

us-09-724-406-10.rag

Fri Jun 29 08:04:16 2001

```

XX PF 28-DEC-1991; 91JP-0359808.
XX PR 28-DEC-1991; 91JP-0359808.
XX PA (KAGA-) ZH KAGAKU KESSEI-RYOHO KENKYUSHO.
XX DR WPI: 1994-187942/23.
XX DR N-PSDB; AAQ65554.
XX PT Mouse-human chimeric anti-HIV antibody heavy and light chains -
XX PT and recombinant antibody consisting of the H- and L-chains,
XX PT useful in AIDS therapy
XX PS Example 3; Fig 4; 22pp; Japanese.
XX CC Murine monoclonal antibodies mu 39.1 and mu 5.5 both neutralise HIV.
XX CC The heavy and light chain variable regions from these antibodies
XX CC were sequenced (AAR55120-R55123). The murine anti-HIV CDRs were
XX CC introduced into human framework regions to construct chimeric
XX CC antibodies (AAR55124-R55127).
XX SQ Sequence 111 AA;

Query Match 98.3%; Score 577; DB 15; Length 111;
Best Local Similarity 97.3%; Pred. No. 1e-40; Indels 0; Gaps 0;
Matches 108; Conservative 2; Mismatches 1;

QY 1 DIVLTQSPASLAVSLGQRATISCKASQSVDFGDSYMNWYQKPGQPPKVLIIYAASNLES 60
Db 1 divltqspaslavslgqratisckasqsvdydgdsymnwyyqkpgppkvllyaaasnlies 60
QY 61 GIPARFSGSGGDTFTLNHPVEEDAATYCCQSNEDPWTFGGKLEIK 111
Db 61 giparfsgsggdtftlnhpveeedaatyccqsgnedpwtfgggtkleik 111

RESULT 2
AAR60302
ID AAR60302 standard; Protein; 111 AA.
AC AAR60302;
XX 09-MAR-1995 (first entry)
XX Anti HIV antibody light chain variable region.
XX Antibody; heavy chain; light chain; human immunodeficiency virus;
XX HIV; acquired immune deficiency syndrome; AIDS; treatment;
XX propylaxis; Mus musculus; Homo sapiens.
XX OS Mus musculus.
XX FH Location/Qualifiers
XX Key 1..23
XX Region /label= Framework region 1.
XX FT 24..38
XX Region /label= CDR1.
XX FT 39..53
XX Region /label= Framework region 2.
XX FT 54..60
XX Region /label= CDR2.
XX FT 61..92
XX Region /label= Framework region 3.
XX FT 93..101
XX Region /label= CDR3.
XX FT 102..111
XX Region /label= Framework region 4.
XX W09415969-A.
XX 21-JUL-1994.
XX PD

XX PF 14-JAN-1993; 93WO-JP00039.
XX PR 14-JAN-1993; 93AU-0032671.
XX PR 14-JAN-1993; 93WO-JP00039.
XX PA (KAGA ) CHEMA SERO THERAPEUTIC RES INST.
XX DR Eda Y, Kimachi K, Maeda H, Osatomi K, Shiosaki K;
XX DR Tokiyoshi S;
XX DR WPI: 1994-249145/30.
XX DR N-PSDB; AAQ70372.
XX PT Recombinant chimeric anti HIV antibody - useful for the treatment
XX PT and prevention of HIV
XX PS Claim 15; Figure 4; 51pp; Japanese.
XX CC The recombinant antibody light chain has neutralising activity
XX CC against HIV. Chimeric antibodies comprising both mouse and human
XX CC sequences are useful in the treatment/prevention of AIDS caused by
XX CC HIV.
XX SQ Sequence 111 AA;

Query Match 98.3%; Score 577; DB 15; Length 111;
Best Local Similarity 97.3%; Pred. No. 1e-40; Indels 0; Gaps 0;
Matches 108; Conservative 2; Mismatches 1;

QY 1 DIVLTQSPASLAVSLGQRATISCKASQSVDFGDSYMNWYQKPGQPPKVLIIYAASNLES 60
Db 1 divltqspaslavslgqratisckasqsvdydgdsymnwyyqkpgppkvllyaaasnlies 60
QY 61 GIPARFSGSGGDTFTLNHPVEEDAATYCCQSNEDPWTFGGKLEIK 111
Db 61 giparfsgsggdtftlnhpveeedaatyccqsgnedpwtfgggtkleik 111

RESULT 3
AAB71895
ID AAB71895 standard; Protein; 113 AA.
AC AAB71895;
XX 09-MAY-2001 (first entry)
XX Monoclonal antibody ST40 light chain.
XX Antibody; ST40; molecular mimetic; CD4; human immunodeficiency virus;
XX HIV; infection.
XX OS Unidentified.
XX PN W0200109191-A1.
XX PD 08-FEB-2001.
XX XX 02-AUG-2000; 2000WO-GB02972.
XX PR 02-AUG-1999; 99EP-0401968.
XX PA (SYNT-) SYNT:EM SA.
XX PI Casset F, Granier C, Kaczorek M, Lahana R, Rees A, Roux F;
XX DR WPI: 2001-168699/17.
XX CC Designing molecular mimetics to mimic a parent molecule activity,
XX CC useful e.g. therapeutically and diagnostically, uses computational
XX CC screening to identify active chemical groups by accessibility within
XX PT the parent molecule
XX PT

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FT Region 74..80
 FT /label= CDR_L2
 FT /note= "claim 9"
 FT 113..121
 FT /label= CDR_L3
 FT /note= "claim 9"
 XX AU9859701-A.
 XX
 XX 08-OCT-1998.
 XX
 XX 30-MAR-1998; 98AU-0059701.
 XX
 XX 08-OCT-1997; 97JP-0276064.
 XX
 XX 01-APR-1997; 97JP-0082953.
 XX
 XX 25-JUN-1997; 97JP-0169088.
 XX
 XX (SANY) SANKYO CO LTD.
 XX
 XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
 XX Masahiko O, Nobufusa S, Shin Y, Tohru T;
 XX
 XX WPI; 1998-543440/47.
 XX
 XX N-PSDB; AA70130.

XX New antibodies and proteins bind conserved epitope of Fas antigen -
 XX used to evaluate drugs in animal models and to treat Fas-associated
 XX diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 XX myocarditis, hepatitis and AIDS
 XX
 XX Reference Example 4; Page 189-190; 292pp; English.

XX This is the amino acid of the light chain of murine anti-human Fas
 XX monoclonal antibody HFE7A. cDNA (see AA70130) encoding the light
 XX chain was obtained from HFE7A-secreting hybridoma (FERM BP-5828)
 XX RNA by RT-PCR (see AA70127-28). The invention provides humanised
 XX HFE7A antibodies (see AA83031-37) produced by CDR grafting. These
 XX antibodies are capable of inducing apoptosis in abnormal cells
 XX expressing Fas, and of inhibiting Fas-induced apoptosis in normal
 XX cells. They are used to evaluate, in animal models, treatments of
 XX diseases that involve Fas/Fas ligand interactions, and also to treat
 XX such diseases, including autoimmune disease (e.g. systemic lupus
 XX erythematosus, Hashimoto's disease, graft versus host disease,
 XX Sjogren syndrome, pernicious anaemia, Addison's disease,
 XX scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid
 XX arthritis, autoimmune haemolytic anaemia, sterility, myasthenia
 XX gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura
 XX and insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
 XX myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
 XX anaemia, hepatitis, AIDS and transplant rejection (all claimed).
 XX
 XX Sequence 238 AA;

Query Match 96.6%; Score 567; DB 19; Length 238;
 Best Local Similarity 97.3%; Pred. No. 1.4e-39;
 Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGQRTATISCKASQSVDFGDSYMNWYQKPGPPKVLIIYAASNLES 60
 Db 21 divltqspaslavslgqratisckasqsvdygdsymnwyyqkpgppklliyaasnles 80
 QY 61 GIPARFSGSGSTDFTLNIHPVEEEDAATYYCQSQNEDPMTFGGKLEIK 111
 Db 81 giparfsgsgstdfnlhphveeedaatyycqsgnedprtfgggtkleik 131

RESULT 6
 AAB14748
 ID AAB14748 standard; Protein; 238 AA.
 XX
 XX AAB14748;
 XX

24-NOV-2000 (first entry)

Mouse anti-Fas antibody HFE7A light chain.

Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
 murine; complementarity determining region; CDR; human Fas;
 Fas ligand; apoptosis modulator; programmed cell death;
 autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
 cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;
 hepatitis; AIDS; graft rejection; light chain.

Mus musculus.

JP2000169393-A.

20-JUN-2000.

30-SEP-1999; 99JP-0278301.

30-SEP-1998; 98JP-0276883.

(SANY) SANKYO CO LTD.

WPI; 2000-485645/43.

N-PSDB; AA72109.

Preventive or treating agent for the diseases caused by an abnormality
 in the Fas/Fas ligand system e.g. autoimmune diseases, contains
 anti-Fas antibody

Example 4; Page 70; 139pp; Japanese.

The invention relates to compositions for the prevention or treatment
 of diseases caused by an abnormality in the Fas/Fas ligand system
 containing an anti-Fas antibody as the active component. The anti-Fas
 antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
 or a humanised version of HFE7A containing identical CDRs
 (complementarity determining regions) to antibody HFE7A. Via its
 interaction with Fas, the antibody of the invention acts as a modulator
 of apoptosis. The composition of the invention may therefore be used in
 the treatment or prevention of conditions such as autoimmune diseases,
 allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
 glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
 and organ graft rejection. The present sequence represents the
 light chain of the murine anti-human Fas monoclonal antibody HFE7A,
 which is produced by hybridoma HFE7A (FERM-BP-5828).

Sequence 238 AA;

Query Match 96.6%; Score 567; DB 21; Length 238;
 Best Local Similarity 97.3%; Pred. No. 1.4e-39;
 Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGQRTATISCKASQSVDFGDSYMNWYQKPGPPKVLIIYAASNLES 60
 Db 21 divltqspaslavslgqratisckasqsvdygdsymnwyyqkpgppklliyaasnles 80
 QY 61 GIPARFSGSGSTDFTLNIHPVEEEDAATYYCQSQNEDPMTFGGKLEIK 111
 Db 81 giparfsgsgstdfnlhphveeedaatyycqsgnedprtfgggtkleik 131

RESULT 7
 AAW90898
 ID AAW90898 standard; Protein; 238 AA.
 XX
 XX AAW90898;
 XX
 XX 08-AUG-2000 (first entry)
 XX Murine anti-Fas antibody HFE7A light chain protein.
 XX

Fas; antibody: murine; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac; dermatological; immunosuppressive; thyromimetic; antihypertensive; nephrotropic; antinfertility; neuroprotective; antihypertensive; antihypertensive; hepatotropic; humanized; systemic lupus erythematosus; HFE7A; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

Mus musculus.

EP990663-A2.

05-APR-2000.

29-SEP-1999; 99EP-0307711.

30-SEP-1998; 98JP-0276881.

30-SEP-1998; 98JP-0276882.

(SANY) SANKYO CO LTD.

Serizawa N, Haryama H, Nakahara K, Tamaki I, Takahashi T;

WPI; 2000-258930/23.

N-PSDB; AA11547.

New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems

Example reference 4; Page 104; 263pp; English.

This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral, immunomodulatory, dermatological, immunosuppressive, thyromimetic, antihypertensive, nephrotropic, antinfertility, neuroprotective, antihypertensive, cardiac and hepatotropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, Sjogren's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a murine anti-Fas monoclonal antibody HFE7A light chain described in the method of the invention.

Sequence 238 AA;

Query Match 96.6%; Score 567; DB 21; Length 238;
Best Local Similarity 97.3%; Pred. No. 1.4e-39;
Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

1 DIVLTQSPASLAVSLGQRATISCKASQSVDFGDSYMNWYQKPGPKVLIYAASNLES 60
|||||

Db 21 divltqspaslavslgqratisckasqsvdydgsymnwqqpgpkvliyaasnl 80
QY 61 GIPARFGSGSGTFTLNHPVEEEDAAATYYCQSNEDPWTFGGTTKLEIK 111
Db 81 giparfsgsgsgtftlnhpveeadaatyyccqsnedprtfgggkgleik 131

RESULT 8

AAR70189
ID AAR70189 standard; Protein; 132 AA.

XX AAR70189;

XX 20-SEP-1995 (first entry)

XX Mouse MAb 3B3 light chain.

XX Chimeric antibody; humanized antibody; antibody engineering;
KW monoclonal antibody; MAB; interleukin-4; IL-4; allergy.
XX Mus sp.

XX Key Location/Qualifiers
FT Peptide 1..20
FT /label= Sig_peptide
FT Region 44..58
FT /label= CDR
FT /note= "complementarity determining region"
FT Region 74..80
FT /label= CDR
FT /note= "complementarity determining region"
FT Region 113..121
FT /label= CDR
FT /note= "complementarity determining region"

XX W09507301-A.

XX 16-MAR-1995.

XX 07-SEP-1994; 94WO-US10308.

XX 07-SEP-1993; 93US-0117366.

XX 14-OCT-1993; 93US-0136783.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Gross MS, Holmes SD, Sylvester DR;

XX WPI; 1995-123387/16.

XX N-PSDB; AAQ83490.

XX Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of IL-4-mediated and IgE-mediated allergic conditions

XX Disclosure; Fig.1; 97pp; English.

XX Spleen cells from mice immunized with human IL-4 were used to prepare hybridomas, which were screened for anti-IL-4 MAb secretion. Only clone 3B9 was positive. cDNA clones of the 3B9 light and heavy chains were cloned into pGEM7f+ and transformed into E. coli DH5-alpha. The clones were sequenced (AAQ83490-91), and used for antibody engineering.

XX Sequence 132 AA;

Query Match 96.4%; Score 566; DB 16; Length 132;
Best Local Similarity 97.3%; Pred. No. 9.6e-40;
Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

1 DIVLTQSPASLAVSLGQRATISCKASQSVDFGDSYMNWYQKPGPKVLIYAASNLES 60

Db 21 divltqspaslavslgqratisckasqsvdygdsgymnwqqkpgppklliyaasnles 80
 QY 61 GIPARFSGSGGTFTLNHPVEEEDAAATYYCQSNEDPWTFGGKLEIK 111
 Db 81 giparfsgsggtftlnhpveeadaatyyccgsnedpftfgggtkleik 131

RESULT 9
 AAY23767
 ID AAY23767 standard; Protein: 132 AA.
 AC AAY23767;
 XX
 XX
 DT 13-SEP-1999 (first entry)
 DE Light chain variable region of murine IL-4 antibody 3B9.
 XX Light chain variable region; interleukin-4; IL-4; antibody 3B9;
 KW chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;
 KW immunoglobulin E-mediated allergic reaction; allergic rhinitis;
 KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
 KW rheumatoid arthritis; host-versus-graft disease; renal disease;
 KW allergy.
 XX
 XX Mus sp.
 OS
 XX US5928904-A.
 PN
 XX 27-JUL-1999.
 XX 07-JUN-1995; 95US-0483632.
 XX 07-JUN-1995; 95US-0483632.
 PR 07-SEP-1993; 93US-0117366.
 PR 14-OCT-1993; 93US-0136783.
 PR 07-SEP-1994; 94WO-US10308.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX Gross MS, Holmes SD, Sylvester DR;
 PI
 XX WPI: 1999-429500/36.
 DR N-PSDB; AAX65884.
 XX
 XX New DNA molecules encoding recombinant antibodies useful for
 treating IL4-mediated conditions
 XX Example 3; Fig 1; 50pp; English.
 PS The present sequence represents the light chain variable region of
 CC murine interleukin-4 (IL-4) antibody 3B9. The sequences are used
 CC in the production chimeric and humanised IL-4 monoclonal antibodies.
 CC The antibodies of the invention are used in therapeutic and
 CC pharmaceutical compositions for treating IL-4 mediated and
 CC immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis,
 CC conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock,
 CC rheumatoid arthritis, host-versus-graft disease and renal disease.
 CC They are also useful in the diagnosis of an allergy or condition
 CC associated with excess IL-4 production through the measurement e.g. by
 CC ELISA of circulating endogenous IL-4 levels in humans.
 XX
 XX Sequence 132 AA;
 SQ

Query Match 96.4%; Score 566; DB 20; Length 132;
 Best Local Similarity 97.3%; Pred. No. 9.6e-40;
 Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGQRATISCKASQSVDFDGSYMNWYQKPGQPPKLLIYAASNLES 60
 Db 21 divltqspaslavslgqratisckasqsvdygdsgymnwqqkpgppklliyaasnles 80

QY 61 GIPARFSGSGGTFTLNHPVEEEDAAATYYCQSNEDPWTFGGKLEIK 111
 Db 81 giparfsgsggtftlnhpveeadaatyyccgsnedpftfgggtkleik 131

RESULT 10
 AAY18120
 ID AAY18120 standard; Protein: 132 AA.
 AC AAY18120;
 XX
 XX
 DT 11-AUG-1999 (first entry)
 DE Light chain sequence for murine 3B9 antibody.
 XX Antibody; interleukin-4; IL4; immunoglobulin E; IgE mediated disease;
 KW allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;
 KW atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;
 KW autoimmune disease; graft versus host disease.
 XX
 OS Mus sp.
 PN US9914110-A.
 XX
 XX 22-JUN-1999.
 XX 07-JUN-1995; 95US-0483636.
 XX 07-JUN-1995; 95US-0483636.
 PR 07-SEP-1993; 93US-0117366.
 PR 14-OCT-1993; 93US-0136783.
 PR 07-SEP-1994; 94WO-US10308.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX Gross MS, Holmes SD, Sylvester DR;
 PI WPI: 1999-370482/31.
 DR N-PSDB; AAX79519.
 XX Recombinant IL4 antibodies
 PT Claim 24; Fig 1; 50pp; English.
 PS This sequence represents the light chain of the murine 3B9
 CC antibody of the invention. The antibody is a chimeric or
 CC humanised interleukin-4 (IL4) monoclonal antibody for the treatment of
 CC immunoglobulin E (IgE) mediated diseases. The antibodies are useful for
 CC the treatment of allergic disorders such as allergic rhinitis,
 CC conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock.
 CC The antibodies are also useful for regulating B and T cell proliferation
 CC and as such are useful in the treatment of autoimmune diseases and graft
 CC versus host disease.
 XX
 XX Sequence 132 AA;
 SQ

Query Match 96.4%; Score 566; DB 20; Length 132;
 Best Local Similarity 97.3%; Pred. No. 9.6e-40;
 Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGQRATISCKASQSVDFDGSYMNWYQKPGQPPKLLIYAASNLES 60
 Db 21 divltqspaslavslgqratisckasqsvdygdsgymnwqqkpgppklliyaasnles 80

QY 61 GIPARFSGSGGTFTLNHPVEEEDAAATYYCQSNEDPWTFGGKLEIK 111
 Db 81 giparfsgsggtftlnhpveeadaatyyccgsnedpftfgggtkleik 131

RESULT 11

AAV59267
ID AAV59267 standard; protein; 111 AA.

AC AAV59267;
DT 17-APR-2000 (first entry)
DE Antibody 4H5 L chain fragment.
KW CD4 antigen; anti-human; antibody; 4H5; drug.
XX Mus sp.

OS JP11332563-A.

PN 07-DEC-1999.

PD 26-MAY-1998; 98JP-0163034.

PF 26-MAY-1998; 98JP-0163034.

PR (ASAH) ASAHI KASEI KOGYO KK.

PA WPI: 2000-091351/08.

XX N-PSDB; AAZ58690.

XX An antibody and the nucleic acid coding the antibody -

XX Disclosure; Page 22-23; 25pp; Japanese.

XX The invention provides an antibody having affinity to CD4 antigen. The

XX anti-human CD4 antibody 4H5 is used for the detection of antigen and

XX application for drugs. It is highly safe in human dose. The present

XX sequence represents a L chain fragment of the antibody 4H5.

XX Sequence 111 AA;

XX Query Match 95.6%; Score 561; DB 21; Length 111;

XX Best Local Similarity 96.4%; Pred. No. 2.1e-39;

XX Matches 107; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

XX QY 1 DIVLTQSPASLAVSLGQRATISCKASQSVDFDGSYMNWYQQKPGPPKVLIIYAASNLES 60

XX Db 1 divltqspaslavslgqratisckasqsvdygdsgymwyqqkpgppklliyaaasnl 60

XX QY 61 GIPARFSGSGGTDFTLNIHPVEEEDAAATYCCQSNEDPWTGGGKLEIK 111

XX Db 61 giparfsgsggtfdtlnihpveeadaatyccqssedpptfgggtkleik 111

XX RESULT 12

XX AAV51144

XX ID AAV51144 standard; Protein; 111 AA.

XX AC AAV51144;

XX DT 31-MAR-2000 (first entry)

XX DE Murine derived protein fragment #6.

XX KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;

XX KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;

XX KW HIV infection; autoimmune disease; murine.

XX OS Mus sp.

XX PN WO9961629-A1.

XX XX 02-DEC-1999.

XX PF 24-MAY-1999; 99WO-JP02711.

XX PI Ono M, Soka T, Morimoto I, Miyamura K;

XX DR WPI: 2000-086720/07.

PR 25-MAY-1998; 98JP-0159957.
PR 26-MAY-1998; 98JP-0163023.
XX (ASAH) ASAHI KASEI KOGYO KK.
PA (ASAH) ASAHI MEDICAL CO LTD.
XX Ono M, Soka T, Morimoto I, Miyamura K;
PI WPI: 2000-086720/07.

XX Devices containing antibodies recognising CD4 or CD34 and their use for
XX the separation of CD4 or CD34 positive cells -
XX Disclosure; Page 95; 111pp; Japanese.

XX This invention describes a novel device (I) for separating cluster
XX differentiation (CD)-positive cells using a recombinant (chimeric or
XX single-chain) antibody recognising CD4 or CD34. The devices are useful
XX for the separation of CD4 or CD34 positive cells, which is useful for
XX the collection of hematopoietic undifferentiated cells, elimination of
XX lymphocytes from cells to be used in bone marrow transplantation, the
XX detection of leukemic cells and the production of medicinal
XX compositions for the treatment of HIV infection and autoimmune diseases.
XX This sequence represents a murine derived protein fragment which is used
XX to illustrate the method of the invention.

XX Sequence 111 AA;

XX Query Match 95.6%; Score 561; DB 21; Length 111;

XX Best Local Similarity 96.4%; Pred. No. 2.1e-39;

XX Matches 107; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

XX QY 1 DIVLTQSPASLAVSLGQRATISCKASQSVDFDGSYMNWYQQKPGPPKVLIIYAASNLES 60

XX Db 1 divltqspaslavslgqratisckasqsvdygdsgymwyqqkpgppklliyaaasnl 60

XX QY 61 GIPARESGSGGTDFTLNIHPVEEEDAAATYCCQSNEDPWTGGGKLEIK 111

XX Db 61 giparfsgsggtfdtlnihpveeadaatyccqssedpptfgggtkleik 111

XX RESULT 13

XX AAY51146

XX ID AAY51146 standard; Protein; 111 AA.

XX AC AAY51146;

XX DT 31-MAR-2000 (first entry)

XX DE Murine derived protein fragment #8.

XX KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;

XX KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;

XX KW HIV infection; autoimmune disease; murine.

XX OS Mus sp.

XX PN WO9961629-A1.

XX XX 02-DEC-1999.

XX PF 24-MAY-1999; 99WO-JP02711.

XX PR 25-MAY-1998; 98JP-0159957.

XX PR 26-MAY-1998; 98JP-0163023.

XX XX (ASAH) ASAHI KASEI KOGYO KK.

XX PA (ASAH) ASAHI MEDICAL CO LTD.

XX PI Ono M, Soka T, Morimoto I, Miyamura K;

XX DR WPI: 2000-086720/07.

DR N-PSDB; AAZ44232.
 XX Devices containing antibodies recognising CD4 or CD34 and their use for
 PT the separation of CD4 or CD34 positive cells -
 PT
 XX PS Disclosure; Page 97-98; 11pp; Japanese.
 XX
 CC This invention describes a novel device (I) for separating cluster
 CC differentiation (CD)-positive cells using a recombinant (chimeric or
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful
 CC for the separation of CD4 or CD34 positive cells, which is useful for
 CC the collection of hematopoietic undifferentiated cells, elimination of
 CC lymphocytes from cells to be used in bone marrow transplantation, the
 CC detection of leukemic cells and the production of medicinal
 CC compositions for the treatment of HIV infection and autoimmune diseases.
 CC This sequence represents a murine derived protein fragment which is used
 CC to illustrate the method of the invention.
 XX
 XX Sequence 111 AA;

Query Match 95.6%; Score 561; DB 21; Length 111;
 Best Local Similarity 96.4%; Pred. No. 2.1e-39;
 Matches 107; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DIVLTQSPASLAVSLGQRATISCKASQSVDFDGSYMNWYQKPGQPPKVLIIYAASNL 60
 Db 1 divltqspaslavslgqratisckasqsvdydgdsymnwyyqkpgppklliyaasnl 60
 QY 61 GIPARFSGSGSTDFTLNIHPVEEEDAATYYCQSQSNEDEPWTFGGTTKLEIK 111
 Db 61 giparfsgsgstdfnlhnpveeedaattyccqssedpptfsgggtkleik 111

RESULT 14
 AAY59264
 ID AAY59264 standard; protein; 305 AA.
 XX
 AC AAY59264;
 XX
 DT 17-APR-2000 (first entry)
 XX
 DE Antibody 4H5 H chain sequence.
 XX
 CC CD4 antigen; anti-human; antibody; 4H5; drug.
 XX
 OS Mus sp.
 XX
 PN JP11332563-A.
 XX
 PD 07-DEC-1999.
 XX
 PF 26-MAY-1998; 98JP-0163034.
 XX
 PR 26-MAY-1998; 98JP-0163034.
 XX
 PA (ASAH) ASAH KASEI KOGYO KK.
 XX
 DR WPI; 2000-091351/08.
 DR N-PSDB; AAZ58663.
 XX
 XX An antibody and the nucleic acid coding the antibody -
 PT
 XX
 XX Disclosure; Page 16-17; 25pp; Japanese.
 XX
 CC The invention provides an antibody having affinity to CD4 antigen. The
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and
 CC application for drugs. It is highly safe in human dose. The present
 CC sequence represents the H chain sequence of the antibody 4H5.
 XX
 XX Sequence 305 AA;

Query Match 95.6%; Score 561; DB 21; Length 305;
 Best Local Similarity 96.4%; Pred. No. 5.7e-39;
 Matches 107; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DIVLTQSPASLAVSLGQRATISCKASQSVDFDGSYMNWYQKPGQPPKVLIIYAASNL 60
 Db 23 divltqspaslavslgqratisckasqsvdydgdsymnwyyqkpgppklliyaasnl 82
 QY 61 GIPARFSGSGSTDFTLNIHPVEEEDAATYYCQSQSNEDEPWTFGGTTKLEIK 111
 Db 83 giparfsgsgstdfnlhnpveeedaattyccqssedpptfsgggtkleik 133
 RESULT 15
 AAY59265
 ID AAY59265 standard; protein; 305 AA.
 XX
 AC AAY59265;
 XX
 DT 17-APR-2000 (first entry)
 XX
 DE Antibody 4H5 L chain sequence.
 XX
 CC CD4 antigen; anti-human; antibody; 4H5; drug.

OS Mus sp.
 XX
 PN JP11332563-A.
 XX
 PD 07-DEC-1999.
 XX
 PF 26-MAY-1998; 98JP-0163034.
 XX
 PR 26-MAY-1998; 98JP-0163034.
 XX
 PA (ASAH) ASAH KASEI KOGYO KK.
 XX
 DR WPI; 2000-091351/08.
 DR N-PSDB; AAZ58664.
 XX
 XX An antibody and the nucleic acid coding the antibody -
 PT
 XX
 XX Disclosure; Page 17-18; 25pp; Japanese.

The invention provides an antibody having affinity to CD4 antigen. The
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and
 CC application for drugs. It is highly safe in human dose. The present
 CC sequence represents the L chain sequence of the antibody 4H5.
 XX
 XX Sequence 305 AA;

Query Match 95.6%; Score 561; DB 21; Length 305;
 Best Local Similarity 96.4%; Pred. No. 5.7e-39;
 Matches 107; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DIVLTQSPASLAVSLGQRATISCKASQSVDFDGSYMNWYQKPGQPPKVLIIYAASNL 60
 Db 156 divltqspaslavslgqratisckasqsvdydgdsymnwyyqkpgppklliyaasnl 215
 QY 61 GIPARFSGSGSTDFTLNIHPVEEEDAATYYCQSQSNEDEPWTFGGTTKLEIK 111
 Db 216 giparfsgsgstdfnlhnpveeedaattyccqssedpptfsgggtkleik 266

Search completed: June 28, 2001, 16:14:35
 Job time: 1323 sec

GenCore version 4.5
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OW protein - protein search, using sw model

Run on: June 28, 2001, 15:58:43 ; Search time 234.85 Seconds
(without alignments)
36.003 Million cell updates/sec

Title: US-09-724-406-10
Perfect score: 587
Sequence: 1 DIVLTQSPASLAVSLGORAT.....CQGSNEDPWTFGGKLEIK 111
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	574	97.8	111	1 KVM569	Ig kappa chain V r
2	571	97.3	111	1 KVM508	Ig kappa chain V r
3	565	96.3	111	1 KVM543	Ig kappa chain V r
4	560	95.4	111	1 KVM583	Ig kappa chain V r
5	550.5	93.8	110	1 KVM510	Ig kappa chain V r
6	550	93.7	112	2 S19971	Ig kappa chain V r
7	550	93.7	131	2 PH1226	Ig kappa chain pre
8	548	93.4	111	1 KVM5C1	Ig kappa chain V r
9	542	92.3	112	2 S19976	Ig kappa chain V r
10	525	89.4	112	2 S19972	Ig kappa chain V r
11	521	88.8	111	2 S09966	Ig kappa chain V r
12	507	86.4	210	2 A56169	Ig kappa chain V-J
13	502	85.5	111	1 KVM584	Ig kappa chain V r
14	501	85.3	131	1 KVM5M6	Ig kappa chain pre
15	499	85.0	111	1 KVM537	Ig kappa chain V r
16	495	84.3	111	1 KVM575	Ig kappa chain V r
17	494	84.2	111	1 KVM540	Ig kappa chain V r
18	490	83.5	111	1 KVM580	Ig kappa chain V r
19	479	81.6	112	2 S45715	Ig kappa chain V r
20	478	81.4	111	2 S09963	Ig kappa chain V r
21	477	81.3	111	2 PL0081	Ig kappa chain V r
22	476	81.1	111	1 KVM585	Ig kappa chain V-J
23	475	80.9	111	2 S09965	Ig kappa chain V r
24	475	80.9	111	2 D45722	Ig kappa chain V-J
25	474	80.7	131	2 S55027	anti-glycoprotein
26	473	80.6	111	2 S09969	Ig light chain pre
27	472	80.4	107	2 S26344	Ig kappa chain V-J
28	471	80.2	109	2 PH0093	Ig kappa chain V r
29	471	80.2	111	1 KVM550	Ig kappa chain V r

ALIGNMENTS

RESULT 1

KVM569
Ig kappa chain V region (PC7769) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
C:Accession: E01937; A01937
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152
A:Accession: E01937
A:Molecule type: protein
C:Residues: 1-111 <WEI>
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match 97.8%; Score 574; DB 1; Length 111;
Best Local Similarity 97.3%; Pred. NO. 3.2e-43;
Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGORATISCKASQSVDFDGSYMNWYQKPGQPKVLIYAASNLES 60
|||||
Db 1 DIVLTQSPASLAVSLGORATISCKASQSVDFDGSYMNWYQKPGQPKVLIYAASNLES 60

QY 61 GIPARESGSGTGDTFTLNHPVEEDAAATYYCQGSNEDPWTFGGKLEIK 111
|||||
Db 61 GIPARESGSGTGDTFTLNHPVEEDAAATYYCQGSNEDPWTFGGKLEIK 111

RESULT 2

KVM508
Ig kappa chain V region (PC6308) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
C:Accession: C01937; A01937
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152
A:Accession: C01937
A:Molecule type: protein
C:Residues: 1-111 <WEI>
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>

F;23-92/Disulfide bonds: #status predicted

Query Match 97.3%; Score 571; DB 1; Length 111;
 Best Local Similarity 96.4%; Pred. No. 5.8e-43;
 Matches 107; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DIVLTQSPASLAVSLGORATISCKASQSDVDGDSYNNWYQKPGQPPKVLIIYAASNL 60
 |||||
 Db 1 DIVLTQSPASLAVSLGORATISCKASQSDVDGDSYNNWYQKPGQPPKVLIIYAASNL 60
 |||||

Qy 61 GIPARFSGSGGTDFTLNHPVEEDAATYYCQSNEDPWTFGGTKLEIK 111
 |||||
 Db 61 GIPARFSGSGGTDFTLNHPVEEDAATYYCQSNEDPWTFGGTKLEIK 111
 |||||

RESULT 3

KVMS43
 Ig kappa chain V region (PC7043) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 21-Jan-2000
 C:Accession: A01937; S42187; S42194; S42190; S42189; S42188; S42191; S42192
 R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
 Nature 276, 785-790, 1978
 A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
 A:Reference number: A93204; MUID:79073152
 A:Accession: A01937
 A:Molecule type: protein
 A:Residues: 1-111 <WEI>
 R:Mo, J.A.; Bona, C.A.; Holmdahl, R.
 Eur. J. Immunol. 23, 2503-2510, 1993
 A:Title: Variable region gene selection of immunoglobulin G-expressing B cells with spec
 A:Reference number: S42176; MUID:94009207
 A:Accession: S42187
 A:Molecule type: DNA
 A:Residues: 10-99 <MO>
 A:Cross-references: EMBL:225444; NID:g407832; PIDN:CAA80931.1; PID:g407833
 A:Note: V-kappa-21E; anti-collagen
 A:Accession: S42194
 A:Molecule type: DNA
 A:Residues: 12-99 <MO>
 A:Cross-references: EMBL:225458; NID:g407844; PIDN:CAA80945.1; PID:g407845
 A:Note: V-kappa-21E; anti-collagen
 A:Accession: S42190
 A:Molecule type: DNA
 A:Residues: 13-99 <MO>
 A:Cross-references: EMBL:225450; NID:g407838; PIDN:CAA80937.1; PID:g407839
 A:Note: V-kappa-21E; anti-collagen
 A:Accession: S42189
 A:Molecule type: DNA
 A:Residues: 15-99 <MO>
 A:Cross-references: EMBL:225448; NID:g407836; PIDN:CAA80935.1; PID:g407837
 A:Note: V-kappa-21E; anti-collagen
 A:Accession: S42188
 A:Molecule type: DNA
 A:Residues: 12-99 <MO>
 A:Cross-references: EMBL:225446; NID:g407834; PIDN:CAA80933.1; PID:g407835
 A:Note: V-kappa-21E; anti-collagen
 A:Accession: S42191
 A:Molecule type: DNA
 A:Residues: 10-99 <MO>
 A:Cross-references: EMBL:225452; NID:g407840; PIDN:CAA80939.1; PID:g407841
 A:Note: V-kappa-21E; anti-collagen
 A:Accession: S42192
 A:Molecule type: DNA
 A:Residues: 10-99 <MO>
 A:Cross-references: EMBL:225454; NID:g407842; PIDN:CAA80941.1; PID:g407843
 A:Note: V-kappa-21E; anti-collagen
 A:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa
 chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F;16-94/Domain: immunoglobulin homology <IMM>

F;23-92/Disulfide bonds: #status predicted

Query Match 96.3%; Score 565; DB 1; Length 111;
 Best Local Similarity 96.4%; Pred. No. 1.9e-42;
 Matches 107; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DIVLTQSPASLAVSLGORATISCKASQSDVDGDSYNNWYQKPGQPPKVLIIYAASNL 60
 |||||
 Db 1 DIVLTQSPASLAVSLGORATISCKASQSDVDGDSYNNWYQKPGQPPKVLIIYAASNL 60
 |||||

Qy 61 GIPARFSGSGGTDFTLNHPVEEDAATYYCQSNEDPWTFGGTKLEIK 111
 |||||
 Db 61 GIPARFSGSGGTDFTLNHPVEEDAATYYCQSNEDPWTFGGTKLEIK 111
 |||||

RESULT 4

KVMS83
 Ig kappa chain V region (PC7183) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
 C:Accession: B01937; A01937
 R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
 Nature 276, 785-790, 1978
 A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
 A:Reference number: A93204; MUID:79073152
 A:Accession: B01937
 A:Molecule type: protein
 A:Residues: 1-111 <WEI>
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k
 chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F;16-94/Domain: immunoglobulin homology <IMM>
 F;23-92/Disulfide bonds: #status predicted

Query Match 95.4%; Score 560; DB 1; Length 111;
 Best Local Similarity 95.5%; Pred. No. 5.2e-42;
 Matches 106; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DIVLTQSPASLAVSLGORATISCKASQSDVDGDSYNNWYQKPGQPPKVLIIYAASNL 60
 |||||
 Db 1 DIVLTQSPASLAVSLGORATISCKASQSDVDGDSYNNWYQKPGQPPKVLIIYAASNL 60
 |||||

Qy 61 GIPARFSGSGGTDFTLNHPVEEDAATYYCQSNEDPWTFGGTKLEIK 111
 |||||
 Db 61 GIPARFSGSGGTDFTLNHPVEEDAATYYCQSNEDPWTFGGTKLEIK 111
 |||||

RESULT 5

KVMS10
 Ig kappa chain V region (PC7210) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
 C:Accession: D01937; A01937
 R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
 Nature 276, 785-790, 1978
 A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
 A:Reference number: A93204; MUID:79073152
 A:Accession: D01937
 A:Molecule type: protein
 A:Residues: 1-110 <WEI>
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k
 chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F;16-94/Domain: immunoglobulin homology <IMM>
 F;23-92/Disulfide bonds: #status predicted

Query Match 93.8%; Score 550.5; DB 1; Length 110;
 Best Local Similarity 94.6%; Pred. No. 3.5e-41;

QY 61 GIPARFSGSGTDFTLNIHPVEEDAATYYCQSNEDPWTFGGKLEIK 111
 |||||
 Db 61 GIPARFSGSGTDFTLNIHPVEEDAATYYCQSIQDPYTFGGGKLEIK 111
 |||||

RESULT 10

S19972
 Ig kappa chain V region (M-T321) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
 C:Accession: S19972
 R:Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.
 submitted to the EMBL Data Library, March 1992
 A:Description: Structural characterization of CD4 mAb.
 A:Reference number: S19963
 A:Accession: S19972
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-112 <WEI>
 A:Cross-references: EMBL:X65094; NID:g52290; PIDN:CAA46222.1; PID:g52291
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 89.4%; Score 525; DB 2; Length 112;
 Best Local Similarity 89.2%; Pred. No. 5.7e-39;
 Matches 99; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYNNWYQKPGQPKVLIYAASNLES 60
 |||||

Db 1 DIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYNNWYQKPGQPKVLIYAASNLES 60
 |||||

QY 61 GIPARFSGSGTDFTLNIHPVEEDAATYYCQSNEDPWTFGGKLEIK 111
 |||||

Db 61 GIPARFSGSGTDFTLNIHPVEEDAATYYCQSNEDPWTFGGKLEIK 111
 |||||

RESULT 11

S09966
 Ig kappa chain V-J region (1E10) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 21-Jan-2000
 C:Accession: S09966
 R:Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
 Eur. J. Immunol. 20, 771-777, 1990
 A:Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodies
 A:Reference number: S09955; MUID:90269328
 A:Accession: S09966
 A:Molecule type: mRNA
 A:Residues: 1-111 <REI>
 A:Cross-references: EMBL:X51854; NID:g55397; PIDN:CAA36147.1; PID:g930231
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 88.8%; Score 521; DB 2; Length 111;
 Best Local Similarity 89.2%; Pred. No. 1.3e-38;
 Matches 99; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYNNWYQKPGQPKVLIYAASNLES 60
 |||||

Db 1 DIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYNNWYQKPGQPKVLIYAASNLES 60
 |||||

QY 61 GIPARFSGSGTDFTLNIHPVEEDAATYYCQSNEDPWTFGGKLEIK 111
 |||||

Db 61 GIPARFSGSGTDFTLNIHPVEEDAATYYCQSNEDPWTFGGKLEIK 111
 |||||

RESULT 12

A56169

Ig kappa chain V region (clone 23.2) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 11-Jan-2000
 C:Accession: A56169
 R:Montardini, C.; Kieber-Emmons, T.; VonFeldt, J.M.; O'Malley, B.; Rosenbaum, H.; God
 J. Biol. Chem. 270, 6628-6638, 1995
 A:Title: Recombinant antibodies in bioactive peptide design.
 A:Reference number: A56169; MUID:95204454
 A:Accession: A56169
 A>Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-210 <NON>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 86.4%; Score 507; DB 2; Length 210;
 Best Local Similarity 86.5%; Pred. No. 3.9e-37;
 Matches 96; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYNNWYQKPGQPKVLIYAASNLES 60
 |||||

Db 1 DIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYNNWYQKPGQPKVLIYAASNLES 60
 |||||

QY 61 GIPARFSGSGTDFTLNIHPVEEDAATYYCQSNEDPWTFGGKLEIK 111
 |||||

Db 61 GIPARFSGSGTDFTLNIHPVEEDAATYYCQSNEDPWTFGGKLEIK 111
 |||||

RESULT 13

KVMS84
 Ig kappa chain V region (PG6684) - mouse (tentative sequence)
 C:Species: Mus musculus (house mouse)
 C:Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 31-Mar-2000
 C:Accession: A01938
 R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
 Nature 276, 785-790, 1978
 A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
 A:Reference number: A93204; MUID:79073152
 A:Accession: A01938
 A:Molecule type: protein
 A:Residues: 1-111 <WEI>
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer
 F:16-94/Domain: immunoglobulin homology <IMM>
 F:23-92/Disulfide bonds: #status predicted

Query Match 85.5%; Score 502; DB 1; Length 111;
 Best Local Similarity 87.4%; Pred. No. 5.6e-37;
 Matches 97; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYNNWYQKPGQPKVLIYAASNLES 60
 |||||

Db 1 DIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYNNWYQKPGQPKVLIYAASNLES 60
 |||||

QY 61 GIPARFSGSGTDFTLNIHPVEEDAATYYCQSNEDPWTFGGKLEIK 111
 |||||

Db 61 GIPARFSGSGTDFTLNIHPVEEDAATYYCQSNEDPWTFGGKLEIK 111
 |||||

RESULT 14

KVMSM6
 Ig kappa chain precursor V regions (M63, AB22, PC9245, PC4050) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 21-Jan-2000
 C:Accession: B90412; B90374; B93822; C93822; C93204; PH1078; A01935
 R:Burstein, Y.; Schechter, I.
 Biochemistry 17, 2392-2400, 1978
 A:Title: Primary structures of N-terminal extra peptide segments linked to the variable expression of immunoglobulin genes.

A:Reference number: A90412; MUID:78235887

A:Contents: M63

A:Accession: B90412

A:Molecule type: protein

A:Residues: 1-35 <BUR>

R:McKean, D.; Potter, M.; Hood, L.

Biochemistry 12, 760-771, 1973

A:Title: Mouse immunoglobulin chains. Pattern of sequence variation among kappa chains

A:Reference number: A90374; MUID:73140225

A:Contents: M63

A:Accession: B90374

A:Molecule type: protein

A:Residues: 21-46, 'Q', '48-53, 'B', '55-57, 'Z', '59-86, 'F', '88-131 <MCK>

A:Note: This sequence has since been revised in reference A93822

R:McKean, D.J.; Bell, M.; Potter, M.

Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978

A:Title: Mechanisms of antibody diversity: multiple genes encode structurally related

A:Reference number: A93822; MUID:79012520

A:Contents: M63; AB22

A:Accession: B93822

A:Molecule type: protein

A:Residues: 1-53, 69-107 <MC2>

A:Accession: C93822

A:Molecule type: protein

A:Residues: 21-119, 'Y', '121-131 <MC3>

R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.

Nature 276, 785-790, 1978

A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.

A:Reference number: A93204; MUID:79073152

A:Contents: PC9245; PC4050

A:Accession: C93204

A:Molecule type: protein

A:Residues: 21-119, 'Y', '121-131 <WEI>

A:Accession: D93204

A:Molecule type: protein

A:Residues: 21-119, 'L', '121-123, 'A', '125-129, 'L', '131 <WE2>

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B

A:Reference number: PH0571; MUID:92381444

A:Accession: PH1078

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 21-122 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1, clone 17p.73

C:Comment: The M63 precursor sequence is shown.

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

tain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status experimental <SIG>

F:21-131/Domain: Ig kappa chain precursor V region #status experimental <MAT>

F:36-114/Domain: immunoglobulin homology <IMM>

F:43-112/Disulfide bonds: #status predicted

Query Match 85.3%; Score 501; DB 1; Length 131;

Best Local Similarity 84.7%; Pred. No. 8.1e-37;

Matches 94; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGORATISCKASQSVDFDGDSTYNNYQKPGQPPKVLIIYAASNL 60

Db 21 NIVLTQSPASLAVSLGORATISCKASQSVDFDGDSTYNNYQKPGQPPKVLIIYAASNL 80

QY 61 GIPARFSGSGSGTDFLTINHPVEEEDAAATYYCOQSNEDPWTGGGKLEIK 111

Db 81 GVPARFSGSGSGTDFLTIDPVEADDAATYYCOQNNEDPWTGGGKLEIK 131

RESULT 15

KVMS37

Ig kappa chain V regions (PC3741, T111) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 21-Jan-2000

C:Accession: A93204; A93822; A01934

R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.

Nature 276, 785-790, 1978

A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.

A:Reference number: A93204; MUID:79073152

A:Contents: PC3741

A:Accession: A93204

A:Molecule type: protein

A:Residues: 1-111 <WEI>

R:McKean, D.J.; Bell, M.; Potter, M.

Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978

A:Title: Mechanisms of antibody diversity: multiple genes encode structurally related

A:Reference number: A93822; MUID:79012520

A:Contents: T111

A:Accession: A93822

A:Molecule type: protein

A:Residues: 1-111 <MCK>

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (

tain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer

F:16-94/Domain: immunoglobulin homology <IMM>

F:23-92/Disulfide bonds: #status predicted

Query Match 85.0%; Score 499; DB 1; Length 111;

Best Local Similarity 85.6%; Pred. No. 1e-36;

Matches 95; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGORATISCKASQSVDFDGDSTYNNYQKPGQPPKVLIIYAASNL 60

Db 1 DIVLTQSPASLAVSLGORATISCKASQSVDFDGDSTYNNYQKPGQPPKVLIIYAASNL 60

QY 61 GIPARFSGSGSGTDFLTINHPVEEEDAAATYYCOQSNEDPWTGGGKLEIK 111

Db 61 GIPARFSGSGSGTDFLTINHPVEEEDAAATYYCOQSNEDPWTGGGKLEIK 111

Search completed: June 28, 2001, 15:58:43

Job time: 371 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 28, 2001, 16:08:20 ; Search time 411.58 Seconds
(without alignments)
35.682 Million cell updates/sec

Title: US-09-724-406-10
Perfect score: 587
Sequence: 1 DIVLQSPASLAVSLGORAT.....COQSNEDPWTFGGTKLEIK 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_16:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_procent:*
12: sp_unclassified:*
13: sp_vertebrate:*
14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	457	77.9	103	11 Q9JL80	Q9JL80 mus musculus
2	393	67.0	108	4 Q9UL77	Q9UL77 homo sapien
3	377.5	64.3	109	4 Q9UL78	Q9UL78 homo sapien
4	374	63.7	108	4 Q9UL70	Q9UL70 homo sapien
5	366	62.4	114	4 Q9UL90	Q9UL90 homo sapien
6	361	61.5	108	4 Q9UL79	Q9UL79 homo sapien
7	360.5	61.4	107	4 Q9UL81	Q9UL81 homo sapien
8	357	60.8	108	4 Q9UL83	Q9UL83 homo sapien
9	353.5	60.2	109	4 Q9UL85	Q9UL85 homo sapien
10	349	59.5	214	11 Q9JL85	Q9JL85 mus musculus
11	340.5	58.0	104	11 Q9JL82	Q9JL82 mus musculus
12	339.5	57.8	109	4 Q9UL86	Q9UL86 homo sapien
13	335	57.1	107	11 Q9ER29	Q9ER29 mus musculus
14	333.5	56.8	106	5 Q9U410	Q9U410 schistosoma
15	329	56.0	97	11 Q9JL76	Q9JL76 mus musculus
16	325	55.4	107	11 Q9JL84	Q9JL84 mus musculus
17	323	55.0	298	11 Q9QYF0	Q9QYF0 mus musculus
18	320	54.5	99	11 Q9JL74	Q9JL74 mus musculus
19	319	54.3	101	11 Q9JL78	Q9JL78 mus musculus

20	293	49.9	109	6 Q9NOW5	Q9NOW5 oryctolagus
21	235.5	40.1	107	4 Q9NSD6	Q9NSD6 homo sapien
22	233	39.7	107	4 Q9UL82	Q9UL82 homo sapien
23	204	34.8	130	4 Q9NF29	Q9NF29 homo sapien
24	172.5	29.4	109	11 Q9ET13	Q9ET13 mus musculus
25	150	25.6	135	4 Q9H524	Q9H524 homo sapien
26	133	22.7	123	11 Q61243	Q61243 mus musculus
27	129	22.0	93	4 Q9UL76	Q9UL76 homo sapien
28	115.5	19.7	337	13 Q9IB02	Q9IB02 spherooides
29	107	18.2	142	13 Q9HQ2	Q9HQ2 ginglymosto
30	106.5	18.1	122	4 Q99603	Q99603 homo sapien
31	106.5	18.1	122	4 Q99604	Q99604 homo sapien
32	106.5	18.1	137	4 Q9UDR1	Q9UDR1 homo sapien
33	106	18.1	136	13 Q9YHR9	Q9YHR9 ginglymosto
34	105	17.9	100	6 Q77624	Q77624 bos taurus
35	105	17.9	136	13 Q9YHP4	Q9YHP4 ginglymosto
36	103.5	17.6	334	13 Q9IB05	Q9IB05 spherooides
37	103	17.5	118	4 Q9UL91	Q9UL91 homo sapien
38	102.5	17.5	228	11 Q70153	Q70153 rattus norv
39	101.5	17.3	509	11 Q08907	Q08907 mus musculus
40	101	17.2	288	4 Q00517	Q00517 homo sapien
41	100	17.0	136	13 Q9YHP2	Q9YHP2 ginglymosto
42	100	17.0	145	4 Q9H022	Q9H022 homo sapien
43	100	17.0	504	4 Q9UIJ6	Q9UIJ6 homo sapien
44	99.5	17.0	503	4 P78324	P78324 homo sapien
45	99	16.9	137	13 Q9YHQ0	Q9YHQ0 ginglymosto

ALIGNMENTS

RESULT 1

Q9JL80 ID Q9JL80 PRELIMINARY; PRT; 103 AA.

AC Q9JL80;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-acetyl-glucosamine antibodies from mice with autoimmune myocarditis."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF206026; AAF69324.1; -
DR InterPro; IPR003006; -
DR InterPro; IPR003596; -
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 103
SQ SEQUENCE 103 AA; 11224 MW; EC87D653DB3AAB21 CRC64;

Query Match 77.9%; Score 457; DB 11; Length 103;
Best Local Similarity 81.6%; Pred. No. 1.2e-42;
Matches 84; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

QY 9 ASLAVSLGGRATISCKASQVDFDGDGSDYNNVYQKPGOPPKVLLIYAASNLESGTPARFSG 68

Db 1 ASLAVSLGGRATISCKASQVDFDGDGSDYNNVYQKPGOPPKVLLIYAASNLESGTPARFSG 60

QY 69 SGSGDTFTLNHPVEEDAAATYCOQSNEDPWTFGGTKLEIK 111

Db 61 SGSGDTFTLNHPVEEDAAATYCOQSNEDPWTFGGTKLEIK 103

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RESULT 2
Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035037; AAD56273.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 67.0%; Score 393; DB 4; Length 108;
Best Local Similarity 65.8%; Pred. No. 1.3e-35;
Matches 73; Conservative 17; Mismatches 17; Indels 4; Gaps 1;

QY 1 DIVLTQSPASLAVSLGORATISCKASQSDVDGDSYMNWYQKPKVLIYAASNL 60
DB 1 DIQMTQSPSLASVSGDRVTITCRASQSI----SSYLWYQKPKGAPNLLIYAAS 56
QY 61 GIPARFSGSGSGTDFLTNIHPVEEEDAAATYYCQSNEDPWTFGGKLEIK 111
DB 57 GVPFRSGSGSGTDFLTITSLQLPEDVATYYCQSYSTSWTFGGTKVEIK 107

RESULT 3
Q9UL78 PRELIMINARY; PRT; 109 AA.
AC Q9UL78;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035036; AAD56272.1; -.
DR HSP; P01789; IMCP.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; Ig; 1.

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DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;

Query Match 64.3%; Score 377.5; DB 4; Length 109;
Best Local Similarity 65.8%; Pred. No. 6.4e-34;
Matches 73; Conservative 14; Mismatches 21; Indels 3; Gaps 1;

QY 1 DIVLTQSPASLAVSLGORATISCKASQSDVDGDSYMNWYQKPKVLIYAASNL 60
DB 1 EIVLTQSPFTLSLSPGERATLSCRASQSV---SSYLWYQKPKGAPRLLIYGAS 57
QY 61 GIPARFSGSGSGTDFLTNIHPVEEEDAAATYYCQSNEDPWTFGGKLEIK 111
DB 58 GIPRFRSGSGSGTDFLTITSLRLEPDCAVYYCQYGGSSPLTFGGTKVEIK 108

RESULT 4
Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035044; AAD56280.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 63.7%; Score 374; DB 4; Length 108;
Best Local Similarity 64.0%; Pred. No. 1.5e-33;
Matches 71; Conservative 16; Mismatches 20; Indels 4; Gaps 1;

QY 1 DIVLTQSPASLAVSLGORATISCKASQSDVDGDSYMNWYQKPKVLIYAASNL 60
DB 1 DIQMTQSPSLASVSGDRVTITCRASQGI----SNYLWYQKPKGKPKSLIYAAS 56
QY 61 GIPARFSGSGSGTDFLTNIHPVEEEDAAATYYCQSNEDPWTFGGKLEIK 111
DB 57 GVPFRSGSGSGTDFLTITSLQLPEDVATYYCQKYNAPRTFGPGTKLEIK 107

RESULT 5
Q9UL80 PRELIMINARY; PRT; 114 AA.
AC Q9UL80;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).

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OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 DR EMBL; AF035034; AAD56270.1; -.
 DR InterPro; IPR003006; -.
 DR InterPro; IPR003596; -.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 FT NON_TER 1
 FT NON_TER 114 114
 SQ SEQUENCE 114 AA; 12775 MW; 070E31E210D1CB01 CRC64;
 Query Match 62.4%; Score 366; DB 4; Length 114;
 Best Local Similarity 62.8%; Pred. No. 1.2e-32;
 Matches 71; Conservative 15; Mismatches 25; Indels 2; Gaps 2;
 QY 1 DIVLTQSPASLAVSLGORATISCKASQSVDFDGSYNNWYQKQPKVLIYAASNL 59
 Db 1 DVVMTQSPSLPVTLPQASISCRSSQSPVSDGNTYLNWFQRPQSPRLIYKVSNRD 60
 QY 60 SGIPARFSGSGGTDFTLNHPVEEDAATYYCQSQSNE-DPWTFGGGKLEIK 111
 Db 61 SGVPDRFSGSGGTDFTLNISRVEDGVYICMGTGTHWPPWTFGGGKVEIK 113
 RESULT 6
 QYUL79 PRELIMINARY; PRT; 108 AA.
 ID Q9UL79;
 AC Q9UL79;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 DR EMBL; AF035035; AAD56271.1; -.
 DR HSP; P01607; IREF.
 DR InterPro; IPR003006; -.
 DR InterPro; IPR003596; -.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 FT NON_TER 1
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 61.5%; Score 361; DB 4; Length 108;
 Best Local Similarity 63.1%; Pred. No. 4e-32;
 Matches 70; Conservative 15; Mismatches 22; Indels 4; Gaps 1;

QY 1 DIVLTQSPASLAVSLGORATISCKASQSVDFDGSYNNWYQKQPKVLIYAASNL 60
 Db 1 DIVMTQSPSLLSASTGDRVTISCRMSQSI-----SSYLAWYQKQKRAPELLIYAASLTQS 56
 QY 61 GIPARFSGSGGTDFTLNHPVEEDAATYYCQSQSNE-DPWTFGGGKLEIK 111
 Db 57 GVPFRSGSGGTDFTLTITISLQSEDFATYYCQYYSPFPFGGQKVEIK 107
 RESULT 7
 QYUL81 PRELIMINARY; PRT; 107 AA.
 ID Q9UL81;
 AC Q9UL81;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 DR EMBL; AF035033; AAD56269.1; -.
 DR HSP; P80362; IWT.
 DR InterPro; IPR003006; -.
 DR InterPro; IPR003596; -.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 FT NON_TER 1
 FT NON_TER 107 107
 SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;
 Query Match 61.4%; Score 360.5; DB 4; Length 107;
 Best Local Similarity 62.2%; Pred. No. 4.5e-32;
 Matches 69; Conservative 20; Mismatches 17; Indels 5; Gaps 2;
 QY 1 DIVLTQSPASLAVSLGORATISCKASQSVDFDGSYNNWYQKQPKVLIYAASNL 60
 Db 1 DIQMTQSPSLASVGDRTITCRASQSI-----SNLWYQKQKRAPELLIYAASLTQS 56
 QY 61 GIPARFSGSGGTDFTLNHPVEEDAATYYCQSQSNE-DPWTFGGGKLEIK 111
 Db 57 GVPFRSGSGGTDFTLTITISLQSEDFATYYCQYS-YSALTFGPGTKVDIR 106
 RESULT 8
 QYUL83 PRELIMINARY; PRT; 108 AA.
 ID Q9UL83;
 AC Q9UL83;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RA Young D.C.;

QY 61 GIPARFSGSGTDFTLNIHPVEEDAATYYCQSNE-DPWTFGGGKLEIK 111
||||| ||||| ||||| | :: || |:||| | - |||||::|||
Dd 57 GIPARFSGSGTEFTITSSLOEDFAIYHCQOYNWPPLTFGGGKVEIK 108

RA Strickland, B. S., Liao L., Cunningham M.W., Diamond B.:
 "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
 acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
 RT Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AF206024; AAF69322.1; -
 DR EMBL: AF206024; AAF69322.1; -
 DR InterPro: IPR003006; -
 DR InterPro: IPR003596; -
 DR Pfam: PF000047; iq: 1.
 DR SMART: SM00406; IGV: 1.
 DR NON_TER 1
 FT NON_TER 104 104
 FT NON_TER 104 AA; 5DA8BBFD5F0AA1AE CRC64;
 SQ SEQUENCE 104 AA; 5DA8BBFD5F0AA1AE CRC64;


```
Query Match          58.0%; Score 340.5; DB 11; Length 104;
Best Local Similarity 64.1%; Pred. No. 6.7e-30;
Matches 66; Conservative 14; Mismatches 22; Indels 1; Gaps 1;

Qy 10 SLAVSLGORATISCKASQSVDFDGSYMNWYQKPGQPKVLIYAASNIESGIPARFSG 68
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 2 SLPVSLGQASISCRSSQSLVHTNGYLIHWYLOKQSPKLLIKYVNSRFGVDPDFSG 61

Qy 69 SGGTDTFLNIHPVEEDAATYCCQSNEDPWFEGGKLEIK 111
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 62 SGGTDTFLKISRVEAEDLGVFCQTHVPYTFGGGKLEIK 104

RESULT 12
Q9UL86 PRELIMINARY; PRT; 109 AA.
AC Q9UL86;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035028; AAD56264.1; -.
DR HSP; P01789; IMCP.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF000047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1 109
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7DAC83 CRC64;

Query Match          57.8%; Score 339.5; DB 4; Length 109;
Best Local Similarity 60.4%; Pred. No. 9.1e-30;
Matches 67; Conservative 16; Mismatches 25; Indels 3; Gaps 1;

Qy 1 DIVLTQSPASLAVSLGORATISCKASQSVDFDGSYMNWYQKPGQPKVLIYAASNLES 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EIVLTQSPGTLSPFGERATLSCRASQSV---SSSYLAWYQKPGQAPRLIYGTSSRAT 57

Qy 61 GIPARFSGSGGTDTFLNIHPVEEDAATYCCQSNEDPWFEGGKLEIK 111
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 58 GIPDRFSGSGGTDTFLTISRLEPEDFAVYCCQYSGSIPTFGPGTKVDIK 108

RESULT 13
Q9ER29 PRELIMINARY; PRT; 107 AA.
ID Q9ER29
AC Q9ER29;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE ANTI HUMAN TNF-ALPHA LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
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Query Match          57.1%; Score 335; DB 11; Length 107;
Best Local Similarity 59.8%; Pred. No. 2.8e-29;
Matches 64; Conservative 17; Mismatches 24; Indels 2; Gaps 1;

Qy 4 LTQSPASLAVSLGORATISCKASQSVDFDGSYMNWYQKPGQPKVLIYAASNLES 61
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MTQSPSSLAMSVGQKVTNSCKSSQSVLNSNTQKNYLANQKPGQSPPELLYVFASTRESG 60

Qy 62 IPARFSGSGGTDTFLNIHPVEEDAATYCCQSNEDPWFEGGKTL 108
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 VPDREFSGSGGTDTFLTISVQVTELDVFCQGHYRTPFTFGSGTKL 107

RESULT 14
Q9U410 PRELIMINARY; PRT; 106 AA.
ID Q9U410
AC Q9U410;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE MONOCLONAL ANTI-IDIOTYPIC ANTIBODY NP30 IMMUNOGLOBULIN LIGHT CHAIN
DE VARIABLE REGION (FRAGMENT).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
OC Trematoda; Digenea; Strigeida; Schistosomatidae; Schistosomatae;
OC Schistosoma.
OX NCBI_TaxID=6182;

Query Match          56.8%; Score 333.5; DB 5; Length 106;
Best Local Similarity 58.7%; Pred. No. 4e-29;
Matches 64; Conservative 16; Mismatches 24; Indels 5; Gaps 1;

Qy 1 DIVLTQSPASLAVSLGORATISCKASQSVDFDGSYMNWYQKPGQPKVLIYAASNLES 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EIVLTQSPGTLSPFGERATLSCRASQSV---SSSYLAWYQKPGQAPRLIYGTSSRAT 57

Qy 61 GIPARFSGSGGTDTFLNIHPVEEDAATYCCQSNEDPWFEGGKLEIK 111
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 58 GIPDRFSGSGGTDTFLTISRLEPEDFAVYCCQYSGSIPTFGPGTKVDIK 108

RESULT 13
Q9ER29 PRELIMINARY; PRT; 107 AA.
ID Q9ER29
AC Q9ER29;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE ANTI HUMAN TNF-ALPHA LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
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Search completed: June 28, 2001, 16:08:20
Job time: 948 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 28, 2001, 16:01:13 ; Search time 138.34 Seconds
(without alignments)
16.163 Million cell updates/sec

Title: US-09-724-406-10
Sequence: 1 DIVLTQSPASLAVSLQRAT.....CQSNEDPWTFGGKLEIK 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 2014635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PTCUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	572	97.4	111	1	US-08-491-845-8
2	571	97.3	131	4	US-08-579-378A-14
3	566	96.4	132	2	US-08-483-636-2
4	566	96.4	132	2	US-08-483-632-2
5	536	91.3	106	3	US-08-466-151-6
6	528	89.9	120	1	US-08-111-080-24
7	528	89.9	120	1	US-08-211-980-24
8	528	89.9	120	5	PCT-US93-07967-24
9	526	89.6	111	3	US-08-466-151-2
10	520	88.6	111	2	US-08-887-352B-5
11	520	88.6	111	4	US-09-109-207C-5
12	500	85.2	131	1	US-08-137-117D-25
13	500	85.2	131	2	US-08-436-717-25
14	498	84.8	131	2	US-08-483-636-58
15	498	84.8	131	2	US-08-483-632-58
16	492	83.8	131	2	US-08-483-636-14
17	492	83.8	131	2	US-08-483-632-14
18	490	83.5	111	1	US-07-634-278-54
19	490	83.5	111	1	US-08-477-728-54
20	490	83.5	111	1	US-08-474-040-54
21	490	83.5	111	1	US-08-487-200-54
22	490	83.5	111	4	US-08-484-537-54
23	490	83.5	131	1	US-07-634-278-67
24	490	83.5	131	1	US-08-477-728-67
25	490	83.5	131	1	US-08-474-040-67
26	490	83.5	131	1	US-08-487-200-67
27	490	83.5	131	4	US-08-484-537-67

28 484 82.5 131 2 US-08-521-751A-10 Sequence 10, Appl
29 484 82.5 239 2 US-08-553-497A-18 Sequence 18, Appl
30 481 81.9 131 4 US-08-579-378A-18 Sequence 18, Appl
31 481 81.9 218 5 PCT-US96-13152-2 Sequence 2, Appl
32 480 81.8 131 3 US-08-836-561-25 Sequence 25, Appl
33 479 81.6 131 1 US-08-137-117D-33 Sequence 33, Appl
34 479 81.6 131 2 US-08-436-717-33 Sequence 33, Appl
35 479 81.6 218 5 PCT-US94-14106-57 Sequence 33, Appl
36 478 81.4 111 1 US-08-275-053-11 Sequence 57, Appl
37 478 81.4 112 3 US-09-065-059-13 Sequence 11, Appl
38 478 81.4 121 1 US-08-111-080-22 Sequence 22, Appl
39 478 81.4 121 1 US-08-211-980-22 Sequence 22, Appl
40 478 81.4 121 5 PCT-US93-07967-22 Sequence 22, Appl
41 477.5 81.3 110 1 US-08-017-570-2 Sequence 22, Appl
42 477.5 81.3 110 1 US-08-471-426-2 Sequence 2, Appl
43 477.5 81.3 110 5 PCT-US94-01709-2 Sequence 2, Appl
44 477 81.3 111 1 US-08-491-845-16 Sequence 16, Appl
45 477 81.3 115 4 US-08-513-968-51 Sequence 51, Appl

ALIGNMENTS

RESULT 1
US-08-491-845-8
; Sequence 8, Application US/08491845
; Patent No. 5773247
; GENERAL INFORMATION:
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: EGA, Yasuyuki
; APPLICANT: SEIOSAKI, Kouichi
; APPLICANT: OSATOMI, Kiyoshi
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: RECOMBINANT ANTI-HIV ANTIBODY AND
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/491,845
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00039
; FILING DATE: 14-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: MAEDA-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-491-845-8

Query Match 97.4%; Score 572; DB 1; Length 111;

RESULT 4
US-08-483-632-2

Sequence 2, Application US/08483632
Patent No. 5928904
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
TREATMENT OF IL4 Mediated Disorders
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESSEE: Intellectual Property
STREET: P.O. Box 1539 / UM2220
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,632
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-632-2

Query Match 96.4%; Score 566; DB 2; Length 132;
Best Local Similarity 97.3%; Pred. No. 8.8e-54;
Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 DIVLTQSPASLAVSLGORATISCKASQSVDFDGSYNNWYQKQPKVLIYAASNLES 60
Db 21 DIVLTQSPASLAVSLGORATISCKASQSVDFDGSYNNWYQKQPKVLIYAASNLES 80
QY 61 GIPARFSGSGCTDFTLNHPVEEEDAATYYCQSQNEDPWTFFGGTKLEIK 111
Db 81 GIPARFSGSGCTDFTLNHPVEEEDAATYYCQSQNEDPWTFFGGTKLEIK 131
RESULT 5
US-08-466-151-6
Sequence 6, Application US/08466151
Patent No. 6037453
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65

CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,151
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/466163
FILING DATE: 06-Jun-1995
APPLICATION NUMBER: 08/405617
FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/185899
FILING DATE: 26-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/879495
FILING DATE: 07-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/744768
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P0718P2C1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-466-151-6

Query Match 91.3%; Score 536; DB 3; Length 106;
Best Local Similarity 95.3%; Pred. No. 1.1e-50;
Matches 101; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 DIVLTQSPASLAVSLGORATISCKASQSVDFDGSYNNWYQKQPKVLIYAASNLES 60
Db 1 DIVLTQSPASLAVSLGORATISCKASQSVDFDGSYNNWYQKQPKVLIYAASNLES 60
QY 61 GIPARFSGSGCTDFTLNHPVEEEDAATYYCQSQNEDPWTFFGGT 106
Db 61 GIPARFSGSGCTDFTLNHPVEEEDAATYYCQSQNEDPWTFFGGT 106
RESULT 6
US-08-111-080-24
Sequence 24, Application 08/111080
Patent No. 5558865
GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
TITLE OF INVENTION: HIV Immunotherapeutics
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA

```

ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/111,080
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/748,562
FILING DATE: 22-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07111
FILING DATE: 24-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,457
FILING DATE: 22-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 31629
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-111-080-24

Query Match      89.9%; Score 528; DB 1; Length 120;
Best Local Similarity 91.8%; Pred. No. 9.5e-50;
Matches 101; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY    1 DIVLTQSPASLAVSLGORATISKASGVDFDGDSDVMNMYQQKPGOPPKVLIYAASNLES 60
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DBB   1 DVLVTQSPASLAVSLGORATISKASGVDFDGDSDVMNMYQQKPGOPPKVLIYAASNVES 60
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QY    61 GIPARFSGSGGTDTFLNIHPVEEDAATYYCQDSNEDPWTFGGGTKLEI 110
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DBB   61 GIPARFYGSGGTDTFTNIHPVEEDAATYYCQSIDDPSTFGGGTKLEI 110
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RESULT 7
US-08-211-980-24
Sequence 24, Application US/08211980
Patent No. 5665569
GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
TITLE OF INVENTION: HIV Immunotherapeutics
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
City: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,980
FILING DATE:

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Query Match	88.6%	Score 520;	DB 2;	Length 111;
Best Local Similarity	90.1%;	Pred. No. 6.2e-49;		
Matches 100;	Conservative	5;	Mismatches 6;	Indels
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Ddb	1	DIVLTQSPASLAVSLGORATISCKASQSYDYDGDSTVMNMYQOKPGOPPKVLIYAA		
QY	61	GIPIAFSGSGSGTDTLTNIHPVEEEDAATYVCOOSNEDPTWTCGGTKLEIK	111	
Ddb	61	GIPIAFSGSGSGTDTLTNIHPVEEEDAATFYCQSHEDPTFTGAGTKLEIK	111	
RESULT	11			

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;
; TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: (202)672-5300
;
; TELEFAX: (202)672-5399
;
; TELEX: 904136
;
; INFORMATION FOR SEQ ID NO: 25:
;
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 131 amino acids
;
; TYPE: amino acid
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; TOPOLOGY: linear
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; MOLECULE TYPE: protein
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; US-08-137-117D-25
;
;
; Query Match 85.2%; Score 500; DB 1; Length 131;
; Best Local Similarity 85.6%; Pred.No. 11e-46;
; Matches 95; Conservative 7; Mismatches 9; Indels 0; Gaps
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; QY 1 DIVLTQSPASLAVSLGQRATISCKASQSVDFDGSYNNWYQKPGQPPKVLIIYAASNLES 60
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; Db 21 DIVLTQSPASLGVSLGQRATISCRASKSVSTSGSYMHWYQKPGQTPKLLIYLAASNLES 80
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; QY 61 GTPARPSGSGSTDTFLNIHPVEEDAATYYCQSNEDPTWTFGGGKLEIK 111
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; Db 81 GTPARPSGSGSTDTFLNIHPVEEDAATYYCQHSRENPTYFGGGKLEIK 131
;
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; RESULT 13
;
; US-08-436-717-25
;
; Sequence 25, Application US/08436717
;
; Patent No. 5817790
;
; GENERAL INFORMATION:
;
; APPLICANT: TSUCHIYA, Masayuki
;
; APPLICANT: SATO, Koh
;
; APPLICANT: BENDIG, Mary
;
; APPLICANT: JONES, Steven
;
; APPLICANT: SALDANHA, Jose
;
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
;
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
;
; NUMBER OF SEQUENCES: 158
;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: Foley & Lardner
;
; STREET: 3000 K Street, N.W., Suite 500
;
; CITY: Washington
;
; STATE: D.C.
;
; COUNTRY: USA
;
; ZIP: 20007-5109
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/08/436,717
;
; FILING DATE:
;
; CLASSIFICATION: 536
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: US/08/137,117
;
; FILING DATE: 20-DEC-1993
;
; APPLICATION NUMBER: WO PCT/JP92/00544
;
; FILING DATE: 24-APR-1992
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: JP 4-32084
;
; FILING DATE: 19-FEB-1992
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: JP 3-95476
;
; FILING DATE: 25-APR-1991
;
; ATTORNEY/AGENT INFORMATION:
;
; NAME: WEGNER, Harold C.
;
; REGISTRATION NUMBER: 25,258
;
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
;
; TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: (202)672-5300
;
; TELEFAX: (202)672-5399
;
;

```


TELEX: 904136
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-436-717-25

Query Match 85.2%; Score 500; DB 2; Length 131;
Best Local Similarity 85.6%; Pred. No. 1.1e-46;
Matches 95; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGORATISCKASQSVDFDGSYNNWYQOKPGQPPKVLIIYAASNL 60
Db 21 DIVLTQSPASLAVSLGORATISCKASQSVDFDGSYNNWYQOKPGQPPKVLIIYAASNL 80
QY 61 GIPARFSGSGTDFTLNIHPVEEEDAAATYYCQSNEDPMTFGGKLEIK 111
Db 81 GVPARFSGSGTDFTLNIHPVEEEDAAATYYCQHSRENPTFGGKLEIK 131

RESULT 14
US-08-483-636-58
; Sequence 58, Application US/08483636
; Patent No. 5914110
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,636
; FILING DATE:
; CLASSIFICATION: 424.
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-483-636-58

Query Match 84.8%; Score 498; DB 2; Length 131;
Best Local Similarity 83.8%; Pred. No. 1.8e-46;
Matches 93; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGORATISCKASQSVDFDGSYNNWYQOKPGQPPKVLIIYAASNL 60
Db 20 DIVMTQSPDLSAVSLGERATINCKASQSVDFDGSYNNWYQOKPGQPPKVLIIYAASNL 79
QY 61 GIPARFSGSGTDFTLNIHPVEEEDAAATYYCQSNEDPMTFGGKLEIK 111
Db 80 GVPDRFSGSGTDFTLTISSLAQEDVAVYYCQSNEDPPTFGGKVEIK 130

RESULT 15
US-08-483-632-58
; Sequence 58, Application US/08483632
; Patent No. 5928904
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,632
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-483-632-58

Query Match 84.8%; Score 498; DB 2; Length 131;
Best Local Similarity 83.8%; Pred. No. 1.8e-46;
Matches 93; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIVLTQSPASLAVSLGORATISKASQSVDFDGDSDSYNNWYQQKPGQPPKVLIIYAASNLES 60
Db 20 DIVMTQSPDLSLAVSLGERATINCKASQSVDFDGDSDSYNNWYQQKPGQPPKLLIIYAASNLES 79
Qy 61 GIPARFSGSGTDFTLNIHPVEEEDAATYYCQGSNEDPWTFGGKLEIK 111
Db 80 GVPDRFSGSGTDFTLTISSLAEDVAVYYCQGSNEDPPTFGGKVEIK 130

Search completed: June 28, 2001, 16:01:13
Job time: 521 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2001, 15:54:35 ; Search time 105.36 Seconds
(without alignments)
36.089 Million cell updates/sec

Title: US-09-724-406-10

Perfect score: 587

Sequence: 1 DIVLTQSPASLAVSLGQRAT.....COQSNEDPWTFGGKLEIK 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	574	97.8	111	1	KV3Q_MOUSE
2	571	97.3	111	1	KV3Q_MOUSE
3	565	96.3	111	1	KV3M_MOUSE
4	560	95.4	111	1	KV3N_MOUSE
5	550.5	93.8	110	1	KV3P_MOUSE
6	548	93.4	111	1	KV3L_MOUSE
7	502	85.5	111	1	KV3R_MOUSE
8	501	85.3	131	1	KV3I_MOUSE
9	499	85.0	111	1	KV3H_MOUSE
10	495	84.3	111	1	KV3S_MOUSE
11	494	84.2	111	1	KV3T_MOUSE
12	493	84.0	111	1	KV3C_MOUSE
13	492	83.8	111	1	KV3J_MOUSE
14	490	83.5	111	1	KV3A_MOUSE
15	480	81.8	111	1	KV3K_MOUSE
16	476	81.1	111	1	KV3U_MOUSE
17	472.5	80.5	112	1	KV3B_MOUSE
18	471	80.2	111	1	KV3D_MOUSE
19	469	79.9	132	1	KV3F_MOUSE
20	468	79.7	112	1	KV3G_MOUSE
21	454	77.3	108	1	KV3V_MOUSE
22	442	75.3	111	1	KV3E_MOUSE
23	406	69.2	134	1	KV4C_HUMAN
24	398	67.8	114	1	KV4A_HUMAN
25	391.5	66.7	133	1	KV4B_HUMAN
26	386	65.8	108	1	KV5P_MOUSE
27	375.5	64.0	133	1	KV2F_HUMAN
28	374.5	63.8	129	1	KV3M_HUMAN
29	374	63.7	129	1	KV1W_HUMAN
30	372	63.4	108	1	KV1B_HUMAN
31	372	63.4	108	1	KV1E_HUMAN
32	371.5	63.3	129	1	KV3H_HUMAN
33	371	63.2	108	1	KV1H_HUMAN

34	371	63.2	108	1	KV1M_HUMAN	P01605	homo sapien
35	371	63.2	108	1	KV1V_HUMAN	P03362	homo sapien
36	365.5	62.3	129	1	KV3L_HUMAN	P18135	homo sapien
37	363	61.8	108	1	KV1K_HUMAN	P01603	homo sapien
38	363	61.8	108	1	KV1N_HUMAN	P01606	homo sapien
39	362.5	61.8	113	1	KV2G_MOUSE	P01631	mus musculus
40	362	61.7	108	1	KV1P_HUMAN	P01608	homo sapien
41	361.5	61.6	107	1	KV6A_MOUSE	P01675	mus musculus
42	361.5	61.6	109	1	KV3B_HUMAN	P01620	homo sapien
43	361.5	61.6	109	1	KV3D_HUMAN	P01622	homo sapien
44	358	61.0	108	1	KV1O_HUMAN	P01607	homo sapien
45	358	61.0	108	1	KV1R_HUMAN	P01610	homo sapien

ALIGNMENTS

RESULT 1				
KV3Q_MOUSE				
ID	KV3Q_MOUSE	STANDARD;	PRT;	111 AA.
AC	P01669;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	IG KAPPA CHAIN V-III REGION PC 7769.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE=79073152; PubMed=103003;			
RA	Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;			
RT	"Rearrangement of genetic information may produce immunoglobulin			
RT	diversity."			
RL	Nature 276:785-790(1978).			
DR	PIR: E01937: KVM569			
DR	InterPro: IPR003006; -			
DR	Pfam: PF00047; Ig; 1.			
KW	Immunoglobulin V region.			
FT	DOMAIN	23		FRAMEWORK 1.
FT	DOMAIN	24	38	COMPLEMENTARITY-DETERMINING 1.
FT	DOMAIN	39	53	FRAMEWORK 2.
FT	DOMAIN	54	60	COMPLEMENTARITY-DETERMINING 2.
FT	DOMAIN	61	92	FRAMEWORK 3.
FT	DOMAIN	93	101	COMPLEMENTARITY-DETERMINING 3.
FT	DOMAIN	102	111	FRAMEWORK 4.
FT	DISULFID	23	92	BY SIMILARITY.
FT	NON_TER	111		
SQ	SEQUENCE	111 AA;	12011 MW;	6FAA345279356829 CRC64;

Query Match 97.8%; Score 574; DB 1; Length 111;
Best Local Similarity 97.3%; Pred. No. 2.3e-51;
Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY	1	DIVLTQSPASLAVSLGQRATISCKASQSDYDGDSDYNNYQKPGQPKVLIYAASNL	60
DB	1	DIVLTQSPASLAVSLGQRATISCKASQSDYDGDSDYNNYQKPGQPKVLIYAASNL	60
QY	61	GIPARFSGSGGTDFTLNIHPVEEDAAATYYCOQSNEDPWTFGGKLEIK 111	
DB	61	GIPARFSGSGGTDFTLNIHPVEEDAAATYYCOQSNEDPWTFGGKLEIK 111	

RESULT 2			
KV3O_MOUSE			
ID	KV3O_MOUSE	STANDARD;	PRT; 111 AA.
AC	P01667;		
DT	21-JUL-1986 (Rel. 01, Created)		
DT	21-JUL-1986 (Rel. 01, Last sequence update)		
DT	15-JUL-1999 (Rel. 38, Last annotation update)		
DE	IG KAPPA CHAIN V-III REGION PC 6308.		

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RA MEDLINE=79073152; PubMed=103003;
RX Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
DR PIR; C01937; KVM508.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12071 MW; 7A4ADE4D6C256D29 CRC64;

Query Match 97.3%; Score 571; DB 1; Length 111;
Best Local Similarity 96.4%; Pred. No. 4.7e-51;
Matches 107; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DIVLTQSPASLAVSLGORATISCKASQSVDFGDSYMNWYQKPGQPKVLIYAASNLES 60
Db 1 DIVLTQSPASLAVSLGORATISCKASQSVDFGDSYMNWYQKPGQPKVLIYAASNLES 60

Qy 61 GIPARFSGSGGTDTFLNIHPVEEEDAATYYCQSNEDPWTFGGKLEIK 111
Db 61 GIPARFSGSGGTDTFLNIHPVEEEDAATYYCQSNEDPWTFGGKLEIK 111

RESULT 3
KV3M_MOUSE
ID KV3M_MOUSE STANDARD; PRT; 111 AA.
AC P01665;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 7043.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RA MEDLINE=79073152; PubMed=103003;
RX Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
DR PIR; A01937; KVM543.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12002 MW; 7A5FCB586C306D29 CRC64;

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Query Match 96.3%; Score 565; DB 1; Length 111;
Best Local Similarity 96.4%; Pred. No. 1.9e-50;
Matches 107; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DIVLTQSPASLAVSLGORATISCKASQSVDFGDSYMNWYQKPGQPKVLIYAASNLES 60
Db 1 DIVLTQSPASLAVSLGORATISCKASQSVDFGDSYMNWYQKPGQPKVLIYAASNLES 60

Qy 61 GIPARFSGSGGTDTFLNIHPVEEEDAATYYCQSNEDPWTFGGKLEIK 111
Db 61 GIPARFSGSGGTDTFLNIHPVEEEDAATYYCQSNEDPWTFGGKLEIK 111

RESULT 4
KV3N_MOUSE
ID KV3N_MOUSE STANDARD; PRT; 111 AA.
AC P01666;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 7183.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RA MEDLINE=79073152; PubMed=103003;
RX Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
DR PIR; B01937; KVM583.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11952 MW; 2058BB50CE306D31 CRC64;

Query Match 95.4%; Score 560; DB 1; Length 111;
Best Local Similarity 95.5%; Pred. No. 6.1e-50;
Matches 106; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DIVLTQSPASLAVSLGORATISCKASQSVDFGDSYMNWYQKPGQPKVLIYAASNLES 60
Db 1 DIVLTQSPASLAVSLGORATISCKASQSVDFGDSYMNWYQKPGQPKVLIYAASNLES 60

Qy 61 GIPARFSGSGGTDTFLNIHPVEEEDAATYYCQSNEDPWTFGGKLEIK 111
Db 61 GIPARFSGSGGTDTFLNIHPVEEEDAATYYCQSNEDPWTFGGKLEIK 111

RESULT 5
KV3P_MOUSE
ID KV3P_MOUSE STANDARD; PRT; 110 AA.
AC P01668;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 7210.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1] NCBI_TaxID=10090;
 RP SEQUENCE.
 RX MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 diversity.";
 RL Nature 276:785-790(1978).
 DR PIR: D01937; KWS10.
 DR InterPro; IPR003006; -.
 DR Pfam; PF00047; Ig; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 100
 FT DOMAIN 101 110
 FT DISULFID 23 92
 FT NON_TER 110 110
 SQ SEQUENCE 110 AA; 11950 MW; 69F1A5CE886B1249 CRC64;

Query Match 93.8%; Score 550.5; DB 1; Length 110;
 Best Local Similarity 94.68; Pred. No. 5.5e-49;
 Matches 105; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 1 DIVLTQSPASLAVSLGORATISCKASQSVDFDGSYNNWYQKQPPKVLIIYAASNL 60
 DB 1 DIVLTQSPASLAVSLGORATISCKASQSLDYDGSYNNWYQKQPPKVLIIYAASNL 60
 QY 61 GIPARFSGSGTDTLNIHPVEEDAATYCCQSNEDPWTFGGKLEIK 111
 DB 61 GIPARFSGSGTDTLNIHPVEEDAATYCHOS-EDPWTFGSGTKLEIK 110

RESULT 6
 KV3L_MOUSE
 ID KV3L_MOUSE STANDARD; PRT; 111 AA.
 AC P01664;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION CBPC 101.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1] NCBI_TaxID=10090;
 RP SEQUENCE.
 RX MEDLINE=79012520; PubMed=99744;
 RA McKean D.J., Bell M., Potter M.;
 RT "Mechanisms of antibody diversity: multiple genes encode structurally
 related mouse kappa variable regions.";
 RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
 CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
 DR PIR: A01936; KWSCL.
 DR InterPro; IPR003006; -.
 DR Pfam; PF00047; Ig; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT DOMAIN 102 111
 FT DISULFID 23 92
 FT NON_TER 111 111
 SQ SEQUENCE 111 AA; 11964 MW; E2B1AD98AD965962 CRC64;

Query Match 93.4%; Score 548; DB 1; Length 111;
 Best Local Similarity 93.7%; Pred. No. 9.9e-49;
 Matches 104; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 1 DIVLTQSPASLAVSLGORATISCKASQSVDFDGSYNNWYQKQPPKVLIIYAASNL 60
 DB 1 DIVLTQSPASLAVSLGORATISCKASQVDYTGESYNNWYQNPQSPKLLIYAASNL 60
 QY 61 GIPARFSGSGTDTLNIHPVEEDAATYCCQSNEDPWTFGGKLEIK 111
 DB 61 GIPARFSGSGTDTLNIHPVEEDAATYCCQSNEDPWTFGGKLEIK 111

RESULT 7
 KV3R_MOUSE
 ID KV3R_MOUSE STANDARD; PRT; 111 AA.
 AC P01670;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION PC 6684.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1] NCBI_TaxID=10090;
 RP SEQUENCE.

RX MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 diversity.";
 RL Nature 276:785-790(1978).
 DR PIR: A01938; KWS84.
 DR InterPro; IPR003006; -.
 DR Pfam; PF00047; Ig; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT DOMAIN 102 111
 FT DISULFID 23 92
 FT NON_TER 111 111
 SQ SEQUENCE 111 AA; 12039 MW; 1E46988341858526 CRC64;

Query Match 85.5%; Score 502; DB 1; Length 111;
 Best Local Similarity 87.4%; Pred. No. 4.3e-44;
 Matches 97; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGORATISCKASQSVDFDGSYNNWYQKQPPKVLIIYAASNL 60
 DB 1 DIVLTQSPASLAVSLGORATISCKASQSVTSYSHWYQKQPPKLLIYASNL 60
 QY 61 GIPARFSGSGTDTLNIHPVEEDAATYCCQSNEDPWTFGGKLEIK 111
 DB 61 GVPARFSGSGTDTLNIHPVEEDAATYCHOSRELPTFGGKLEIK 111

RESULT 8
 KV3L_MOUSE
 ID KV3L_MOUSE STANDARD; PRT; 131 AA.
 AC P01661;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION MOPC 63 PRECURSOR.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 1-35.
RX MEDLINE=78235887; PubMed=98179;
RA Burstein Y., Schechter I.;
RT "Primary structures of N-terminal extra peptide segments linked to
RT the variable and constant regions of immunoglobulin light chain
RT precursors: implications on the organization and controlled
RT expression of immunoglobulin genes.";
RL Biochemistry 17:2392-2400(1978).
RN [2]
RP SEQUENCE OF 21-131.
RX MEDLINE=73140225; PubMed=4691517;
RA McKean D.J., Potter M., Hood L.E.;
RT "Mouse immunoglobulin chains. Pattern of sequence variation among
RT kappa chains with limited sequence differences.";
RL Biochemistry 12:760-771(1973).
RN [3]
RP REVISIONS.
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
DR PIR; A01935; KVM5M6.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 131 IG KAPPA CHAIN V-III REGION MOPC 63.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 59 73 FRAMEWORK 2.
FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 81 112 FRAMEWORK 3.
FT DOMAIN 113 121 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 122 131 FRAMEWORK 4.
FT DISULFID 43 112 BY SIMILARITY.
FT NON_TER 131 131
SQ SEQUENCE 131 AA; 14291 MW; D212EC9F08DC880A CRC64;

Query Match 85.38; Score 501; DB 1; Length 131;
Best Local Similarity 84.78; Pred. No. 6.6e-44;
Matches 94; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGQRATISCKASQSDVDFGDSYMNWYQKPGQPKVLIVAAASNL 60
DB 21 NLVLTQSPASLAVSLGQRATISCKASQSDVSGNSFMHWYQKPGQPKVLIVAAASNL 80
QY 61 GIPARFSGSGGTDFTLNHPVEEEDAATYCCQSNEDPWTFGGKLEIK 111
DB 81 GVPARFSGSGSRDFTLTIDPVEADDAATYCCQNNEDPWTFGGKLEIK 131

RESULT 9
KV3H_MOUSE STANDARD; PRT; 111 AA.
AC P01660;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 3741/TEPC 111.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (PC 3741).
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR PIR; B01938; KVM575.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 61 92 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 93 101 FRAMEWORK 3.
FT DOMAIN 102 111 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12010 MW; F041E89AA7858523 CRC64;

```

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RL Nature 276:785-790(1978).
RN [2]
RP SEQUENCE (TEPC 111).
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
CC 1- MISCELLANEOUS; THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL.
DR PIR; A01934; KVM537.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
KW Immunoglobulin V region..
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12099 MW; EC46C9D259213BE4 CRC64;

Query Match 85.0%; Score 499; DB 1; Length 111;
Best Local Similarity 85.6%; Pred. No. 8.7e-44;
Matches 95; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGQRATISCKASQSDVDFGDSYMNWYQKPGQPKVLIVAAASNL 60
DB 1 DIVLTQSPASLAVSLGQRATISCKASQSDVSGNSFMHWYQKPGQPKVLIVAAASNL 60
QY 61 GIPARFSGSGGTDFTLNHPVEEEDAATYCCQSNEDPWTFGGKLEIK 111
DB 61 GIPARFSGSGSRDFTLTINPVEADDAATYCCQSNEDPWTFGGKLEIK 111

RESULT 10
KV3S_MOUSE STANDARD; PRT; 111 AA.
ID KV3S_MOUSE
AC P01671;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 7175.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR PIR; B01938; KVM575.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12010 MW; F041E89AA7858523 CRC64;

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FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 102 111 FRAMEWORK 4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12041 MW; D7DF0609303453CE CRC64;

Query Match 83.8%; Score 492; DB 1; Length 111;
Best Local Similarity 83.8%; Pred. No. 4.4e-43;
Matches 93; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGQRATISCKASQSVDFDGSYNNWYQKPGQPKVLIYAASNLES 60
Db 1 NIVLTQSPASLAVSLGQRATISCKASQSVDFDGSYNNWYQKPGQPKVLIYAASNLES 60

QY 61 GIPARFSGSGGTDTFLNIHPVEEEDAAATYYCQSNEDPWTFFGGTKLEIK 111
Db 61 GVPARFSGSGRTDFTLTIDPVEADDAATYYCQNNEDPYTFGGGKLEIK 111

RESULT 14
KV3A_MOUSE STANDARD; PRT; 111 AA.
ID P01654;
AC P01654;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 2880/PC 1229.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
CC -!- MISCELLANEOUS: THE PC 2880 AND PC 1229 SEQUENCES ARE IDENTICAL.
DR PIR: A01930; KVM580.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 39 53 FRAMEWORK 2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 61 92 FRAMEWORK 3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 102 111 FRAMEWORK 4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11980 MW; AFEAC6A9D26FC12D CRC64;

Query Match 83.5%; Score 490; DB 1; Length 111;
Best Local Similarity 82.9%; Pred. No. 7.1e-43;
Matches 92; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGQRATISCKASQSVDFDGSYNNWYQKPGQPKVLIYAASNLES 60
Db 1 DIVLTQSPASLAVSLGQRATISCKASQSVDFDGSYNNWYQKPGQPKVLIYAASNLES 60

QY 61 GIPARFSGSGGTDTFLNIHPVEEEDAAATYYCQSNEDPWTFFGGTKLEIK 111
Db 61 GVPARFSGSGRTDFTLTIDPVEADDAATYYCQNNEDPYTFGGGKLEIK 111

RESULT 15
KV3K_MOUSE STANDARD; PRT; 111 AA.
ID P01663;
AC P01663;
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DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 4050.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
CC PIR: A01935; KVM56.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 39 53 FRAMEWORK 2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 61 92 FRAMEWORK 3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 102 111 FRAMEWORK 4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12005 MW; 39D87619313453CB CRC64;

Query Match 81.8%; Score 480; DB 1; Length 111;
Best Local Similarity 82.0%; Pred. No. 7.2e-42;
Matches 91; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

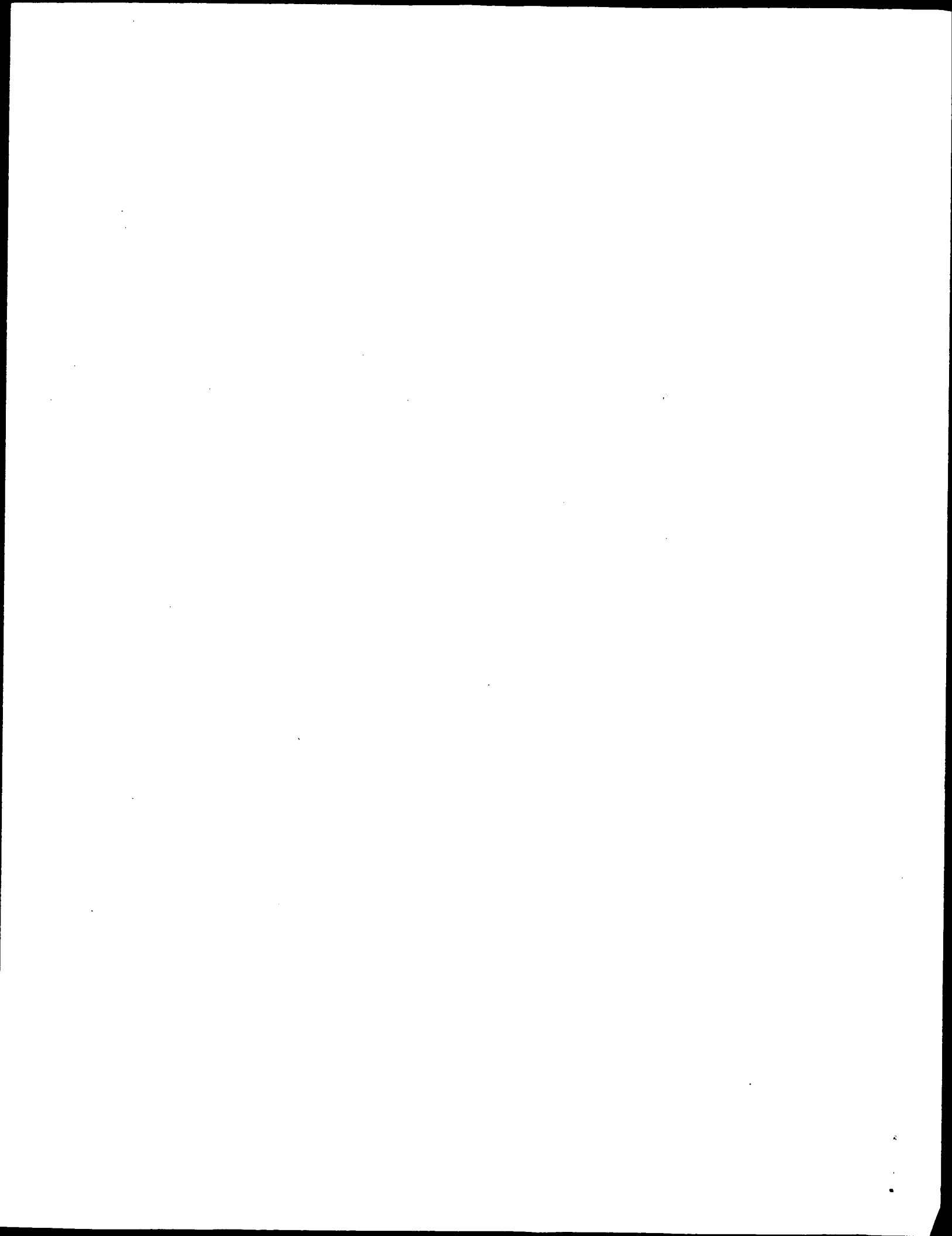
QY 1 DIVLTQSPASLAVSLGQRATISCKASQSVDFDGSYNNWYQKPGQPKVLIYAASNLES 60
Db 1 NIVLTQSPASLAVSLGQRATISCKASQSVDFDGSYNNWYQKPGQPKVLIYAASNLES 60

QY 61 GIPARFSGSGGTDTFLNIHPVEEEDAAATYYCQSNEDPWTFFGGTKLEIK 111
Db 61 GVPARFSGSGRTDFTLTIDPVEADDAATYYCQNNEDPYTFGGGKLEIK 111

Search completed: June 28, 2001, 15:54:35
Job time: 123 sec.
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us-09-724-406-10.rsp

• Fri Jun 29 08:04:19 2001



GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2001, 15:28:27 ; Search time 19 Seconds
(without alignments)
352.005 Million cell updates/sec

Title: US-09-724-406-2
Perfect score: 635
Sequence: 1 QIQIQSGPEVVKPGASVKI.....NYGNWFAYWGQGTQVTVSA 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_0401.*
1: /SID56/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID56/gcgdata/geneseq/geneseq/AA1981.DAT.*
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22: /SID56/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	543.5	85.6	139	18 W29750	Anti-HMFG MAB CTMO
2	539.5	85.0	138	21 W56873	MAB CT-M-01 heavy
3	537.5	84.6	139	14 R33950	CTMO1 VH. Synthet
4	521.5	82.1	469	14 R40384	Monoclonal antibod
5	501.5	79.0	116	16 R79241	Heavy chain variab
6	497.5	78.3	122	18 W01577	Lead binding MAB 1
7	496	78.1	249	9 P80154	Biosynthetic antib
8	495	78.0	123	21 W78325	Anti-zeta-chain an
9	495	78.0	532	21 W78328	Bispecific anti-ze
10	494	77.8	119	18 W01585	Lead binding MAB 1
11	494	77.8	121	18 W07437	Anti-DNA antibody

12	490	77.2	119	19 W49814	Amino acid sequenc
13	490	77.2	138	14 R32666	Mouse C4G1 Ig heav
14	490	77.2	138	19 W49810	Variable region of
15	488.5	76.9	118	18 W27359	Heavy chain variab
16	487.5	76.8	116	17 W03742	Murine monoclonal
17	486	76.5	117	17 R88716	Mouse antibody hea
18	485.5	76.5	116	21 B10443	Murine monoclonal
19	485	76.4	136	8 P70624	Sequence encoded b
20	485	76.4	136	18 W10584	Anti-hepatitis B h
21	485	76.4	136	18 W16340	Mouse-human chimae
22	485	75.4	136	18 W10239	Chimeric anti-hepa
23	485	75.4	136	19 W47510	Human anti-hepatit
24	485	75.4	136	19 W41054	Human anti-hepatit
25	485	75.4	136	19 W47517	Human anti-hepatit
26	485	75.4	136	20 W89535	Chimeric anti-hepa
27	484.5	76.3	118	16 R79159	Human IgE receptor
28	484.5	76.3	118	18 W27356	Heavy chain variab
29	484.5	76.3	382	18 W26651	Chimeric receptor
30	484.5	76.3	403	18 W26648	Chimeric receptor
31	484.5	76.3	473	18 W26646	Chimeric receptor
32	484.5	76.3	514	18 W26647	Chimeric receptor
33	484.5	76.3	651	18 W26647	Chimeric receptor
34	484.5	76.3	692	18 W26650	Chimeric receptor
35	484	76.2	555	22 B19871	Activating polypep
36	484	76.2	565	22 B19873	Activating polypep
37	484	76.2	577	22 B19872	Activating polypep
38	484	76.2	704	22 B19888	MLV envelope glyco
39	483.5	76.1	139	15 R53328	KM-796 heavy chain
40	483.5	76.1	139	20 Y28384	Anti-GM2 heavy cha
41	483.5	76.1	139	20 Y28356	Antibody chain use
42	483	76.1	117	9 P80148	Biosynthetic antib
43	481.5	75.8	120	12 R13721	Control fusion pro
44	480.5	75.7	118	13 R22420	Murine heavy chain
45	480.5	75.7	118	15 R54757	Mouse HMFG1 heavy

ALIGNMENTS

RESULT 1
ID W29750 standard; Protein; 139 AA.
XX
AC W29750:
XX
DT 14-JAN-1998 (first entry)
XX
DE Anti-HMFG MAB CTMO1 heavy chain variable region.
XX
DE Humanised antibody; CDR-grafted antibody; chimeric antibody; CTMO1;
KW complementarity determining region; human milk fat globule; HMFG;
KW monoclonal antibody; MAB; mouse; cancer; breast cancer;
XX ovary carcinoma; lung cancer; uterus cancer; diagnosis; therapy.
XX Mus musculus.
XX
XX Key Location/Qualifiers
FT Peptide I..19
FT Misc-difference 344 /label= Leader_peptide
FT Misc-difference 344 /note= "encoded by ACG"
XX
XX EP781845-A2.
XX
XX 02-JUL-1997.
XX
XX 24-SEP-1992; 92EP-0308680.
XX
XX 26-SEP-1991; 91GB-0020467.
XX
XX (CLLT) CELLTech THERAPEUTICS LTD.
XX
XX Adair JR, Baker TS, Hamann PR, Hinman LM, Lyons AH;

Qy	1	QIOLQSGPEWVPGASVKISCKASGYTDDYIIHWAKPKQGLIEWIGWYIPGSGNTKY	60
Db	20	QIQIQQSGPEIIVPGASVKISCKASGYTDDYIYINMKQKPGGLIEWIGWIDPGSGNTKY	79
Qy	61	NEKPKGKATLTVDTSSTAPMQLSSLTSEDYAYFCA--NYGNYFA--YWGQGTQVTVS	116
Db	80	NEKfkgkatltvdtsststaymqiLssltsedvayfcaeketkytyamdywgqgtsvts	138

RESULT 3
R33950
IN p33950 standard: Protein: 139 AA.

R33950;
16-JUL-1993 (first entry)
CTMO1 VH.

Heavy; light; chain; variable; domain; CTMO1; PCR; primer; carcinoma; immunoglobulin; murine; monoclonal; antibody; MAB; IgG-kappa; ovary; humanized; diagnosis; therapy; breast; uterus; lung.

X	Synthetic.
S	
X	Key
H	Location/Qualifiers
X	Peptide
T	1..19
T	/note= "Signal peptide"
T	20..139
T	/note= "Mature protein"
X	
X	EP534742-A.
N	
N	
X	31-MAR-1993.
XD	
XX	24-SEP-1992; 92EP-0308680.
FF	
XX	26-SEP-1991; 91GB-0020467.
PR	
XX	(CLLT) CELLTECH LTD.
XA	
XX	Adair JR, Baker TS, Hamann PR, Hinman LM, Lyons AH;
P	Menendez AT, Owens RJ;
IPI	
XX	WPI: 1993-102837/13.
DR	N-PSDB: Q38877.
OR	
XX	
PT	Anti-human milk fat globule humanised antibodies - useful as
PT	conjugate for in-vivo diagnosis and therapy of e.g. ovarian or
PT	breast cancer
XX	
PS	Disclosure: page 17-18; 57pp; English.

XX The sequences given in R33950-51 represent the heavy and light chain
 CC variable domains of CTMO1 respectively. The DNA encoding these
 CC peptides was isolated by PCR using the primer sequences given in
 CC Q38879-80. Examination of these amino acid sequences revealed
 CC considerable homology with other characterised immunoglobulin genes.
 CC The murine monoclonal antibody (WAB), CTMO1, was confirmed to be an
 CC IGG-kappa antibody. CTMO1 was used in the production of a humanised
 CC antibody for in vivo diagnosis and therapy of carcinomas of ovary,
 CC breast, uterus and lung.
 XX Sequence 139 AA;

Query Match 84.6%; Score 537.5; DB 14; Length 139;
 Best Local Similarity 86.7%; Pred. No. 1.7e-36;
 Matches 104; Conservative 5; Mismatches 8; Indels 3; Gaps 2;

QY 1 QIQLOQSGPEVVKPGASVKISKASGYFTDYITWVKQKPGQGLEWIGWYPGSGNTKY 60
 DB 20 QIQLOQSGPELVKPGASVKISKASGYFTDYINWVKQKPGQGLEWIGWIDPQSGNTKY 79
 QY 61 NEKFKGKATLTVDTSSTAFMQSLTSDTAVYFCANYGNYWFA--YWGQGTQVTVSA 117
 DB 80 NEKFKGKATLTVDTSSTAFMQSLTSDTAVYFCAREKTYTYYVAMDYWGQGTSTVSA 139

RESULT 4

R40384
 ID R40384 standard; Protein: 469 AA.

AC R40384;

DT 08-FEB-1994 (first entry)

XX Monoclonal antibody M(alpha)2-3 Heavy-chain.

KW anti-snake small neurotoxin antibody; heavy chain; IgG2;
 KW immunoglobulin; bispecific bivalent antibody; cell-targetting;
 KW cytotoxic agent.

FH Key Location/Qualifiers
 FT Peptide 1..19
 FT Region /label= signal_peptide
 FT Region 20..139
 FT Region /label= variable
 FT Region 140..236
 FT Region /label= constant
 FT Region 237..252
 FT Region /label= joining
 FT Region 253..362
 FT Region /label= constant
 FT Region 363..469
 FT Region /label= constant

XX EP556111-A.

XX 18-AUG-1993.

XX 09-FEB-1993; 93EP-0400323.

XX 11-FEB-1992; 92FR-0001505.

XX (BOUL/) BOULAIN J.

XX (CONS) COMMISSARIAT ENERGIE ATOMIQUE.

XX Boulain J, Ducancel F, Gillet D, Menez A;

XX WPI; 1993-260351/33.

XX N-PSDB; Q48037.

XX New immunoglobulin hybrid proteins - with immunoglobulin
 PT fragments linked to dimeric protein, for diagnosis or

PT therapeutic use

XX Example 1; Fig 3A; 37pp; French.

XX A fragment of the heavy chain (VH + CH1) from the anti-snake small
 CC neurotoxin monoclonal antibody M(alpha)2-3 was PCR-amplified from
 CC hybridoma-derived cDNA using primers Q48039 and Q48040. A light
 CC chain' fragment (VL + CL) was amplified from the same source using
 CC primers Q48041 and Q48042. The two amplified fragments were
 CC inserted into the same vector; the H-chain fragment was inserted
 CC (in-frame) between codons 6-7 of the phoA coding sequence and the
 CC L-chain fragment was inserted into a cassette which contained a
 CC phoA S-D sequence, a signal peptide and the first 6 codons of phoA.
 CC The cassette was positioned between the termination codon and
 CC the transcription termination sequence of phoA. The fusion
 CC construct is expected to encode a hybrid protein comprising two
 CC identical Ab-derived units. The invention also covers hybrid
 CC proteins containing two different Ab-derived units (i.e. to produce
 CC bispecific antibodies). When a toxic protein is used in place of
 CC phoA, the hybrid molecules can be used as cell-targetting
 CC therapeutic agents.

XX Sequence 469 AA;

Query Match 82.1%; Score 521.5; DB 14; Length 469;
 Best Local Similarity 83.3%; Pred. No. 1.3e-36;

Matches 100; Conservative 5; Mismatches 12; Indels 3; Gaps 1;

QY 1 QIQLOQSGPEVVKPGASVKISKASGYFTDYITWVKQKPGQGLEWIGWYPGSGNTKY 60
 DB 20 QIQLOQSGPELVKPGASVKISKASGYFTDYINWVKQKPGQGLEWIGWIDPQSGNTKY 79

QY 61 NEKFKGKATLTVDTSSTAFMQSLTSDTAVYFCANYGNYWFA--YWGQGTQVTVSA 117
 DB 80 NEKFKGKATLTVDTSSTAFMQSLTSDTAVYFCAREKTYTYYVAMDYWGQGTSTVSA 139

RESULT 5

R79241
 ID R79241 standard; Protein: 116 AA.

AC R79241;

DT 21-DEC-1995 (first entry)

XX Heavy chain variable region for monoclonal antibody 4A10.

XX Monoclonal antibody; heavy metal; mercury; variable region;
 XX heavy chain.

XX Synthetic.

XX WO9520607-A.

XX 03-AUG-1995.

XX 27-JAN-1995; 95WO-US01199.

XX 27-JAN-1994; 94US-0187407.

XX (BION-) BIONEERASKA INC.

XX Lopez O, Wagner FW, Wylie DE;

XX WPI; 1995-275415/36.

XX N-PSDB; Q97498.

XX New polypeptide(s) which bind heavy metals, esp. mercury - derived from
 PT monoclonal antibodies, used for detecting, removing, adding or
 PT neutralising heavy metals

XX Claim 13; Page 54; 106pp; English.

Sequence 116 AA:

Query Match	78.3%	Score 497.5;	DB 18;	Length 122;
Best Local Similarity	77.0%;	Pred. No. 3.5e-35;		
Matches	94:	Conservative	9:	Mismatches 14:
				Indels 5:
				Gaps

RESULT	7
P80154	
ID	P80154 standard; protein; 249 AA.
XX	
AC	P80154;
XX	
DT	01-JAN-1980 (first entry)

XX	Biosynthetic antibody binding site.
DE	
XX	
KW	Biosynthetic antibody binding site; framework region; assay; imaging; multifunctional protein.
KW	

W08809344-A.

01-DEC-1988

19-MAY-1988: 88WO-IIS01737

21-MAY-1987: 87US-0052800

(CREA-) CREATIVE BIOMOLECULES, INC.

Huston JS, Oppermann H:

WPT: 1988-353928/49.

N-PSDB; N80180.

sequence for biological activity, ion sequestering or binding to a solid support.

• 7 roddns nrtne

PT New oligonucleotide, polypeptide, antibody useful for treating
 PT autoimmune disease, immune deficiencies, T-cell malignancies and
 XX infectious diseases -
 PS Example 9; Page 74-76; 79pp; English.
 XX
 CC The present invention describes a nucleic acid molecule (I) encoding at
 CC least one complementary determining region (CDR) of a variable region of
 CC an antibody which specifically interacts with the extracellular domain of
 CC the human zeta-chain. The antibody whose CDR of a variable region is
 CC encoded by (I), is obtained by immunising a rat with Jurkat cells and
 CC subsequently with a conjugate comprising a carrier molecule and a
 CC peptide having 11 N-terminal amino acids of a rat zeta-chain. The
 CC anti-zeta-chain antibody is useful for the treatment and prevention of
 CC autoimmune diseases, immune deficiencies, T-cell malignancies, and
 CC infectious diseases and the suppression of immune response preferably in
 CC order to avoid graft rejection after organ transplantation, malignancies,
 CC or viral infections. The antibody, and fragments of it, can be useful for
 CC the enhancement or suppression of NK-cell dependent immunity or for the
 CC determination of zeta-chain or eta-chain expression on NK-cells, for
 CC T-lymphocytes or their precursors. The present sequence represents a
 CC bispecific anti-zeta-chain/anti-EpCAM antibody, from an example from
 CC the present invention.
 XX Sequence 532 AA;
 SQ

Query Match 78.0%; Score 495; DB 21; Length 532;
 Best Local Similarity 74.8%; Pred. No. 2.4e-34;
 Matches 92; Conservative 13; Mismatches 12; Indels 6; Gaps 1;
 QY 1 QIQLOQSGPEVVKPGASVKISKASGYTFTDYITWVKQPGQGLEWIGWYPCSGNTKY 60
 Db 142 qvqlqsgaeivkpgssvkiskasytftsydmhwikqpgnglewigyppgngntky 201
 QY 61 NEKFKGKATLTVDYSSSTAFWQLSSLTSEDYAVFCANTGNVW-----FAYWGQGTQV 114
 Db 202 nqkfngkatltadksstaymqsltsedsavycardwhyssyirpfaywggtltv 261
 QY 115 VSA 117
 Db 262 vss 264

RESULT 10
 W01585
 ID W01585 standard; Protein; 119 AA.
 XX
 AC W01585;
 XX
 DT 22-AUG-1997 (first entry)
 DE
 XX Lead binding MAb 11D11 heavy chain variable region.
 KW Monoclonal antibody; Fd fragment; lead cation; perfume; cosmetic;
 KW pharmaceutical; health care; skin treatment; pesticide; herbicide;
 KW heavy metal.
 XX
 OS Mus musculus.
 XX
 PN W09639518-A1.
 XX
 PD 12-DEC-1996.
 XX
 PF 05-JUN-1996; 96WO-US09258.
 XX
 PR 10-OCT-1995; 95US-0541373.
 PR 05-JUN-1995; 95US-0462798.
 XX
 PA (BION-) BIONEERASKA INC.
 XX
 PI Lopez O, Murray PJ, Wylie DE;

XX WPI; 1997-043140/04.
 DR N-PSDB; T58259.
 XX
 PT DNA encoding heavy metal binding polypeptide sequences - used for
 PT detecting, removing, adding or neutralising heavy metals, such as
 PT lead cations
 XX
 PS Claim 12; Page 73; 125pp; English.
 XX
 CC The present sequence represents the heavy chain variable region for
 CC monoclonal antibody (MAb) 11D11, which immunoreacts with a lead cation.
 CC The sequence was derived from RNA isolated from mouse hybridoma cells.
 CC The protein can be used for binding heavy metals, such as lead cations.
 CC It can be used for detecting, removing, adding or neutralising the
 CC heavy metals in biological and inanimate systems. It can be used in
 CC e.g. aqueous liquid systems, in biological or environmental systems or
 CC in such compositions as perfumes, cosmetics, pharmaceuticals, health
 CC care products, skin treatment products, pesticides, herbicides,
 CC solvents used in the production of semi-conductor and integrated
 CC circuit components and production materials for electronic components.
 CC The products can provide for applications involving minute amounts of
 CC specific heavy metals.
 XX Sequence 119 AA;
 SQ

Query Match 77.8%; Score 494; DB 18; Length 119;
 Best Local Similarity 76.5%; Pred. No. 6.8e-35;
 Matches 91; Conservative 14; Mismatches 12; Indels 2; Gaps 1;
 QY 1 QIQLOQSGPEVVKPGASVKISKASGYTFTDYITWVKQPGQGLEWIGWYPCSGNTKY 60
 Db 1 qvqlqsgaeivkpgssvkiskasytftsydmhwikqpgnglewigyppgngntky 201
 QY 61 NEKFKGKATLTVDYSSSTAFWQLSSLTSEDYAVFCANTGNVW-----FAYWGQGTQV 117
 Db 61 nekfgkatltadksstaymqsltsedsavycardwhyssyirpfaywggtltv 261
 RESULT 11
 W07437
 ID W07437 standard; Protein; 121 AA.
 XX
 AC W07437;
 XX
 DT 12-AUG-1997 (first entry)
 DE
 XX Anti-DNA antibody 4b2 group heavy chain variable region.
 KW Heavy chain; variable region; anti-DNA; monoclonal; antibody;
 KW 4b2 group; hairpin; diagnosis; inflammatory glomerulonephritis;
 KW systemic lupus erythematosus; screening; treatment; prevention;
 KW SLE; disease; consensus; putative.
 XX
 OS Synthetic.
 XX
 FH Key
 FT Region
 FT 1..30
 FT /label= framework_I
 FT 31..35
 FT /label= CDR_I
 FT 36..49
 FT /label= framework_II
 FT 50..66
 FT /label= CDR_II
 FT 67..98
 FT /label= framework_III
 FT 99..110
 FT /label= CDR_III
 FT 111..121
 FT /label= J_region
 XX

PN WO9636361-A1.
 XX 21-NOV-1996.
 XX 16-MAY-1996; 96WO-US07113.
 XX 18-MAY-1995; 95US-0443540.
 XX (UNMI) UNIV MICHIGAN.
 XX Glick GD, Swanson PC;
 XX WPI; 1997-011854/01.
 XX N-PSDB; T43806.
 XX Anti-DNA antibody which specifically binds DNA hairpin - useful to
 PT develop prods. for diagnosis and treatment of disorders, e.g.
 PT glomerulonephritis or systemic lupus erythematosus
 XX Example; Fig 9; 102pp; English.
 PS
 XX The present sequence is the heavy chain variable region of the
 CC group 4b2 putative consensus anti-DNA monoclonal antibody (MAB),
 CC which has a high affinity for single stranded DNA, low or no
 CC affinity for double stranded DNA and specifically binds a DNA
 CC hairpin. The MAB can be used to diagnose disorders associated with the
 CC pathological complexation of DNA, e.g. inflammatory
 CC glomerulonephritis and systemic lupus erythematosus. It can also be
 CC used to generate reagents to screen for pharmaceutical agents, and
 CC treat and/or prevent an above disorder.
 CC The sequence was derived by aligning homologous anti-DNA MAB,
 CC whose sequences have been published, as well as several MAB of
 CC other specificities obtained from a database search.
 XX
 SQ Sequence 121 AA;
 Query Match 77.8%; Score 494; DB 18; Length 121;
 Best Local Similarity 78.3%; Pred. No. 6.9e-35;
 Matches 94; Conservative 8; Mismatches 14; Indels 4; Gaps 1;
 QY 1 QIQLQSGPEVVKPGASVKISCKASGYTFDYITWVKQKPGQGLEWIGWYPCSGNTKY 60
 DB 1 qvqlqsgaelarpasvklscasgyftsgiswvkgtrtgqglwlgelypgsgntky 60
 QY 61 NEKFKGKATLVDTSSSFAFMQLSLTSEDFAVYFCANYGNY----WFAYWGQGTQVTVS 116
 DB 61 nekfkgtatltdksssttymqlsltsedsavfycarqsyysvfwfaywgqgtltvts 120
 RESULT 12
 W49814
 ID W49814 standard; Protein; 119 AA.
 AC W49814;
 XX
 XX 24-SEP-1998 (first entry)
 DE Amino acid sequence of the mouse antibody C4G1 mature heavy chain.
 KW Heavy chain; humanised; immunoglobulin; Ig; mouse C4G1; antibody;
 KW inhibition; antigen; cardiovascular disease; thromboembolic disorder;
 KW cancer; acute myocardial infarction; unstable angina; stroke;
 KW transient ischemic episode; pulmonary embolism; deep vein thrombosis;
 KW extracorporeal cardiopulmonary circulation.
 XX Mus sp.
 OS
 XX Key Location/Qualifiers
 FH 31..35
 FT Domain /note= "complementarity determining region"
 FT 50..66
 FT Domain /note= "complementarity determining region"
 FT

FT Domain 99..108
 FT /note= "complementarity determining region"
 XX
 PN US5777085-A.
 XX 07-JUL-1998.
 XX 17-MAY-1995; 95US-0458516.
 XX 03-MAY-1993; 93US-0059159.
 XX 20-DEC-1991; 91US-0812111.
 XX 09-JUN-1992; 92US-0895952.
 XX 11-SEP-1992; 92US-0944159.
 XX (PROT-) PROTEIN DESIGN LABS INC.
 XX Co MS, Tso JY;
 XX WPI; 1998-398136/34.
 XX New humanised immunoglobulin which binds GPIIb/IIIa - derived from
 PT mouse C4G1 antibody, used for inhibiting platelet aggregation for
 PT treating cardiovascular and thromboembolic disorders.
 XX Claim 1; Fig 5E; 35pp; English.
 CC This is the amino acid sequence of the humanised antibody C4G1 heavy
 CC chain, used in the method of the invention involving the creation
 CC of a humanised immunoglobulin (Ig) derived from the mouse C4G1 antibody.
 CC The humanised Ig is capable of binding to GPIIb/IIIa and inhibiting
 CC platelet aggregation and also the releasing reaction of platelets. The
 CC Ig can be used for treating cardiovascular diseases and thromboembolic
 CC disorders, e.g. acute myocardial infarction, unstable angina, stroke,
 CC transient ischemic episodes, deep vein thrombosis and pulmonary embolism,
 CC extracorporeal cardiopulmonary circulation. The Ig can also be used in
 CC diagnosing the presence and location of a thrombus, or certain types of
 CC cancer cells which develop GPIIb/IIIa on their surfaces, for the
 CC detection of GPIIb/IIIa antigens or for isolating platelets.
 XX
 SQ Sequence 119 AA;
 Query Match 77.2%; Score 490; DB 19; Length 119;
 Best Local Similarity 78.2%; Pred. No. 1.5e-34;
 Matches 93; Conservative 11; Mismatches 13; Indels 2; Gaps 2;
 QY 1 QIQLQSGPEVVKPGASVKISCKASGYTFDYITWVKQKPGQGLEWIGWYPCSGNTKY 60
 DB 1 qvqlqsgaelvgpgtsrvscasgyaftnylliewktrpgqglwlgvlypgsgntny 60
 QY 61 NEKFKGKATLVDTSSSFAFMQLSLTSEDFAVYFCANY-GNY-WFAYWGQGTQVTVSA 117
 DB 61 nekfkgtatltdksssttymqlsltsedsavfycarrdngywgwrgtltvtvsa 119
 RESULT 13
 R39266
 ID R39266 standard; Protein; 138 AA.
 AC R39266;
 XX
 XX 29-NOV-1993 (first entry)
 DT Mouse C4G1 Ig heavy-chain.
 DE
 XX Immunoglobulin; H-chain; platelet membrane glycoprotein; GPIIb/IIIb;
 KW monoclonal antibody; platelet agglutination; humanised antibody.
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH 1..20
 FT Peptide /label= signal_peptide
 FT

KW Complementarity determining region; CDR: murine; mouse; human;
 KW high affinity; immunoglobulin E; receptor; monoclonal antibody;
 KW IgE; MAb; heavy chain; variable region; humanised; semi-chimeric;
 KW chimeric; treatment; prevention; disease; allergy; CRA4.

XX Chimeric - Homo sapiens.
 OS Chimeric - Mus spp.
 OS Synthetic.

XX JP09191886-A.
 PN XX
 XX 29-JUL-1997.
 PD XX
 XX 19-JAN-1996; 96JP-0024816.
 PF XX
 XX 19-JAN-1996; 96JP-0024816.
 PR XX

XX (ASAK) ASahi BREWERIES LTD.
 PA (NIKK-) NIKKA WHISKEY KK.
 PA (TORI) TORII YAKUHIH KK.
 PA (TSUR/) TSURA T.
 PA XX
 XX WPI; 1997-429186/40.

DR Humanised, semi-chimeric and chimeric antibodies against human
 XX high-affinity IgE receptor - useful medicinally and have low
 PT antigenicity in humans
 PT
 XX Claim 8; Page 16; 26pp; Japanese.

PS The present sequence, the heavy chain variable region of a
 XX chimeric human CRA4 antibody (Ab), comprises complementarity
 CC determining regions (CDR) from a murine, anti-human high affinity
 CC immunoglobulin E (IgE) receptor, monoclonal Ab (MAb). The
 CC humanised chimeric MAb can be used to treat or prevent diseases,
 CC specifically allergies, associated with the receptor, and has very
 CC low antigenicity in humans.

XX Sequence 118 AA;
 SQ

Query Match 76.9%; Score 488.5; DB 18; Length 118;
 Best Local Similarity 78.8%; Pred. No. 2e-34;
 Matches 93; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

Qy 1 QIQLQSGPEVVKPGASVKISCKASGYFTDYITWVKRPGQGLEWIGWYFGSGNTKY 60

Db 1 qvqlqsgpelvkgasvrisckasgyfttsyihwvkqpggglewlgwlypkvntky 60

Qy 61 NEKFKGKATLVDTSSSTAFMQLSSLTSEDYNYFCANYGNW-FAYWGQGTQVTVSA 117

Db 61 nerfkgkatlttdkssstaymqlssltedsavvfcaltaratamywgggtttvtvss 118

Search completed: June 18, 2001, 15:29:16
 Job time: 49 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2001, 15:28:27 ; Search time 11.88 seconds
(without alignments)
198.394 Million cell updates/sec

Title: US-09-724-406-2

Perfect score: 635

Sequence: 1 QIQLQSGPEVVRPGASVKI.....NYGNYWFAYGQGTQTVSA 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents_AA.*

- 1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	543.5	85.6	139	1 US-08-253-877C-8	Sequence 8, Appli
2	543.5	85.6	139	2 US-08-452-164A-8	Sequence 8, Appli
3	539.5	85.0	138	3 US-08-603-024-2	Sequence 2, Appli
4	501.5	79.0	116	2 US-08-888-366-2	Sequence 2, Appli
5	497.5	78.3	122	4 US-08-767-128-4	Sequence 4, Appli
6	494	77.8	119	4 US-08-767-128-20	Sequence 20, Appli
7	490	77.2	119	1 US-08-458-516-11	Sequence 11, Appli
8	490	77.2	138	1 US-08-458-516-7	Sequence 7, Appli
9	483.5	76.1	139	2 US-08-116-778E-1	Sequence 1, Appli
10	483.5	76.1	139	2 US-08-438-562-1	Sequence 1, Appli
11	483.5	75.7	139	2 US-08-483-528B-91	Sequence 91, Appli
12	480.5	75.7	118	2 US-08-428-257A-74	Sequence 74, Appli
13	480.5	75.7	118	4 US-07-987-264-14	Sequence 14, Appli
14	477.5	75.2	128	1 US-08-202-040-21	Sequence 21, Appli
15	477.5	75.2	128	3 US-08-964-690-21	Sequence 21, Appli
16	476	75.0	121	3 US-08-881-037-65	Sequence 65, Appli
17	475.5	74.9	139	1 US-08-253-877C-19	Sequence 19, Appli
18	475.5	74.9	139	2 US-08-452-164A-19	Sequence 19, Appli
19	475.5	74.9	139	3 US-08-603-024-18	Sequence 18, Appli
20	474	74.6	119	1 US-08-458-516-10	Sequence 10, Appli
21	474	74.6	222	1 US-08-458-516-22	Sequence 22, Appli
22	474	74.6	235	1 US-08-458-516-23	Sequence 23, Appli
23	474	74.6	449	1 US-08-458-516-13	Sequence 13, Appli
24	473	74.5	121	4 US-08-579-378A-7	Sequence 7, Appli
25	473	74.5	121	5 PCT-US93-11612-7	Sequence 7, Appli
26	473	74.5	140	5 PCT-US93-11612-4	Sequence 4, Appli
27	470	74.0	118	3 US-09-065-059-5	Sequence 5, Appli

28	470	74.0	135	2 US-08-860-174A-4	Sequence 4, Appli
29	470	74.0	274	2 US-08-860-174A-12	Sequence 12, Appli
30	469.5	73.9	269	2 US-08-428-257A-72	Sequence 72, Appli
31	469.5	73.9	269	2 US-08-491-988-3	Sequence 3, Appli
32	469.5	73.9	402	2 US-08-491-988-9	Sequence 9, Appli
33	469.5	73.9	415	2 US-08-491-988-7	Sequence 7, Appli
34	469.5	73.9	435	2 US-08-491-988-5	Sequence 5, Appli
35	468	73.7	140	4 US-08-579-378A-4	Sequence 4, Appli
36	466.5	73.5	137	2 US-08-116-778E-3	Sequence 3, Appli
37	466.5	73.5	137	2 US-08-438-562-3	Sequence 3, Appli
38	466.5	73.5	137	2 US-08-483-528B-93	Sequence 93, Appli
39	466	73.4	119	4 US-08-767-128-10	Sequence 10, Appli
40	465.5	73.3	135	1 US-08-137-117D-27	Sequence 27, Appli
41	465.5	73.3	135	2 US-08-436-717-27	Sequence 27, Appli
42	465.5	73.3	137	1 US-08-392-419-2	Sequence 2, Appli
43	465.5	73.3	139	1 US-08-137-117D-35	Sequence 35, Appli
44	465.5	73.3	139	2 US-08-436-717-35	Sequence 35, Appli
45	465	73.2	119	2 US-08-553-497A-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1

US-08-253-877C-8

; Sequence 8, Application US/08253877C

; Patent No. 5773001

; GENERAL INFORMATION:

; APPLICANT: Hamann, Philip R.

; APPLICANT: Hinman, Lois

; APPLICANT: Hollander, Irwin

; APPLICANT: Holcomb, Ryan

; APPLICANT: Hallett, William

; APPLICANT: Tscu, Hwei-Ru

; APPLICANT: Weiss, Martin J.

; TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor

; NUMBER OF SEQUENCES: 73

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: American Cyanamid Company

; STREET: One Cyanamid Plaza

; CITY: Wayne

; STATE: New Jersey

; COUNTRY: U.S.A.

; ZIP: 07470-8426

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA: US/08/253,877C

; FILING DATE: 03-JUN-1994

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Barnhard, Elizabeth M.

; REGISTRATION NUMBER: 31,088

; REFERENCE/DOCKET NUMBER: 32,368

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-831-3246

; TELEFAX: 201-831-3305

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 139 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-253-877C-8

Query Match 85.6%; Score 543.5; DB 1; Length 139;
Best Local Similarity 87.5%; Pred. No. 2.4e-44;
Matches 105; Conservative 5; Mismatches 7; Indels 3; Gaps 2;

Qy 1 QIQLQSGPEVVKPGASVKISCKASGYTFDYITWVKQKPGQGLEWIGWYPCSGNTKY 60
Db 20 QIQLQSGPELVKPGASVKISCKASGYTFDYIYNWVKQKPGQGLEWIDPDSGNTKY 79
Qy 61 NEKFKGKATLTVDTSSTAFMQLSLTSEDYAVFCA-NYGNWFA--YWGQGTQVTVSA 117
Db 80 NEKFKGKATLTVDTSSTAFMQLSLTSEDYAVFCA-NYGNWFA--YWGQGTQVTVSA 139

RESULT 2
US-08-452-164A-8
; Sequence 8, Application US/08452164A
; Patent No. 5877296
; GENERAL INFORMATION:
; APPLICANT: Hamann, Philip R.
; APPLICANT: Hinman, Lois
; APPLICANT: Hollander, Irwin
; APPLICANT: Holcomb, Ryan
; APPLICANT: Hallett, William
; APPLICANT: Tsou, Hwei-Ru
; APPLICANT: Weiss, Martin J.
; TITLE OF INVENTION: Conjugates of Methylothio Antitumor
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Home Products Corporation
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/452,164A
; FILING DATE: 26-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 32,368-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-683-2158
; TELEFAX: 201-683-4117
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-452-164A-8

Query Match 85.6%; Score 543.5; DB 2; Length 139;
Best Local Similarity 87.5%; Pred. No. 2.4e-44;
Matches 105; Conservative 5; Mismatches 7; Indels 3; Gaps 2;

Qy 1 QIQLQSGPEVVKPGASVKISCKASGYTFDYITWVKQKPGQGLEWIGWYPCSGNTKY 60
Db 20 QIQLQSGPELVKPGASVKISCKASGYTFDYIYNWVKQKPGQGLEWIDPDSGNTKY 79
Qy 61 NEKFKGKATLTVDTSSTAFMQLSLTSEDYAVFCA-NYGNWFA--YWGQGTQVTVSA 117
Db 80 NEKFKGKATLTVDTSSTAFMQLSLTSEDYAVFCA-NYGNWFA--YWGQGTQVTVSA 139

RESULT 3
US-08-603-024-2
; Sequence 2, Application US/08603024

; Patent No. 6015562
; GENERAL INFORMATION:
; APPLICANT: Hinman, Lois M.
; APPLICANT: Menendez, Ana T.
; APPLICANT: Hamann, Philip R.
; TITLE OF INVENTION: TARGETED FORMS OF METHYLTHIO
; TITLE OF INVENTION: ANTITUMOR AGENTS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Home Products Corporation
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: NJ
; COUNTRY: USA
; ZIP: 07054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/603,024
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,932-03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 973-683-2158
; TELEFAX: 973-683-4117
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 138 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-603-024-2

Query Match 85.0%; Score 539.5; DB 3; Length 138;
Best Local Similarity 87.4%; Pred. No. 5.7e-44;
Matches 104; Conservative 5; Mismatches 7; Indels 3; Gaps 2;

Qy 1 QIQLQSGPEVVKPGASVKISCKASGYTFDYITWVKQKPGQGLEWIGWYPCSGNTKY 60
Db 20 QIQLQSGPELVKPGASVKISCKASGYTFDYIYNWVKQKPGQGLEWIDPDSGNTKY 79
Qy 61 NEKFKGKATLTVDTSSTAFMQLSLTSEDYAVFCA-NYGNWFA--YWGQGTQVTVS 116
Db 80 NEKFKGKATLTVDTSSTAFMQLSLTSEDYAVFCA-NYGNWFA--YWGQGTQVTVS 138

RESULT 4
US-08-888-366-2
; Sequence 2, Application US/08888366
; Patent No. 5972656
; GENERAL INFORMATION:
; APPLICANT: Lopez, Osvaldo
; APPLICANT: Wylie, Dwane E.
; APPLICANT: Wagner, Fred W.
; TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefo
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/888,366
; APPLICATION NUMBER: US/08/888,366
; FILING DATE: 03-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/187,407
; FILING DATE: 27-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,542
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/493,299
; FILING DATE: 14-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/324,392
; FILING DATE: 14-MAR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.390USC1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-888-366-2

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Query Match 79.0%; Score 501.5; DB 2; Length 116;
Best Local Similarity 80.3%; Pred. No. 1.8e-40;
Matches 94; Conservative 9; Mismatches 13; Indels 1; Gaps 1;

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QY 1 QIQLQSGPEVVKPGASVKISKASGYTFTDYITWKQKPGQGLEWIGWYPSGNTKY 60
DB 1 EVQLQSGPELVKPGALVKISKASGYTFTSYDINWVKQKPGQGLEWIGWYPSGNTKY 60
QY 61 NEKFKGKATLVDTSSSTAFAEQLSLTSEDYAVYFCARCG-YAMDYWGQGTQVTVSS 116
DB 61 NEKFKGKATLVDTSSSTAFAEQLSLTSEDYAVYFCARCG-YAMDYWGQGTQVTVSS 116

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RESULT 5
US-08-767-128-4
; Sequence 4, Application US/08767128
; Patent No. 6111079
; GENERAL INFORMATION:
; APPLICANT: WYLIE, DWANE E.
; APPLICANT: LOPEZ, OSVALDO
; APPLICANT: MURRAY, PETER JOSEPH
; APPLICANT: GOEBEL, PETER
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; NUMBER OF INVENTION: NUCLEOTIDES CODING THEREFORE
; CORRESPONDENCE ADDRESS: 46
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6111079west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,128

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; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09258
; FILING DATE: 05-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/541,373
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,798
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.49USF1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/371-5278
; TELEFAX: 612/332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-08-767-128-4

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Query Match 78.3%; Score 497.5; DB 4; Length 122;
Best Local Similarity 77.0%; Pred. No. 4.4e-40;
Matches 94; Conservative 9; Mismatches 14; Indels 5; Gaps 2;

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QY 1 QIQLQSGPEVVKPGASVKISKASGYTFTDYITWKQKPGQGLEWIGWYPSGNTKY 60
DB 1 QVQLQSGAGLVKPGASVKLSCKASGYTFTDYIIHWYKQSGQGLEWIGWYPSGSIKY 60
QY 61 NEKFKGKATLVDTSSSTAFAEQLSLTSEDYAVYFCARCG-YAMDYWGQGTQVTV 115
DB 61 NEKFKGKATLVDTSSSTAFAEQLSLTSEDYAVYFCARCG-YAMDYWGQGTQVTV 120
QY 116 SA 117
DB 121 SA 122

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RESULT 6
US-08-767-128-20
; Sequence 20, Application US/08767128
; Patent No. 6111079
; GENERAL INFORMATION:
; APPLICANT: WYLIE, DWANE E.
; APPLICANT: LOPEZ, OSVALDO
; APPLICANT: MURRAY, PETER JOSEPH
; APPLICANT: GOEBEL, PETER
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; NUMBER OF INVENTION: NUCLEOTIDES CODING THEREFORE
; CORRESPONDENCE ADDRESS: 46
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6111079west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSQL Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,128
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER:
FILING DATE: 04-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: PCT/US96/09258
FILING DATE: 05-JUN-1996
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/541,373
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/462,798
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.49USFI
TELEPHONE/COMMUNICATION INFORMATION: 612/371-5278
TELEFAX: 612/332-9081

TELETYPE: INFORMATION FOR SEO ID NO: 20:

SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
IS-08-767-128-20

Query Match

	Pred. NO.	9.2e-40;	
Query Match	76.8%;		
Best Local Similarity	76.5%;		
Matches	91; Conservative	14; Mismatches	12;
		Indels	2; Gaps
			1;

[illegible]

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7
RESULT
US-08-458-516-11
; Sequence 11, Application US/08458516
; Patent No. 5777085
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GLIB/IIIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza,
; City: San Francisco
; STATE: California
; COUNTRY: USA

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ZIP: 94105
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/458,516
 FILING DATE:
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/059,159
 FILING DATE: 03-MAY-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M.
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 11823-37-3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-326-2400
 TELEFAX: 415-326-2422
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 119 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: N-terminal fragment
 US-08-08-458-516-11

Query Match 77.28; Score 490; DB 1; Length 119;

Query Match	Pred. No. 2.2e-39;	Gaps 2;
Best Local Similarity 78.28;		
Matches 93; Conservative	11; Mismatches 13;	Indels 2;
		Gaps 2;

[illegible]

RESULT 8

US-08-458-516-7
: Sequence 7, Application US/08458516

Patent No. 5777085
GENERAL INFORMATION:

APPLICANT: Co, Man Sung
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: GPIIB/IIIa
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA

ZIP: 94105

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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,
,      COMPUTER: IBM PC compatible
,      OPERATING SYSTEM: PC-DOS/MS-DOS
,      SOFTWARE: PatentIn Release #1.0, Version #1.25
,
,      CURRENT APPLICATION DATA:
,      APPLICATION NUMBER: US/08/458,516
,      FILING DATE:
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/059,159
FILING DATE: 03-MAY-1993
ATTORNEY/AGENT INFORMATION:


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RESULT          9
US-08-116-778E-1
; Sequence 1, Application US/08116778E
; Patent No. 5830470
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, YOSHIO
; APPLICANT: KUNAWA, NOSHISASA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,778E
; FILING DATE: 07-SEP-93
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 249-59
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: -19...-1

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[illegible]

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1  RESULT 10
2  US-08-438-562-1
3  ; Sequence 1, Application US/08438562
4  ; Patent No. 5874255
5  ; GENERAL INFORMATION:
6  ; APPLICANT: NAKAMURA, KAZUYASU
7  ; APPLICANT: KOIKE, MASAMICHI
8  ; APPLICANT: SHITARA, KENYA
9  ; APPLICANT: HANAI, NOBUO
10 ; APPLICANT: KUNANA, YOSHIHISA
11 ; APPLICANT: HASEGAWA, MAMORU
12 ; TITLE OF INVENTION: HUMANIZED ANTIBODIES
13 ; NUMBER OF SEQUENCES: 49
14 ; CORRESPONDENCE ADDRESS:
15 ; ADDRESSEE: HIXON & VANDERHYE P.C.
16 ; STREET: 1100 NORTH GLEBE ROAD
17 ; CITY: ARLINGTON
18 ; STATE: VIRGINIA
19 ; COUNTRY: U.S.A.
20 ; ZIP: 22201-4714
21 ; COMPUTER READABLE FORM:
22 ; MEDIUM TYPE: Floppy disk
23 ; COMPUTER: IBM PC compatible
24 ; OPERATING SYSTEM: PC-DOS/MS-DOS
25 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
26 ; CURRENT APPLICATION DATA:
27 ; APPLICATION NUMBER: US/08438,562
28 ; FILING DATE: 10-MAY-95
29 ; CLASSIFICATION: 424
30 ; PRIOR APPLICATION DATA:
31 ; APPLICATION NUMBER: 08/116,778
32 ; FILING DATE: 07-SEP-93
33 ; CLASSIFICATION: 424

```

us-09-724-406-2.ra1

Fri Jun 29 08:04:38 2001

```
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249-76
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: sig_peptide
LOCATION: -19..-1
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"
FEATURE:
NAME/KEY: domain
LOCATION: 31..35
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
FEATURE:
NAME/KEY: domain
LOCATION: 50..66
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
US-08-438-562-1

Query Match 76.1%; Score 483.5; DB 2; Length 139;
Best Local Similarity 75.0%; Pred. No. 1.le-38;
Matches 90; Conservative 14; Mismatches 13; Indels 3; Gaps 1;

QY 1 QIQLOQSGPEVVKPGASVKISCKASGYTFTDYITWVKQKPGQGLEWIGWYIPNGSGNTKY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 EVQLQSGPELVKPGASVKISCKASGYTFTDYNMDVWVKQSHGKSLWIGYIPNGSGTGY 79

QY 61 NEKFQKATLTVDTSSTAFMQLSLTSEDYAYFCANYGNW---FAYWGQGTQVTVSA 117
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 NQFKSKATLTVDKSSSTAYMELSLTSDSAVYICATYGHYGYMFAIWGQGLTVTVSA 139

RESULT 11
US-08-483-528B-91
; Sequence 91, Application US/08483528B
; Patent No. 5939532
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUNAWA, YOSHIIHISA
; APPLICANT: HASEGAWA, MANORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHIE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON

ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249-76
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: sig_peptide
LOCATION: -19..-1
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"
FEATURE:
NAME/KEY: domain
LOCATION: 31..35
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
FEATURE:
NAME/KEY: domain
LOCATION: 50..66
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
US-08-438-562-1

Query Match 76.1%; Score 483.5; DB 2; Length 139;
Best Local Similarity 75.0%; Pred. No. 1.le-38;
Matches 90; Conservative 14; Mismatches 13; Indels 3; Gaps 1;

QY 1 QIQLOQSGPEVVKPGASVKISCKASGYTFTDYITWVKQKPGQGLEWIGWYIPNGSGNTKY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 EVQLQSGPELVKPGASVKISCKASGYTFTDYNMDVWVKQSHGKSLWIGYIPNGSGTGY 79

QY 61 NEKFQKATLTVDTSSTAFMQLSLTSEDYAYFCANYGNW---FAYWGQGTQVTVSA 117
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 NQFKSKATLTVDKSSSTAYMELSLTSDSAVYICATYGHYGYMFAIWGQGLTVTVSA 139

RESULT 12
US-08-428-257A-74
; Sequence 74, Application US/08428257A
; Patent No. 5865808
; GENERAL INFORMATION:
; APPLICANT: Spooner, Robert A.
; APPLICANT: Epenetos, A.A.
; TITLE OF INVENTION: Compounds to target cells
; NUMBER OF SEQUENCES: 80
```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jules E. Goldberg
; STREET: 261 Madison Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10016-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/428,257A
; FILING DATE: 07/05/95
; CLASSIFICATION: 514
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-428-257A-74

Query Match 75.7%; Score 480.5; DB 2; Length 118;
Best Local Similarity 75.4%; Pred. No. 1.7e-38;
Matches 89; Conservative 15; Mismatches 13; Indels 1; Gaps 1;
QY 1 QIQLQSGPEVVKPGASVKISKASGYFTDYITWVKQKPGQGLEWIGWYPGSGNTKY 60
Db 1 QVQLQSGAELMKPGASVKISKATGYTFSAYWIEWVKQKPGHGLEWIGELPGSNNSRY 60
QY 61 NEKFKGKATLTVDTSSTAFMQLSLTSEDYAVYFCA-NYGNWYFAYWGQGTQVTVSA 117
Db 61 NEKFKGKATFTADTSSNTAYMQLSLTSEDSAVYCSRSYDFAMFAYWGQGTPTVTVSA 118

RESULT 13
US-07-987-264-14
; Sequence 14, Application US/07987264
; Patent No. 6204366
; GENERAL INFORMATION:
; APPLICANT: VERHOEYEN, MARTINE ELISA
; TITLE OF INVENTION: SPECIFIC BINDING AGENTS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/987,264
; FILING DATE: 08-MAR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9019553.8
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB PCT/GB91/01511
; FILING DATE: 05-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 200232/P3095USA
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-987-264-14

Query Match 75.7%; Score 480.5; DB 4; Length 118;
Best Local Similarity 75.4%; Pred. No. 1.7e-38;
Matches 89; Conservative 15; Mismatches 13; Indels 1; Gaps 1;
QY 1 QIQLQSGPEVVKPGASVKISKASGYFTDYITWVKQKPGQGLEWIGWYPGSGNTKY 60
Db 1 QVQLQSGAELMKPGASVKISKATGYTFSAYWIEWVKQKPGHGLEWIGELPGSNNSRY 60
QY 61 NEKFKGKATLTVDTSSTAFMQLSLTSEDYAVYFCA-NYGNWYFAYWGQGTQVTVSA 117
Db 61 NEKFKGKATFTADTSSNTAYMQLSLTSEDSAVYCSRSYDFAMFAYWGQGTPTVTVSA 118

RESULT 14
US-08-202-047-21
; Sequence 21, Application US/08202047
; Patent No. 5800815
; GENERAL INFORMATION:
; APPLICANT: CHESNUT, Robert W.
; APPLICANT: POLLEY, Margaret J.
; APPLICANT: PAULSON, James C.
; APPLICANT: JONES, S. Tarran
; APPLICANT: SALDANHA, Jose W.
; APPLICANT: BENDIG, Mary M.
; TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,047
; FILING DATE: 25-FEB-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14137-77
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..128
; OTHER INFORMATION: /label= MOUSE_IIA

US-08-202-047-21

Query Match	75.2%	Score	477.5;	DB 1;	Length	128;			
Best Local Similarity	71.3%;	Pred. No.	3.5e-38;						
Matches	92;	Conservative	12;	Mismatches	12;	Indels	13;	Gaps	2;
QY	1	OIQLOQQSEPVVKPGASVKISCKRASGVTFTDYIITWVKKPKGGLEWTGWLPGSNTKY	60						
Ddb	1	EVLQSQSGPELVKPGASVKISCKRASGVTFTDYIMNVWKSPGKSLEWIGDINPNGGYTSY	60						
QY	61	NKEFKGATLAVDTSSSTAFMQLSSLTSETDYFCAFYCANTGYW-----FAYWG	108						
Ddb	61	NQKPKGATLAVDKSSSTAFMQLSSLTSDSVAIVYCARGXYSSSYMKAXXXAFAFDWG	119						
QY	109	QGQTQTVTSA	117						
Ddb	120	QGTTTTVTSS	128						

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RESULT 15
US-08-964-690-21
: Sequence 21, Application US/08964690
: Patent No. 6033667
: GENERAL INFORMATION:
: APPLICANT: CHESNUT, Robert W.
: APPLICANT: POLLEY, Margaret J.
: APPLICANT: PAULSON, James C.
: APPLICANT: JONES, S. Tarran
: APPLICANT: SALDANHA, Jose W.
: APPLICANT: BENDIG, Mary M.
: TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses
: NUMBER OF SEQUENCES: 45
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend Khourie and Crew
: STREET: One Market Plaza, Steuart Tower, Suite 2000
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94105
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING: IBM PC compatible
: SOFTWARE: PC-DOS/MS-DOS
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/964,690
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/202,047
: FILING DATE: 25-FEB-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Smith, William M.
: REGISTRATION NUMBER: 30,223
: REFERENCE/DOCKET NUMBER: 14137-77
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-326-2400
: TELEFAX: 415-326-2422
: INFORMATION FOR SEQ ID NO: 21:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 128 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: FEATURE:
: NAME/KEY: Protein
: LOCATION: 1..128
: OTHER INFORMATION: /label= MOUSE_I1A
US-08-964-690-21

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Query Match          75.2%; Score 477.5; DB 3; Length 128;
Best local Similarity 71.3%; Pred. No. 3.5e-39;
Matches 92; Conservative 12; Mismatches 12; Indels 13; Gaps

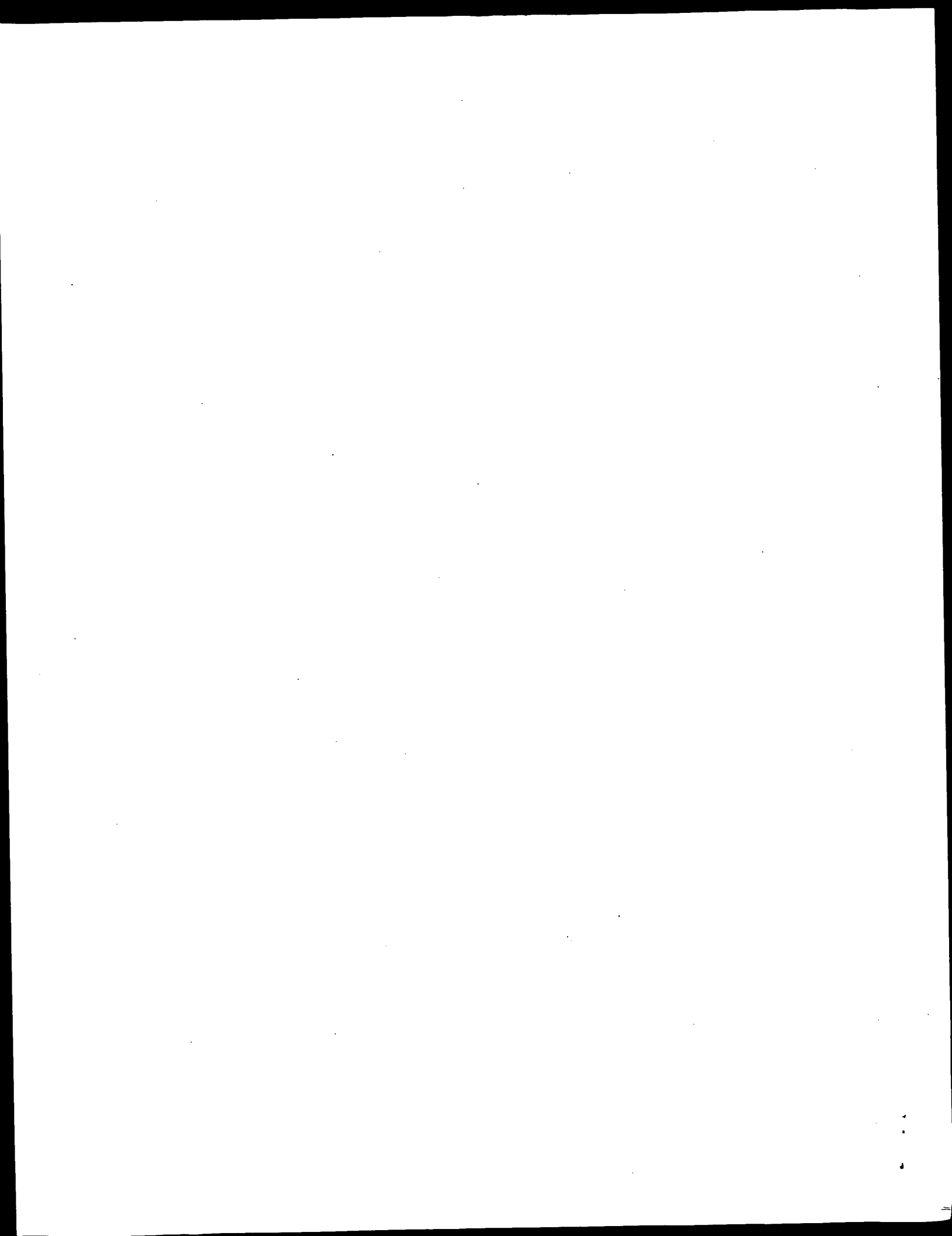
      QY      1 OIOLOQSGPEVWPAGSAVKISCKASGYFTDYITWVKRPGOGLEWIGWIPGSGNTKY 60
                ::::::::::::::::::::::::::::|::|::|::|::|::|::|::|::|::|::|
Ddb         1 EVQLOQSGPELVPAGSAVKISCKASGYFTDYVMNWKSPGKSLIEWIGDINFGNGTSY 60
                ::::::::::::::::::::::::::::::|::|::|::|::|::|::|::|::|::|::|

      QY      61 NEKFGRATLTVTSSSTAFMQLSLSITSDTAYFCANYNW-----PAYWG 108
                |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Ddb         61 NQKFGRATLTVDKSSSTAYMQLSLSITSDSVAIYYCAR-GXYYSSSYMXAXXYAFDYWG 119
                |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

      QY      109 QGTQTVSA 117
                ||| |::|::|
Db          120 QGTTVTSS 128
                ||| |::|::|

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Search completed: June 18, 2001, 15:29:31
Job time: 64 sec



Query Match 79.9%; Score 507.5; DB 2; Length 115;
 Best Local Similarity 80.9%; Pred. No. 1.1e-37;
 Matches 93; Conservative 11; Mismatches 10; Indels 1; Gaps 1;

QY 1 QIOLQSGPEVVKPGASVKISCKASGYFTDYITWVKQKPGQGLEWIGWIPGSGNTKY 60
 DB 1 EVQLQSGPELVKPGASVKISCKASGYFTDYITWVKQKPGQGLEWIGWIPGSGNTKY 60

QY 61 NEKFKGKATLTVDTSSTAFMQLSSLTSEDYAVYFCARSSGGYLGWGGQTTLT 114
 DB 61 NEKFKGKATLTADKSSSTAYMQLSSLTSEDYAVYFCARSSGGYLGWGGQTTLT 115

RESULT 7
 PH0998
 Ig heavy chain V region (clone 165.3) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PH0998
 R:Trillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
 J. Exp. Med. 176, 761-779, 1992
 A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell
 A:Reference number: PH0971; MUID:92381444
 A:Accession: PH0998
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-111 <FHL>
 A:Experimental source: B cell, strain [NZB x NZW]F1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 503; DB 2; Length 111;
 Best Local Similarity 84.7%; Pred. No. 2.7e-37;
 Matches 94; Conservative 5; Mismatches 8; Indels 4; Gaps 1;

QY 1 QIOLQSGPEVVKPGASVKISCKASGYFTDYITWVKQKPGQGLEWIGWIPGSGNTKY 60
 DB 1 QIOLQSGPELVKPGASVKISCKASGYFTDYITWVKQKPGQGLEWIGWIPGSGNTKY 60

QY 61 NEKFKGKATLTVDTSSTAFMQLSSLTSEDYAVYFCANYNWFA----YV 107
 DB 61 NEKFKGKATLTVDTSSTAYMQLSSLTSEDYAVYFCARGDILLRLIDY 111

RESULT 8
 PL0245
 Ig heavy chain V region (anti-DNA, Dp17VH) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
 C:Accession: PL0245
 R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
 J. Exp. Med. 171, 265-297, 1990
 A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
 A:Reference number: PL0231; MUID:90111618
 A:Accession: PL0245
 A:Molecule type: mRNA
 A:Residues: 1-112 <SHL>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-23/Region: framework 1
 F:8-91/Domain: immunoglobulin homology <IMM>
 F:24-28/Region: complementarity-determining 1
 F:29-42/Region: framework 2
 F:43-59/Region: complementarity-determining 2
 F:60-91/Region: framework 3
 F:92-102/Region: complementarity-determining 3
 F:103-112/Region: framework 4

Query Match 78.7%; Score 499.5; DB 2; Length 112;
 Best Local Similarity 83.0%; Pred. No. 5.5e-37;
 Matches 93; Conservative 5; Mismatches 11; Indels 3; Gaps 1;

QY 8 GPEVVKPGASVKISCKASGYFTDYITWVKQKPGQGLEWIGWIPGSGNTKYNEKFKG 67
 DB 1 GPELVKPGASVKISCKASGYFTDYITWVKQKPGQGLEWIGWISGNTKYNEKFEK 60

QY 68 ATLTVDTSSSTAFMQLSSLTSEDYAVYFCANYG---NYWFAYWGGQTQVTVS 116
 DB 61 ATLTVDTSSSTAYMQLSSLTSEDYAVYFCVRRNGLRRAWFAYWGGQTQVTVS 112

RESULT 9
 G28195
 Ig heavy chain V region (anti-haloperidol antibody B) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 23-Jul-1999
 C:Accession: G28195
 R:Sherman, M.A.; Deans, R.J.; Bolger, M.B.
 J. Biol. Chem. 263, 4059-4063, 1988
 A:Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amino aci
 A:Reference number: A28195; MUID:88153717
 A:Accession: G28195
 A:Molecule type: mRNA
 A:Residues: 1-120 <SHE>
 A:Cross-references: GB:M19772; NID:g195520; PIDN:AAA38340.1; PID:g195521
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 78.5%; Score 498.5; DB 2; Length 120;
 Best Local Similarity 77.5%; Pred. No. 7.2e-37;
 Matches 93; Conservative 12; Mismatches 12; Indels 3; Gaps 1;

QY 1 QIOLQSGPEVVKPGASVKISCKASGYFTDYITWVKQKPGQGLEWIGWIPGSGNTKY 60
 DB 1 QVQLQSGPELVKPGASVKISCKASGYFTDYITWVKQKPGQGLEWIPGSGNTKY 60

QY 61 NEKFKGKATLTVDTSSTAFMQLSSLTSEDYAVYFCANYNWYF---AYWQGGTQVTVSA 117
 DB 61 NEKFKGKATLTADKSSSTAYMQLSSLTSEDYAVYFCAREGSTEYDEADYWGXTTLTVSS 120

RESULT 10
 E29380
 Ig heavy chain precursor V region (AC-1001) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 23-Jul-1999
 C:Accession: E29380
 R:Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.
 J. Biol. Chem. 263, 13579-13583, 1987
 A:Title: Nucleotide and translated amino acid sequences of cDNA coding for the variab
 A:Reference number: A92612; MUID:88007582
 A:Accession: E29380
 A:Molecule type: mRNA
 A:Residues: 1-137 <CHE>
 A:Cross-references: GB:M17164; GB:J02815; NID:g195411; PIDN:AAA38295.1; PID:g195412
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 78.2%; Score 496.5; DB 2; Length 137;
 Best Local Similarity 78.8%; Pred. No. 1.2e-36;
 Matches 93; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 1 QIOLQSGPEVVKPGASVKISCKASGYFTDYITWVKQKPGQGLEWIGWIPGSGNTKY 60
 DB 20 QVQLQSGPELVKPGASVKISCKASGYFTDYITWVKQKPGQGLEWIGWIPGSGNTKY 79

QY 61 NEKFKGKATLTVDTSSTAFMQLSSLTSEDYAVYFCA-NYGNWYFAYWGGTQVTVSA 117

RESULT 15
C30562
Ig heavy chain V region (27.7.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 16-Aug-1996
C:Accession: C30562
R:Sikder, S.K.; Borden, P.; Gruzo, F.; Akolkar, P.N.; Bhattacharya, S.B.; N

J. Immunol. 142, 888-893, 1989
 A:Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-bi
 A:Reference number: A30562; MUID:89110066
 A:Accession: C30562
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-119 <SIK>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.1%; Score 483; DB 2; Length 119;
 Best Local Similarity 76.5%; Pred. No. 1.6e-35;
 Matches 91; Conservative 13; Mismatches 13; Indels 2; Gaps 1;
 Oy 1 QIQLOQSGPEVVKPGASVKISCKASGYTFDYITWVKQPGGLEWIGMIYPGSGNTKY 60
 Db 1 QVQLOQSGAELMKPGASVKISCKATGYTFSSYIEWVKQPGHGLEWIGIILPGSGSTNY 60
 Oy 61 NEKFKKATLTVDTSSTAFMQLSSLTSEDYVFCAN--YGNVWFAYWGQGTQVTVSA 117
 Db 61 NEKFKKATFTADTSSNTAFMQLSSLTSEDSAVYICARHYGSSSPAYWGQGLTVTVSA 119

Search completed: June 18, 2001, 15:30:16
 Job time: 94 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 18, 2001, 15:28:57 ; Search time 9.63 seconds
(without alignments)
416.188 Million cell updates/sec

Title: US-09-724-406-2

Perfect score: 635

Sequence: 1 QIQLQSGPEVVKPGASVKI.....NYGNWFAYWGQGTQVTVSA 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	467	73.5	120	1	HV03_MOUSE
2	466.5	73.5	139	1	HV07_MOUSE
3	453	71.3	117	1	HV12_MOUSE
4	452	71.2	140	1	HV02_MOUSE
5	451	71.0	117	1	HV13_MOUSE
6	451	71.0	117	1	HV52_MOUSE
7	450	70.9	138	1	HV48_MOUSE
8	437.5	68.9	118	1	HV51_MOUSE
9	436.5	68.7	137	1	HV11_MOUSE
10	427	67.2	121	1	HV01_MOUSE
11	418.5	65.9	120	1	HV50_MOUSE
12	415	65.4	136	1	HV15_MOUSE
13	412	64.9	117	1	HV09_MOUSE
14	405	63.8	117	1	HV06_MOUSE
15	405	63.8	117	1	HV14_MOUSE
16	403	63.5	117	1	HV04_MOUSE
17	399	62.8	117	1	HV05_MOUSE
18	396	62.4	117	1	HV10_MOUSE
19	396	62.4	117	1	HV49_MOUSE
20	386.5	60.9	147	1	HV1C_HUMAN
21	364	57.3	117	1	HV1B_HUMAN
22	356	56.1	117	1	HV1G_HUMAN
23	342.5	53.9	114	1	HV00_MOUSE
24	329	51.8	117	1	HV1A_HUMAN
25	325	51.2	142	1	HV01_RAT
26	320.5	50.5	119	1	HV40_MOUSE
27	320.5	50.5	136	1	HV16_MOUSE
28	319	50.2	144	1	HV43_MOUSE
29	313.5	49.4	119	1	HV37_MOUSE
30	311.5	49.1	122	1	HV3G_HUMAN
31	309.5	48.7	126	1	HV3K_HUMAN
32	308.5	48.6	124	1	HV1D_HUMAN
33	306.5	48.3	119	1	HV38_MOUSE

```

34 306.5 48.3 120 1 HV1H_HUMAN
35 306 48.2 115 1 HV32_MOUSE
36 305 48.0 117 1 HV41_MOUSE
37 304 47.9 121 1 HV3J_HUMAN
38 302.5 47.6 122 1 HV3A_HUMAN
39 301 47.4 113 1 HV30_MOUSE
40 299 47.1 118 1 HV39_MOUSE
41 299 47.1 137 1 HV46_MOUSE
42 298 46.9 115 1 HV33_MOUSE
43 297 46.8 117 1 HV42_MOUSE
44 296 46.6 113 1 HV27_MOUSE
45 295 46.5 113 1 HV29_MOUSE

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ALIGNMENTS

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RESULT 1
HV03_MOUSE STANDARD; PRT; 120 AA.
AC HV03_MOUSE
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83131846; PubMed=6186498;
RA Siekevitz M., Geffer M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsonate
RT idotype response of the strain A mouse.";
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -I- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
CC PIR: A02028; HVM5G7.
CC InterPro: IPR003006;
CC Pfam: PF00047; ig; 1.
CC Immunoglobulin V region; Antiarsonate antibody; Hybridoma.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;

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Query Match 73.5%; Score 467; DB 1; Length 120;

Best Local Similarity 73.3%; Pred. No. 4.5e-40;

Matches 88; Conservative 14; Mismatches 14; Indels 4; Gaps 1;

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QY 2 IQLQSGPEVVKPGASVKISCKASGYTFDYITVWVKPGGLEWIGHIYPGSGNFKYN 61
Db 1 VQLQSGAELEVRAGSSVKRCKASGYTFYSIGNVWVKRPGGLEWIGHIYPGSGNFKYN 60
QY 62 EKFKGKATITVDTSSSTAFPMQLSLTSEDYVYFCANY----GNWYFAYWGQGTQVTVSA 117
Db 61 EKFKGKATITVDTSSSTAFPMQLSLTSEDYVYFCARSYVYGSYFYDYWGQGTTLTVSS 120

```

RESULT 2

```

HV07_MOUSE STANDARD; PRT; 139 AA.
ID HV07_MOUSE
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION B1-8/186-2 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6789376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NpB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THE BL-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
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CC -----
DR EMBL; J00529; AAA38170.1; -
DR PIR; A02034; MHMS18.
DR InterPro; IPR003006; -
DR Pfam; PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 139 IG HEAVY CHAIN V REGION BL-8/186-2.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 58 FRAMEWORK 2.
FT DOMAIN 59 68 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 69 85 FRAMEWORK 3.
FT DOMAIN 86 117 FRAMEWORK 4.
FT DOMAIN 118 124 D SEGMENT.
FT DOMAIN 125 139 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 139 139
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;

Query Match 73.5%; Score 466.5; DB 1; Length 139;
Best Local Similarity 73.3%; Pred. No. 6e-40;
Matches 88; Conservative 14; Mismatches 15; Indels 3; Gaps 1;
QY 1 QIOLQSGPEVVKPGASVKISKASGYTFTDYITWVKQKPGGLEWIGWIPGSGNTKY 60
D 1 QVQLQPGAEVVKPGASVKISKASGYTFTDYITWVKQKPGGLEWIGWIPGSGNTKY 79
QY 61 NEKFKGKATLTVDTSSTAFMQLSLTSEDYAVYFCAN--YGNVWFAYWGQGTQVTVSA 117
D 80 NEKFKSKATLTVDKPSSTAYMQLSLTSEDYAVYFCARYDYSSYFDYWGQGTTLTVSS 139
RESULT 3
HV12_MOUSE STANDARD; PRT; 117 AA.
ID HV12_MOUSE
AC P01756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION MOPC 104E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=83075344; PubMed=6816276;
RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RT heavy chain constant region domains.";

RL Biochemistry 21:5415-5424(1982).
CC -!- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC PROTEIN HAS ALSO BEEN DETERMINED.
CC -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR; A02039; MHMS4E.
DR InterPro; IPR003006; -
DR Pfam; PF00047; Ig; 1.
KW Immunoglobulin V region; Glycoprotein.
FT DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. .).
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;
Query Match 71.3%; Score 453; DB 1; Length 117;
Best Local Similarity 71.8%; Pred. No. 1.1e-38;
Matches 84; Conservative 16; Mismatches 17; Indels 0; Gaps 0;
QY 1 QIOLQSGPEVVKPGASVKISKASGYTFTDYITWVKQKPGGLEWIGWIPGSGNTKY 60
D 1 EVQLQSGPELVKPGASVKMSKASGYTFTDYIMKWKQSHGKSLWIGDINPNNGGTSY 60
QY 61 NEKFKGKATLTVDTSSTAFMQLSLTSEDYAVYFCAN--YGNVWFAYWGQGTQVTVSA 117
D 61 NQKFKGKATLTVDKSSSTAYMQLSLTSEDYAVYFCARYDYFDVWGAGTTTVTVSS 117
RESULT 4
HV02_MOUSE STANDARD; PRT; 140 AA.
ID HV02_MOUSE
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 93G7 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/J;
RX MEDLINE=82152818; PubMed=6801765;
RA Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain.";
RL Science 216:309-311(1982).
CC -----
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CC or send an email to license@isb-sib.ch).
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DR EMBL; J00493; AAA38128.1; -
DR PIR; A02028; HVMSG7.
DR InterPro; IPR003006; -
DR Pfam; PF00047; Ig; 1.
KW Immunoglobulin V region; Antiarrsonate antibody; Hybridoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.
FT NON_TER 140 140
SQ SEQUENCE 140 AA; 15514 MW; 25A4ACBBE31DA5CE8 CRC64;
Query Match 71.2%; Score 452; DB 1; Length 140;
Best Local Similarity 71.9%; Pred. No. 1.7e-38;
Matches 87; Conservative 15; Mismatches 15; Indels 4; Gaps 2;
QY 1 QIOLQSGPEVVKPGASVKISKASGYTFTDYITWVKQKPGGLEWIGWIPGSGNTKY 60

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Db 20 EVQLQSGAEIVRAGSSVKMSCKASGYTFYSGINWVKRPGGLEWIGVINGVINY 79
Qy 61 NEKFKGKATLVDTSSSTAFMQLSSLTSDTAVYFCA--NY--GNVWFAYWGQGTQVTVS 116
Db 80 NEKFKGKATLVDTSSSTAFMQLSSLTSDTAVYFCA--NY--GNVWFAYWGQGTQVTVS 139
Qy 117 A 117
Db 140 S 140

RESULT 5
HV13_MOUSE
ID HV13_MOUSE STANDARD; PRT; 117 AA.
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Cleveland B., Davie J.M., Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
RL rearrangements in heavy chain v-region gene segments.";
CC Nature 283:35-40(1980).
CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC WHICH OCCUR IN THE D AND J SEGMENTS.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR; A26242; MMS35.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; ig; 1.
KW Immunoglobulin V region.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match 71.0%; Score 451; DB 1; Length 117;
Best Local Similarity 71.8%; Pred. No. 1.8e-38;
Matches 84; Conservative 15; Mismatches 18; Indels 0; Gaps 0;

Qy 1 QIQLQSGPEVVKPGASVKISCKASGYTFDYITWVKRPGGLEWIGVINGVINGVINY 60
Db 1 EVQLQSGPELVKPGASVKMSCKASGYTFDYIMKWKQSHGKSLWIGDINPNNGTSTY 60
Qy 61 NEKFKGKATLVDTSSSTAFMQLSSLTSDTAVYFCA--NY--GNVWFAYWGQGTQVTVS 117
Db 61 NQKFKGKATLVDTSSSTAFMQLSSLTSDTAVYFCA--NY--GNVWFAYWGQGTQVTVS 117

RESULT 6
HV52_MOUSE
ID HV52_MOUSE STANDARD; PRT; 117 AA.
AC P06327;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION VH58 AL/A4 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85099340; PubMed=2578321;
RA Yancopoulos G.D., Alt F.W.;

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RT "Developmentally controlled and tissue-specific expression of
RL unrearranged VH gene segments.";
CC Cell 40:271-281(1985).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M13787; AAA38499.1; -.
DR PIR; A02029; HVMSAL.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH58 AL/A4.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12971 MW; 8B0BC138856DFC9D CRC64;

Query Match 71.0%; Score 451; DB 1; Length 117;
Best Local Similarity 85.8%; Pred. No. 1.8e-38;
Matches 83; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QIQLQSGPEVVKPGASVKISCKASGYTFDYITWVKRPGGLEWIGVINGVINGVINY 60
Db 20 QVQLQSGPELVKPGALVKISCKASGYTFDYINWVKRPGGLEWIGVINGVINGVINY 79
Qy 61 NEKFKGKATLVDTSSSTAFMQLSSLTSDTAVYFCA 97
Db 80 NEKFKGKATLVDTSSSTAFMQLSSLTSENSAVYFCA 116

RESULT 7
HV48_MOUSE
ID HV48_MOUSE STANDARD; PRT; 138 AA.
AC P03980;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION TEPC 1017 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84248078; PubMed=6429663;
RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA Tucker P.W.;
RT "Illegitimate recombination generates a class switch from C mu to C
RL delta in an IgD-secreting plasmacytoma.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR PIR; A02033; HVMS77.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 138 IG HEAVY CHAIN V REGION TEPC 1017.
FT DOMAIN 21 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.

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OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
FN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=81234548; PubMed=6788376;
RA	Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K., Baltimore D.;
RT	"Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region.";
RL	Cell 24:625-637(1981).
CC	-I- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC	MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL (NPB ANTIBODIES).
CC	-----
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CC	-----
CC	EMBL; J00539; AAA38172.1; -.
DR	PIR; A02038; G2MS43.
DR	InterPro; IPR003006; -.
DR	Pfam; PF00047; ig; 1.
KW	Immunoglobulin V region; Signal.
FT	SIGNAL
FT	CHAIN
FT	DOMAIN
FT	DOMAIN
FT	DOMAIN
FT	DOMAIN
FT	DOMAIN
FT	DOMAIN
FT	DOMAIN
FT	DISULFID
FT	NON_TER
SQ	SEQUENCE

Query Match		68.78; Score 436.5; DB 1; Length 137;		
Best Local Similarity		70.68; Pred. No. 5.8e-37;		
Matches		84; Conservative 12; Mismatches 20; Indels 3; Gaps 2;		
Qy	1	QIOLQSGPEVVKPGASVKISCKASGYTFTDYITWVKQPGQGLEWIGWYPCSGNTKY 60		
Db	20	QVQLQQGAEFVKPGASVKLSCKASGYTFTSYLHMVWNRQPRGLEWIGRIDPNSGGTTY 79		
Qy	61	NEKFKGKATLVTDTSSSTAFMQLSSLTSEDYAVYFCANY--GNWYFAYWGQGTQVTVSA 117		
Db	80	NEHFRSKATLTDKPSSTAYMQLSSLTSEDSAVYCYARYLGRY-FDYWGQGTTLTVSS 137		
RESULT 10				
ID	HV01_MOUSE	STANDARD;	PRT;	121 AA.
AC	P01745;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	IG HEAVY CHAIN V REGION MPC 11.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
FN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=81053741; PubMed=6253904;			
RA	Zakut R., Cohen J., Givol D.;			
RT	"Cloning and sequence of the cDNA corresponding to the variable			
RT	region of immunoglobulin heavy chain MPC11.";			


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RL Nucleic Acids Res. 8:3591-3601(1980).
RN [2]
RP REVISIONS.
RA Zakut R., Cohen J., Givol D.;
RL Nucleic Acids Res. 8:4839-4840(1980).
CC -I- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
CC FROM A MYELOMA THAT SECRETES IGG2B.
DR PIR: A02037; GVMS11.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig: 1.
KW Immunoglobulin V region.
FT NON_TER 121
SQ SEQUENCE 121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;

Query Match 67.2%; Score 427; DB 1; Length 121;
Best Local Similarity 67.2%; Pred. No. 4.6e-36;
Matches 82; Conservative 16; Mismatches 18; Indels 6; Gaps 2;

QY 1 QIQLOQSGPEVVKPGASVKISCKASGYTFDYITVWVKPGQGLEWIGWYIPGSGNTKY 60
DB 1 EAOLQSGAELVRPGTSVKISCAAGYTFNWIWGWKRPGRHGLEWIGDIYPPGGFTNY 60
QY 61 NEKFKGKATLTVDTSSTAFMQLSSTSEDTAVYFCANFY-----WFAWYWGQGTQVTV 115
DB 1 NDNLKGRATLTADTSSSTAYIQLSSTSEDSAIYHCAR-GIYNNSPYFDSWGQGTTLTV 119
QY 116 SA 117
DB 120 SS 121

RESULT 11
HV50_MOUSE
ID HV50_MOUSE STANDARD; PRT; 120 AA.
AC P06329;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION AC38 15.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR: A02037; MHWS15.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig: 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 105 D SEGMENT.
FT DOMAIN 106 120 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13311 MW; 914453F426F09834 CRC64;

Query Match 65.9%; Score 418.5; DB 1; Length 120;
Best Local Similarity 65.0%; Pred. No. 3.2e-35;
Matches 78; Conservative 17; Mismatches 22; Indels 3; Gaps 1;

QY 1 QIQLOQSGPEVVKPGASVKISCKASGYTFDYITVWVKPGQGLEWIGWYIPGSGNTKY 60
DB 1 EAOLQSGAELVRPGTSVKISCAAGYTFNWIWGWKRPGRHGLEWIGDIYPPGGFTNY 60
QY 61 NEKFKGKATLTVDTSSTAFMQLSSTSEDTAVYFCANFY-----GNYWFAWYWGQGTQVTVSA 117
DB 1 NDNLKGRATLTADTSSSTAYIQLSSTSEDSAIYHCAR-GIYNNSPYFDSWGQGTTLTV 119

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DB 61 NEKFKSKATLTVDKSSSATYMQLSPTSDSAVYICARWDYEGDRYFDVWGTGTTVTSS 120

RESULT 12
HV15_MOUSE
ID HV15_MOUSE STANDARD; PRT; 136 AA.
AC P01759;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION BCL1 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82222252; PubMed=6806821;
RA Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
RA Blattner F.R.;
RT "Simultaneous expression of immunoglobulin mu and delta heavy chains
RT by a cloned B-cell lymphoma: a single copy of the VH gene is shared
RL by two adjacent CH genes.";
CC Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
CC
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CC
CC EMBL: J00494; AAA38130.1; -.
CC PIR: A02042; HVMSB1
CC InterPro: IPR003006; -.
CC Pfam: PF00047; Ig: 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 136 IG HEAVY CHAIN V REGION BCL1.
FT NON_TER 136 136
SQ SEQUENCE 136 AA; 15078 MW; 6827CFBC6DB3F35E CRC64;

Query Match 65.4%; Score 415; DB 1; Length 136;
Best Local Similarity 68.6%; Pred. No. 8.2e-35;
Matches 81; Conservative 13; Mismatches 22; Indels 2; Gaps 2;

QY 1 QIQLOQSGPEVVKPGASVKISCKASGYTFDYITVWVKPGQGLEWIGWYIPGSGNTKY 60
DB 20 QVQLQSGPEVVRPGVSVKISCKSGSYTFDYAMHWKQSHAKSLEWIGVISTYNGNTSY 79
QY 61 NEKFKGKATLTVDTSSTAFMQLSSTSEDTAVYFCANFY-----YGYWFAWYWGQGTQVTVSA 117
DB 80 NOKFKGKATMTVDKSSSTVHMLARLTSEDSANLYCARYGNY-FDYWGQGTTLTVSS 136

RESULT 13
HV09_MOUSE
ID HV09_MOUSE STANDARD; PRT; 117 AA.
AC P01753; P11271;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 186-1 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;

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Fri Jun 29 08:04:40 2001

us-09-724-406-2.rsp

RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.,
RT "Heavy chain variable region contribution to the Npb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region."
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
DR PIR: B02034; HVMS61.
DR InterPro: IPR003006; -
DR Pfam: PF00047; Ig: 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 186-1.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12890 MW; 16191A088CB17F5A CRC64;

Query Match 64.9%; Score 412; DB 1; Length 117;
Best Local Similarity 79.4%; Pred. No. 1.4e-34;
Matches 77; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

QY 1 QIQLOQSGPEVVKPGASVKISCKASGYTFTDYITWVKRPGQGLEWIGWYPGSGNTKY 60
DB 20 QVLOQPGAEIVKPGASVKISCKASGYTFTSYMMHWVKRPGQGLEWIGRIDPNSSGTTY 79
QY 61 NEKFKGKATLTVDTSSTAFMQLSLTSEDVAVYCA 97
DB 80 NEKFKGKATLTVDTSSTAFMQLSLTSEDVAVYCA 116

RESULT 14
HV06_MOUSE STANDARD; PRT; 117 AA.
AC P01750;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 102 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.,
RT "Heavy chain variable region contribution to the Npb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region."
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
DR PIR: A02032; HVMS02.
DR InterPro: IPR003006; -
DR Pfam: PF00047; Ig: 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 102.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12867 MW; 740A65DD851FCA8C CRC64;

Query Match 63.8%; Score 405; DB 1; Length 117;
Best Local Similarity 77.1%; Pred. No. 7e-34;
Matches 74; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

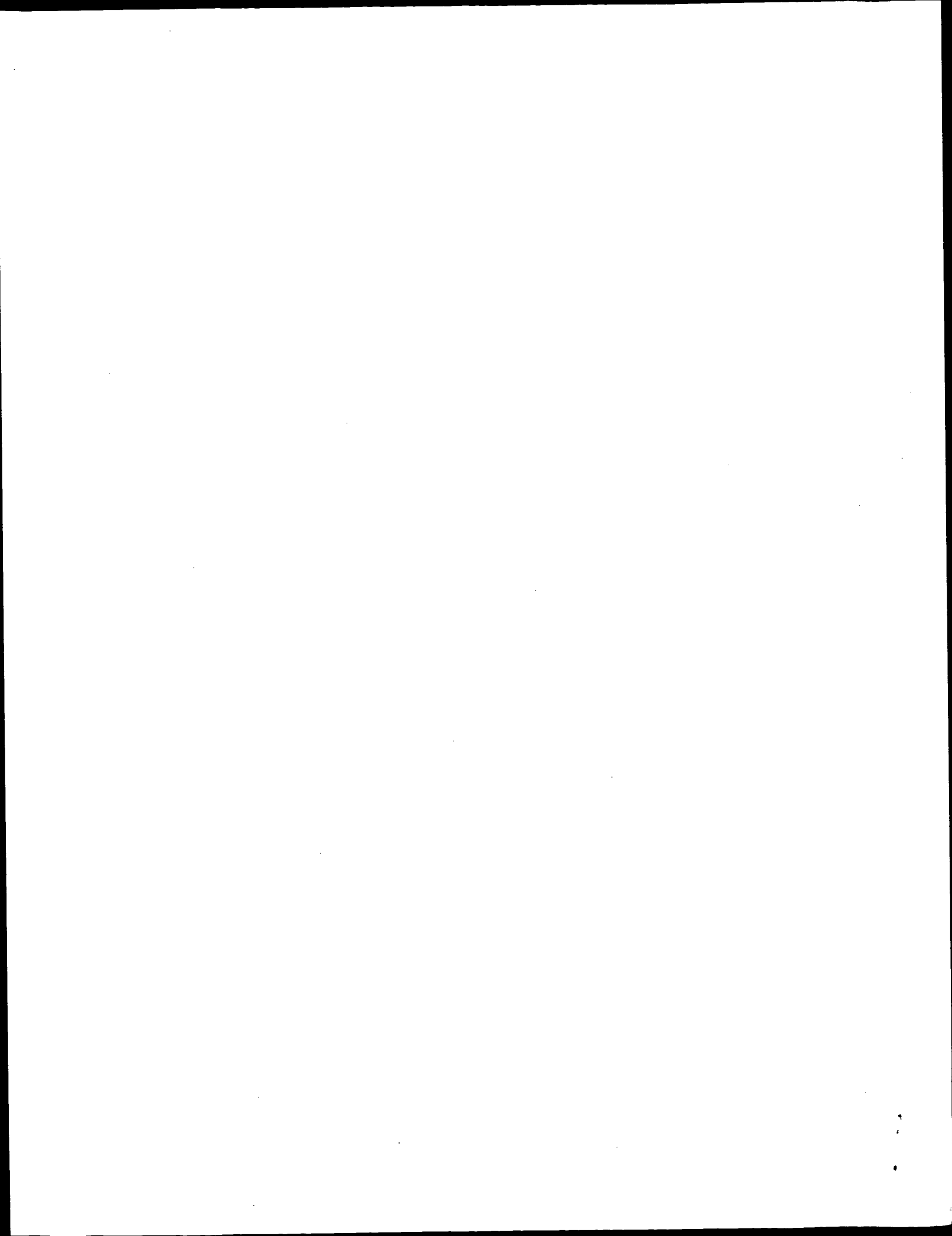
QY 2 IQLOQSGPEVVKPGASVKISCKASGYTFTDYITWVKRPGQGLEWIGWYPGSGNTKY 61
DB 21 VLOQPGAEIVKPGASVKISCKASGYTFTSYMMHWVKRPGQGLEWIGRIDPNSSGTTY 80
QY 62 EKFEGKATLTVDTSSTAFMQLSLTSEDVAVYCA 97
DB 81 QKFKGKATLTVDKSSSTAYMQLSLTSEDVAVYCA 116

RESULT 15
HV14_MOUSE STANDARD; PRT; 117 AA.
AC P01758;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 108A PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81245215; PubMed=6789211;
RA Givol D., Zakut R., Efron K., Rechavi G., Ram D., Cohen J.B.,
RT "Diversity of germ-line immunoglobulin VH genes."
RL Nature 292:426-430(1981).
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CC -----
CC EMBL: J00488; AAA38519.1; -
DR PIR: A02041; HVMS8A.
DR InterPro: IPR003006; -
DR Pfam: PF00047; Ig: 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 108A.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12972 MW; 428CB44DF25D1BC2 CRC64;

Query Match 63.8%; Score 405; DB 1; Length 117;
Best Local Similarity 77.3%; Pred. No. 7e-34;
Matches 75; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 1 QIQLOQSGPEVVKPGASVKISCKASGYTFTDYITWVKRPGQGLEWIGWYPGSGNTKY 60
DB 20 EVLOQSGPELVKPGASVKISCKASGYTFTDYNMHWVKRPGQGLEWIGYIYPNGTGY 79
QY 61 NEKFKGKATLTVDTSSTAFMQLSLTSEDVAVYCA 97
DB 80 NQKFKSKATLTVDNSSSTAYMQLSLTSEDVAVYCA 116

Search completed: June 18, 2001, 15:30:28
Job time: 91 sec



Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	470	74.0	117	11	Q9QXF0	Q9qxf0 mus musculus
2	460	72.4	117	11	Q9QXE9	Q9qxe9 mus musculus
3	434.5	68.4	109	11	Q9JL75	Q9jl75 mus musculus
4	434.5	68.4	118	11	Q9Z1C4	Q9z1c4 mus musculus
5	424.5	66.9	110	11	Q9JL83	Q9jl83 mus musculus
6	420	66.1	119	4	Q9JL94	Q9jl94 homo sapien
7	419.5	66.1	110	11	Q9JL77	Q9jl77 mus musculus
8	417	65.7	117	11	Q9Z1C6	Q9z1c6 mus musculus
9	411.5	64.8	114	11	Q9JL81	Q9jl81 mus musculus
10	404	63.6	119	5	Q9GZ22	Q9gz22 schistosoma
11	401.5	63.2	124	4	Q9JL92	Q9jl92 homo sapien
12	394	62.0	125	4	Q9JL95	Q9jl95 homo sapien
13	384	60.5	109	11	Q9JL85	Q9jl85 mus musculus
14	377.5	59.4	116	4	Q9JL89	Q9jl89 homo sapien
15	365	57.5	157	4	Q9S978	Q9s978 homo sapien
16	353	55.6	150	4	Q9Y298	Q9y298 homo sapien
17	343	54.0	102	11	Q9JL79	Q9jl79 mus musculus
18	338	53.2	119	4	Q9JL73	Q9jl73 homo sapien
19	320.5	50.5	298	11	Q9GVF0	Q9gvf0 mus musculus

RESULT 2
Q9QXE9
ID Q9QXE9 PRELIMINARY;
PRT: 117 AA.

Q90X99; 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Clemens A., Rademakers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ225174; CAB65237.1; -
DR InterPro; IPR003006; -
DR InterPro; IPR003596; -
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1 117
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13000 MW; CDDE2AF84D499734 CRC64;

Query Match 72.4%; Score 460; DB 11; Length 117;
Best Local Similarity 73.5%; Pred. No. 2.5e-40;
Matches 86; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

QY 1 QIQLQSGPEVVKPGASVKISKASGYFTDYITWVKQKPGQGLEWIGWYPGSGNTKY 60
Db 1 EVQLQSGPELVKPGASVKMSKASGYFTDYIMKWKQSHGKSLKLEIDINPNNGTSY 60

QY 61 NEKFKGKATLTVDTSSTAFMQLSLTSEDYAVFCANYGYWYFAYWGQGTQVTVSA 117
Db 61 NQKFKGKATLTVDKSSSTAYMQLSLTSEDSAVYICARDRIYAMDYWGQGTSTVSS 117

RESULT 3
Q9JL75 PRELIMINARY; PRT; 109 AA.
ID Q9JL75
AC Q9JL75
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
acetyl-glucosamine antibodies from mice with autoimmune myocarditis."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF206031; AAF69329.1; -
DR InterPro; IPR003006; -
DR InterPro; IPR003596; -
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1 109
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 12118 MW; FF65E441BBF936A6 CRC64;

Query Match 68.4%; Score 434.5; DB 11; Length 109;
Best Local Similarity 76.1%; Pred. No. 1e-37;
Matches 83; Conservative 11; Mismatches 14; Indels 1; Gaps 1;

QY 10 EVVKPGASVKISKASGYFTDYITWVKQKPGQGLEWIGWYPGSGNTKYNEKFKGKAT 69
Db 1 ELVKPGASVKMSKASGYFTSYVHWVWVKQKPGQGLEWIGYINPYNDGTYNEKFKGKAT 60

QY 70 LTVDTSSSTAFMQLSLTSEDYAVFCANYGYWYFAYWGQGTQVTVSA 117
Db 61 LNSDKSSSTAYMQLSLTSEDSAVYICARDGNYRGFDYWGQGTTLTVSS 109

RESULT 4
Q921C4 PRELIMINARY; PRT; 118 AA.
ID Q921C4
AC Q921C4
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE ANTI-PORCINE VCAM MAB 3F4 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RA Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RA Matis L.M., Evans M.J.;
RT "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
IgG2/G4 constant regions block human leukocyte binding to porcine
endothelial cells."
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN
CC EMBL; U78801; AAD00293.1; -
DR InterPro; IPR003006; -
DR InterPro; IPR003596; -
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1 118
FT NON_TER 118 118
SQ SEQUENCE 118 AA; 13036 MW; 90BEC559D31EC4FC CRC64;

Query Match 68.4%; Score 434.5; DB 11; Length 118;
Best Local Similarity 68.1%; Pred. No. 1.1e-37;
Matches 81; Conservative 16; Mismatches 19; Indels 3; Gaps 2;

QY 1 QIQLQSGPEVVKPGASVKISKASGYFTDYITWVKQKPGQGLEWIGWYPGSGNTKY 60
Db 1 QVQVQSGAELARPWASVKLSKASGYFTDYIMKWKQSHGKSLKLEIDINPNNGTSY 60

QY 61 NEKFKGKATLTVDTSSTAFMQLSLTSEDYAVFCANYGYWYFAYWGQGTQVTVSA 117
Db 61 TQKFRGKATLTADKSSSTAYMQLSLTSEDSAVYICARRTVGGY-EDYWGQGTTLTVSS 118

RESULT 5
Q9JL83 PRELIMINARY; PRT; 110 AA.
ID Q9JL83
AC Q9JL83
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
acetyl-glucosamine antibodies from mice with autoimmune myocarditis."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF206023; AAF69321.1; -
DR InterPro; IPR003006; -
DR InterPro; IPR003596; -

DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Igv; 1.
FT NON_TER 110 110
SQ SEQUENCE 110 AA; 12052 MW; 84E6F2AD219AF95E CRC64;

Query Match 66.9%; Score 424.5; DB 11; Length 110;
Best Local Similarity 74.1%; Pred. No. 1.1e-36;
Matches 83; Conservative 10; Mismatches 14; Indels 5; Gaps 2;
QY 9 PEVAPGASVKISCKASGYTFDYITVWKQPGQGLEWIGWYPSGNTKYNEKFKGKA 68
Db 1 PELVRPGASVKISCKASGYTFSSNMWVVKLPQGGLEWIGRIYPCGDAYNGKFKGKA 60
QY 69 TLTVTSSTAPFQWLSLSTSDTAVYFCANYGNYW---FAYWGGGTQVTVSA 117
Db 61 TLTVTSSTAPFQWLSLSTSDTAVYFCAR--SNWDVRFAYWGGGTQVTVSA 110

RESULT 6

Q9UL94 PRELIMINARY; PRT; 119 AA.
AC Q9UL94;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.
DR EMBL: AF035020; AAD56256.1; -.
DR InterPro: IPR003006; -.
DR InterPro: IPR003596; -.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Igv; 1.
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13205 MW; 13E64F5345F4A16E CRC64;

Query Match 66.1%; Score 420; DB 4; Length 119;
Best Local Similarity 65.5%; Pred. No. 3.6e-36;
Matches 78; Conservative 15; Mismatches 24; Indels 2; Gaps 1;

QY 1 QIOLQSGPEVVKPGASVKISCKASGYTFDYITVWKQPGQGLEWIGWYPSGNTKY 60
Db 1 EVQLVESGAEVKKPGASVKVSKASGYTFGTGYMHVVRQAPGQGLEWGNPNSTNY 60
QY 61 NEKFKGKATLVDTSSSTAPFQWLSLSTSDTAVYFCANYG--NYWFAWGGGTQVTVSA 117
Db 61 AQKFGKVTWKDTSISTAYMELSLRLSDDTAVYFCARGGGLWFDWPGGGLTVTVSS 119

RESULT 7

Q9JL77 PRELIMINARY; PRT; 110 AA.
AC Q9JL77;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-DBA/2;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-acetyl-glucosamine antibodies from mice with autoimmune myocarditis";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF206029; AAR69327.1; -.
DR InterPro: IPR003006; -.
DR InterPro: IPR003596; -.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Igv; 1.
FT NON_TER 110 110
SQ SEQUENCE 110 AA; 12138 MW; 2EDE81FB5862C9AF CRC64;

Query Match 66.1%; Score 419.5; DB 11; Length 110;
Best Local Similarity 73.1%; Pred. No. 3.7e-36;
Matches 79; Conservative 13; Mismatches 15; Indels 1; Gaps 1;

QY 11 VVKPGASVKISCKASGYTFDYITVWKQPGQGLEWIGWYPSGNTKYNEKFKGKATL 70
Db 3 LVRPGASVKISCKASGYTFSSNMWVVKLPQGGLEWIGRIYPCGDAYNGKFKGKA 62
QY 71 TVDTSSSTAPFQWLSLSTSDTAVYFCANY--GNTWFAWGGGTQVTVSA 117
Db 63 TVDTSSSTAPFQWLSLSTSDTAVYFCAR--GNTWFAWGGGTQVTVSA 110

RESULT 8

Q9Z1C6 PRELIMINARY; PRT; 117 AA.
AC Q9Z1C6;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ANTI-PORCINE VCAM MAB 2A2 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RA Mueller J.P., Glannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RA Matis L.M., Evans M.J.;
RT "Humanized porcine VCAM-specific monoclonal antibodies with chimeric IgG2/G4 constant regions block human leukocyte binding to porcine endothelial cells";
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.
DR EMBL: U78799; AAD00291.1; -.
DR InterPro: IPR003006; -.
DR InterPro: IPR003596; -.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Igv; 1.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13122 MW; 4F65B193AFB77E5B CRC64;

Query Match 65.7%; Score 417; DB 11; Length 117;
Best Local Similarity 65.8%; Pred. No. 7.1e-36;
Matches 77; Conservative 14; Mismatches 26; Indels 0; Gaps 0;

QY 1 QIOLQSGPEVVKPGASVKISCKASGYTFDYITVWKQPGQGLEWIGWYPSGNTKY 60
Db 1 EVQLVESGAEVKKPGASVKVSKASGYTFGTGYMHVVRQAPGQGLEWGNPNSTNY 60

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -|- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
DR EMBL: AF035C19; AAD56255.1; -.
DR InterPro: IPR003006; -.
DR InterPro: IPR003596; -.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 125 125
SQ SEQUENCE 125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;

Query Match 62.0%; Score 394; DB 4; Length 125;
Best Local Similarity 59.2%; Pred. No. 1.8e-33;
Matches 74; Conservative 17; Mismatches 26; Indels 8; Gaps 1;

Qy 1 QIOLQSGPVPKPGASVKISCKASGYTFTDYITWVKQPGQGLEWIGWYPGSGNTRY 60
Db 1 EVQLVSGAEVKPGASVKVSKASGYTFTGYMHVVRAPQGLEWGWNPNSGGIN 60

Qy 61 NEKFKGKATLVDTSSSTAFMQLSSLTSEDYAVYFCAN-----YGNWYAYWGQGTQ 112
Db 61 AOKVQGVWTRDTTSTAYMELSLRSDYAVYCARSGGGRIAAAGDAFDWQGTG 120

Qy 113 VTVSA 117
Db 121 VTSS 125

RESULT 13
Qy 13
ID Q9JL85 PRELIMINARY; PRT; 109 AA.
AC Q9JL85;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C.
RA Makiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF206021; AAF69319.1; -.
DR InterPro: IPR003006; -.
DR InterPro: IPR003596; -.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11944 MW; DFE615FE6CED4EDE CRC64;

Query Match 60.5%; Score 384; DB 11; Length 109;
Best Local Similarity 65.7%; Pred. No. 1.7e-32;
Matches 71; Conservative 17; Mismatches 20; Indels 0; Gaps 0;

Qy 10 EVVKGASVKISCKASGYTFTDYITWVKQPGQGLEWIGWYPGSGNTRYNEKFKCAT 69
Db 2 ELVKGASVKLSCTASGFNIEDTYMHVVKQRPQGLEWIGRIDPATGSKYDPKFGKAT 61

Qy 70 LTVDTSSSTAFMQLSSLTSEDYAVYFCANYGWYAYWGQGTQTVTSA 117
Db 62 ITSDTSSNTAYLQLSSLTSEDYAVYCYVRGAVFDYWGQGTALTVSS 109

RESULT 14
Qy 14
ID Q9JL89 PRELIMINARY; PRT; 116 AA.
AC Q9JL89;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -|- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
DR EMBL: AF035025; AAD56261.1; -.
DR InterPro: IPR003006; -.
DR InterPro: IPR003596; -.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12605 MW; C8F9131DE13EA898 CRC64;

Query Match 59.4%; Score 377.5; DB 4; Length 116;
Best Local Similarity 63.5%; Pred. No. 8.6e-32;
Matches 73; Conservative 17; Mismatches 22; Indels 3; Gaps 2;

Qy 6 QSGDEVKPGASVKISCKASGYTFTDYITWVKQPGQGLEWIGWYPGSGNTRYNEKFK 65
Db 2 QSGAEVKPGASVKISCKASGYTFTDYITWVKQPGQGLEWIGWYPGSGNTRYNEKFK 61

Qy 66 GKATLVDTSSSTAFMQLSSLTSEDYAVYFCAN--NYGNWYAYWGQGTQTVTSA 117
Db 62 GRVITADKSTAYMELSSLTSEDYAVYFCASSNMGWYFVLDLWGRGTLTVTSS 116

RESULT 15
Qy 15
ID Q95978 PRELIMINARY; PRT; 157 AA.
AC Q95978;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE VH1 PROTEIN PRECURSOR (FRAGMENT).
GN VH1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-PERIPHERAL BLOOD;
RA Jox A., Zander T., Kueppers R., Irsch J., Kanzler H., Kornacker M.,
RA Bohlen H., Diehl V., Wolf J.;

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OM protein - protein search, using sw model

Run on: June 28, 2001, 15:52:32 ; Search time 362.28 Seconds
(without alignments)
0.837 Million cell updates/sec

Title: US-09-724-406-4
Perfect score: 29
Sequence: 1 DVTIT 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_0601.*

- 1: /SID58/gcgdata/geneseq/geneseq/AA1981.DAT.*
- 2: /SID58/gcgdata/geneseq/geneseq/AA1981.DAT.*
- 3: /SID58/gcgdata/geneseq/geneseq/AA1982.DAT.*
- 4: /SID58/gcgdata/geneseq/geneseq/AA1983.DAT.*
- 5: /SID58/gcgdata/geneseq/geneseq/AA1984.DAT.*
- 6: /SID58/gcgdata/geneseq/geneseq/AA1985.DAT.*
- 7: /SID58/gcgdata/geneseq/geneseq/AA1986.DAT.*
- 8: /SID58/gcgdata/geneseq/geneseq/AA1987.DAT.*
- 9: /SID58/gcgdata/geneseq/geneseq/AA1988.DAT.*
- 10: /SID58/gcgdata/geneseq/geneseq/AA1989.DAT.*
- 11: /SID58/gcgdata/geneseq/geneseq/AA1990.DAT.*
- 12: /SID58/gcgdata/geneseq/geneseq/AA1991.DAT.*
- 13: /SID58/gcgdata/geneseq/geneseq/AA1992.DAT.*
- 14: /SID58/gcgdata/geneseq/geneseq/AA1993.DAT.*
- 15: /SID58/gcgdata/geneseq/geneseq/AA1994.DAT.*
- 16: /SID58/gcgdata/geneseq/geneseq/AA1995.DAT.*
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- 18: /SID58/gcgdata/geneseq/geneseq/AA1997.DAT.*
- 19: /SID58/gcgdata/geneseq/geneseq/AA1998.DAT.*
- 20: /SID58/gcgdata/geneseq/geneseq/AA1999.DAT.*
- 21: /SID58/gcgdata/geneseq/geneseq/AA2000.DAT.*
- 22: /SID58/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	29	100.0	346 15 AAR55059	Elk tyrosine kinases
2	29	100.0	346 16 AAR82606	Eph transmembrane
3	29	100.0	346 17 AAR91930	Human cytokine elk
4	29	100.0	346 18 AAW36055	Human elk-L protei
5	29	100.0	346 18 AAW19249	Human elk ligand p
6	29	100.0	346 19 AAW44323	Human elk-L. Homo
7	29	100.0	683 21 AAY96781	Ephrin-B1-Ephrin-B
8	29	100.0	706 18 AAW31199	Bacillus popilliae
9	28	96.6	173 16 AAR71930	Zag gene FAM bindi
10	28	96.6	200 22 AAB63700	Human gastric canc
11	28	96.6	254 21 AAG42791	Arabidopsis thalia

12	28	96.6	255	21	AAG42790	Arabidopsis thalia
13	28	96.6	328	21	AAG42789	Arabidopsis thalia
14	28	96.6	515	21	AAB10981	H. tuberculata hem
15	27	93.1	101	21	AAY93885	Amino acid sequenc
16	27	93.1	177	19	AAW48849	Mouse receptor tyr
17	27	93.1	197	21	AAB42709	Human ORFX ORF2473
18	27	93.1	275	19	AAW48847	Rat receptor tyros
19	27	93.1	398	20	AAW37578	Amino acid sequenc
20	27	93.1	472	19	AAW48848	Human receptor tyr
21	26	89.7	120	13	AAR27497	WNI 222-5 antibody
22	26	89.7	120	13	AAR27498	WNI 58-9 antibody
23	26	89.7	124	17	AAR90831	2B5 heavy chain va
24	25	86.2	58	22	AAB59288	Beta4Gal-T1 protei
25	25	86.2	76	21	AAB39058	Human secreted pro
26	25	86.2	116	17	AAW03742	Murine monoclonal
27	25	86.2	123	18	AAW28331	Staphylococcus aur
28	25	86.2	142	19	AAY85892	S. pneumoniae deri
29	25	86.2	154	21	AAY91476	Human secreted pro
30	25	86.2	162	13	AAR21140	Polypeptide encode
31	25	86.2	183	21	AAB18980	Amino acid sequenc
32	25	86.2	197	20	AAW92992	S. aureus MurB pro
33	25	86.2	207	21	AAY91632	Human secreted pro
34	25	86.2	208	12	AAR13210	Streptococcal pyro
35	25	86.2	208	14	AAR45018	Streptococcal ent
36	25	86.2	208	22	AAB67345	Streptococcus pyro
37	25	86.2	235	19	AAW62784	Streptococcus pyro
38	25	86.2	235	19	AAW62785	Mutant streptococc
39	25	86.2	235	19	AAW62786	Mutant streptococc
40	25	86.2	235	19	AAW62787	Mutant streptococc
41	25	86.2	235	19	AAW62788	Mutant streptococc
42	25	86.2	307	20	AAW92991	S. aureus MurB pro
43	25	86.2	307	21	AAY70128	Staphylococcus aur
44	25	86.2	326	22	AAW46973	S. aureus MurB pro
45	25	86.2	367	21	AAB40201	Gene 1 human secre

ALIGNMENTS

RESULT 1
AAR55059
ID AAR55059 standard; Protein; 346 AA.
XX
AC AAR55059;
XX
DT 28-JAN-1995 (first entry)
XX
DE Elk tyrosine kinase receptor ligand.
XX
KW Vectors; elk-L protein; elk; ligands; cell growth; differentiation.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..24
FT Protein /note= "signal peptide"
FT /note= "mature elk-L protein"

XX
PN WO9411384-A.
XX
PD 26-MAY-1994.
XX
PF 15-NOV-1993; 93WO-US10955.
XX
PR 13-NOV-1992; 92US-0977693.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Baum PR, Beckmann MP, Lyman S;
XX WPI, 1994-183415/22.
XX N-PSDB; AAQ65486.
DR

XX New DNA encoding ligand for elk tyrosine kinase receptor - also
 PT related polypeptides, vectors, antibodies and probes, useful e.g.
 PT in studying cell differentiation or growth
 XX
 PS Claim 7; Page 30; 35pp; English.
 XX
 CC The sequence is that of the elk-L protein able to bind elk, a
 CC tyrosine kinase receptor. The DNA may be incorporated into vectors
 CC which can be used to study the role of elk and its ligands in cell
 CC growth and differentiation.
 XX
 SQ Sequence 346 AA;

Query Match 100.0%; Score 29; DB 15; Length 346;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5
 DB 131 dyyit 135
 |||||

RESULT 2
 AAR82606
 ID AAR82606 standard; Protein; 346 AA.
 XX
 AC AAR82606;
 DT 16-MAY-1996 (first entry)
 XX
 DE Eph transmembrane tyrosine kinase family ligand, Efl-3.
 XX
 KW Efl-2; EHK1-L; Eph transmembrane tyrosine kinase family ligand;
 KW neurological disorder; identification; diagnosis.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..29
 FT Domain /label= signal_peptide
 FT /label= transmembrane_domain
 FT Misc-difference 159
 FT /note= "borders main conserved regions"
 XX
 PN WO9527060-A2.
 XX
 PD 12-OCT-1995.
 XX
 PF 04-APR-1995; 95WO-US04208.
 XX
 PR 21-OCT-1994; 94US-0327423.
 PR 04-APR-1994; 94US-0222075.
 PR 12-APR-1994; 94US-0229402.
 PR 01-SEP-1994; 94US-0299567.
 XX
 PA (REG-) REGENERON PHARM INC.
 XX
 PI Aldrich TH, Davis S, Gale N, Goldfarb M, Maisonnier PC;
 PI Yancopoulos GD;
 XX
 WPI; 1995-358635/46.
 XX
 PT Ligands which bind Eph family receptors - used in the diagnosis of
 PT neurological disorders
 XX
 PS Disclosure; Fig 2; 58pp; English.
 XX
 CC Efl-3 (also known as EHK-L) is an Eph transmembrane tyrosine kinase
 CC family ligand. It has homology with B61 (Efl-1) and Efl-2. Efl-3
 CC appears to comprise a conventional transmembrane protein with a

CC cytoplasmic domain. Efl-3 is useful for identifying other ligands
 CC for Efl-1, -2, -3, Ecl and Elk receptors. The ligands are useful in
 CC promoting a differential function and/or influencing the phenotype,
 CC such as growth and/or proliferation, of receptor bearing cells. They
 CC may be used in the diagnosis, and treatment of neurological disorders.
 XX
 SQ Sequence 346 AA;

Query Match 100.0%; Score 29; DB 16; Length 346;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5
 DB 131 dyyit 135
 |||||

RESULT 3
 AAR91930
 ID AAR91930 standard; Protein; 346 AA.
 XX
 AC AAR91930;
 DT 11-DEC-1996 (first entry)
 XX
 DE Human cytokine elk-ligand (elk-L).
 XX
 KW Human; cytokine; elk-ligand; elk-L; tyrosine kinase receptor;
 KW neurotrophic; neuroprotective; placenta; radiolabelled probe;
 KW treatment; neural tissue; excitotoxicity; injury; disorder;
 KW neural culture reagent; immunogenic fragment; antibody.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..24
 FT /label= sig_peptide
 FT Peptide 25..346
 FT /label= mat_peptide
 XX
 PN US5512457-A.
 XX
 PD 30-APR-1996.
 XX
 PF 13-NOV-1992; 92US-0977693.
 XX
 PR 15-MAR-1994; 94US-0213403.
 PR 13-NOV-1992; 92US-0977693.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Baum PR, Beckmann MP, Carpenter MK, Lyman S;
 XX
 WPI; 1996-229866/23.
 DR N-PSDB; AAT28770.
 XX
 PT DNA coding for neurotrophic human elk ligand cytokine - useful as
 PT probe to isolate other elk ligand sequences
 XX
 PS Claim 1; Columns 27-30; 18pp; English.
 XX
 CC The present sequence is the human cytokine elk-ligand (elk-L),
 CC which binds a member of the tyrosine kinase receptor family. Elk-L
 CC exhibits neurotrophic and neuroprotective properties, and has a
 CC calculated mol. wt. 35180 daltons and a pI of 9.006. The elk-L
 CC cDNA, isolated from a human placental cDNA library, can be
 CC radiolabelled and used as a probe for isolating other mammalian
 CC elk-L cDNA. Elk-L can be used to treat neural tissue disorders,
 CC partic. excitotoxicity associated injuries or disorders, and as a
 CC neural culture reagent, while immunogenic fragments of elk-L can be
 CC used to generate specific anti-elk-L antibodies.

SQ Sequence 346 AA;

Query Match 100.0%; Score 29; DB 17; Length 346;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYVIT 5
|
|
|
|
Db 131 dyvit 135

RESULT 4

AAW36055
ID AAW36055 standard; Protein; 346 AA.

XX AC AAW36055;

XX DT 06-MAR-1998 (first entry)

XX DE Human elk-L protein.

XX KW Human; elk-L; cytokine; ligand; tyrosine kinase receptor; fusion protein;
XX KW extracellular domain; immunoglobulin; neurological disease.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Peptide 1..24

XX FT Protein /note= "signal peptide"

XX FT Domain 25..346

XX FT Domain 25..237

XX FT Domain /note= "extracellular domain; this region is used to
generate a fusion protein with the Fc portion
of the human immunoglobulin G1"

XX FT Domain 238..265

XX FT Domain /note= "transmembrane domain"

XX FT Domain 266..346

XX FT Modified-site /note= "intracellular domain"

XX FT Cleavage-site 139..141

XX FT Cleavage-site /note= "Asn is N-glycosylated"

XX FT Cleavage-site 266..267

XX FT Cleavage-site /note= "KEX2 protease cleavage site"

XX FT Cleavage-site 267..268

XX FT Cleavage-site /note= "KEX2 protease cleavage site"

XX FT Cleavage-site 270..271

XX FT Cleavage-site /note= "KEX2 protease cleavage site"

XX PN US5670625-A.

XX PD 23-SEP-1997.

XX XX 02-JUN-1995; 95US-0460741.

XX XX 15-MAR-1994; 94US-0213403.

XX XX 13-NOV-1992; 92US-0977693.

XX XX 02-JUN-1995; 95US-0460741.

XX PA (IMMV) IMMUNEX CORP.

XX PI Baum PR, Beckmann MP, Lyman S;

XX DR WPI; 1997-479524/44.

XX DR N-PSDB; AAT97976.

XX FT Soluble fusion proteins of human elk-L ligand and Fc immunoglobulin
XX FT fragment - and their dimers and oligomers, useful as
XX FT neuro-protectants and neurotrophic agents

XX PS Claim 1; Columns 27-30; 18pp; English.

XX XX This is the amino acid sequence of the human elk-L protein, a new

CC cytokine that is the ligand for the elk tyrosine kinase receptor. The
CC extracellular domain of the protein (amino acids 1-213) is used to
CC generate a fusion protein comprising the Fc polypeptide of the human
CC immunoglobulin G1 (extending from the hinge region to the C-terminus).
CC The fusion protein (which has the same activities as the natural elk-L
CC protein) has neuroprotective and neurotrophic activity so is potentially
CC useful for treating a wide range of neurological diseases.
XX SQ Sequence 346 AA;

Query Match 100.0%; Score 29; DB 18; Length 346;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYVIT 5
|
|
|
|
Db 131 dyvit 135

RESULT 5

AAW19249

ID AAW19249 standard; Protein; 346 AA.

XX AC AAW19249;

XX DT 18-AUG-1997 (first entry)

XX DE Human elk ligand protien.

XX KW Human; elk; ligand; elk-L; cytokine; testing; measuring;

XX KW purification; neuroprotection; treatment; diabetic; hereditary;

XX KW nutritional; neuropathy; neurodegenerative disease;

XX KW tissue culture.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Peptide 1..24

XX FT Peptide /label= sig_peptide

XX FT Peptide 25..346

XX FT Peptide /label= mat_peptide

XX PN US5627267-A.

XX PD 06-MAY-1997.

XX XX 13-NOV-1992; 92US-0977693.

XX XX 15-MAR-1994; 94US-0213403.

XX XX 13-NOV-1992; 92US-0977693.

XX XX 01-JUN-1995; 95US-0458077.

XX PA (IMMV) IMMUNEX CORP.

XX PI Baum PR, Beckmann MP, Lyman S;

XX XX WPI; 1997-271366/24.

XX DR N-PSDB; AAT69766.

XX FT Human elk ligand protein - for diagnostic or therapeutic use, e.g.
XX FT as neuro-protective agent

XX PS Claim 1; Columns 29-32; 18pp; English.

XX XX The present sequence is a human elk ligand (elk-L) protein,
XX CC which binds elk, has a calculated molecular weight of 35180 and an
XX CC isoelectric point of 9.006. Elk-L is a cytokine that can be used to
XX CC test cells for elk expression, measure the biological activity of
XX CC elk, purify elk by affinity chromatography and as a neuroprotective
XX CC agent to treat diabetic, hereditary and nutritional neuropathies
XX CC and neurodegenerative diseases. It may also be added to tissue
XX CC cultures to prolong the life of neurons. The elk-L cDNA was

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Isolated from a human placental cDNA library, and is present as a
 CC cDNA insert in the recombinant vector deposited in strain
 CC ATCC 69085.
 XX
 XX
 SQ Sequence 346 AA;

Query Match 100.0%; Score 29; DB 18; Length 346;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5
 |||||
 Db 131 dyyit 135

RESULT 6
 AAW44323
 ID AAW44323 standard; Protein; 346 AA.
 XX
 AC AAW44323;
 XX
 DT 27-MAY-1998 (first entry)
 XX
 DE Human elk-L.

XX Human; elk-L; elk ligand; cytokine; antibody; cell surface receptor;
 KW tyrosine kinase receptor; neural disease; trophic mechanism.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..24
 FT /label= signal
 FT Protein 25..346
 FT /label= elk-L

US5728813-A.

17-MAR-1998.

12-NOV-1996; 96US-0747240.

15-MAR-1994; 94US-0213403.

13-NOV-1992; 92US-0977693.

02-JUN-1995; 95US-0460741.

12-NOV-1996; 96US-0747240.

(IMMV) IMMUNEX CORP.

Baum PR, Beckmann MP, Lyman S;

WPI; 1998-206621/18.

N-PSDB; AAV15226.

Antibodies to elk ligand polypeptides - bind to tyrosine kinase

receptors, useful for treating neural disease

Claim 1; Column 31-32; 17pp; English.

XX The present sequence represents human elk-L (elk ligand). The present
 CC invention describes antibodies to elk-L polypeptides. The elk-L protein
 CC is known to be neuroprotective exhibiting its effect through a trophic
 CC mechanism. Examples of diseases that may be treated with elk-L include
 CC neuropathies e.g. diabetic, hereditary and nutritional neuropathies,
 CC neurodegenerative diseases and other diseases characterised by loss of
 CC function or degeneration of neurons.

Sequence 346 AA;

Query Match 100.0%; Score 29; DB 19; Length 346;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;

RESULT 7

AA96781
 ID AA96781 standard; Protein; 683 AA.
 XX
 AC AA96781;
 XX
 DT 26-SEP-2000 (first entry)
 XX
 DE Ephrin-B1-Ephrin-B1-FC fusion protein.

XX Ephrin-B1; ELK receptor; ligand; dimer; Fc domain; fusion protein;
 KW Efl-6 antagonist; neurological.
 XX
 OS Chimeric - Homo sapiens.
 OS Chimeric - Synthetic.

XX Key Location/Qualifiers

FT Peptide 1..29
 FT /label= Signal_peptide
 FT /note= "derived from ELK-L Ectodomain 1"
 FT Protein 30..237
 FT /label= ELK-L_ectodomain_1
 FT Peptide 238..240
 FT /label= Bridging_peptide
 FT Protein 241..448
 FT /label= ELK-L_Ectodomain_2
 FT Peptide 449..451
 FT /label= Bridging_peptide
 FT Region 452..683
 FT /label= Human_IgG1_Fc_region

WO200037642-A1.

29-JUN-2000.

23-DEC-1999; 99WO-US30900.

23-DEC-1998; 98US-0113387.

(REGE-) REGENERON PHARM INC.

Davis SJ, Gale NW, Yancopoulos GD, Stahl N;

WPI; 2000-442670/38.

N-PSDB; AAA51345.

Polynucleotide encoding a fusion polypeptide, useful for promoting
 differential function and influencing phenotype, comprises two subunits
 containing at least one copy of the receptor binding domain of a ligand

Example 12; Fig 14A-E; 97pp; English.

XX Production of homogenous forms of clustered ligands is broadly applicable
 CC to improve the affinity and/or increase the activity of a ligand as
 CC compared to the native form of the ligand. Ephrin fusion proteins have
 CC been constructed, which may be useful for treating neurological
 CC disorders. The ephrin fusion proteins are preferably capable of binding
 CC to ELK receptor and are especially Efl-6 antagonists. The fusion proteins
 CC were constructed after it was demonstrated that similar improved
 CC activities could be achieved using Tie-2 receptor ligands.
 CC Angiopoietin-1 (Ang-1) is a Tie-2 receptor ligand and is an agonist for
 CC Tie-2, whereas angiopoietin-2 (Ang-2) is a naturally occurring antagonist
 CC of the Tie-2 receptor. The fibronectin domains (FD) of Ang-1 and Ang-2 are
 CC the receptor-binding domains and dimerized versions, of e.g. Ang-1-FD-Fc
 CC (Ang-1 fibronectin domain fused to an Fc domain), can bind to the Tie-2
 CC receptor with much higher affinity than monomeric Ang-1-FD (dimerization

CC occurs between the Fc components of adjacent molecules). However,
 CC Ang-1-FD-Fc is not able to induce phosphorylation (activate) the Tie-2
 CC receptor on endothelial cells unless it is further clustered with goat
 CC anti-human Fc antibodies. The novel fusion proteins, mutant versions of
 CC Ang-1-FD and Ang-2-FD, were designed that were intrinsically more highly
 CC clustered. Tie-2 agonist fusion proteins may be used as haematopoietic
 CC factors. Tie-2 receptor antagonist fusion proteins may be used to
 CC diagnose or treat, e.g. myeloproliferative or other proliferative
 CC disorders of blood forming organs, e.g. thrombocythemias, polycythemia
 CC and leukemias.

XX Sequence 583 AA;

Query Match 100.0%; Score 29; DB 21; Length 583;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYVIT 5
 Db 131 dyvit 135
 |||||

RESULT 8
 AAW31199
 ID AAW31199 standard; Protein; 706 AA.

XX AC AAW31199;

XX DT 13-FEB-1998 (first entry)

XX DE Bacillus popilliae crystal protein.

XX KW Crystal protein; beetle; Scarabaeidae; maybug; cockchafer;
 XX KW agricultural pest; spore; Bacillus thuringiensis; cytolysing protein;
 XX KW fusion protein; transgenic plant.

XX OS Bacillus popilliae.

XX FH Key Location/Qualifiers
 XX FT Protein 1..706
 XX FT /label= crystal protein

XX PN DE19642729-A1.

XX PD 24-APR-1997.

XX PF 17-OCT-1996; 96DE-1042729.

XX PR 18-OCT-1995; 95DE-1040223.

XX PA (UVHE-) UNIV HEIDELBERG.

XX PI Krieger L, Schnetter W, Zhang J;

XX DR WPI; 1997-237512/22.

XX DR N-PSDB; AAT89348.

XX PT DNA encoding Bacillus popilliae crystal protein - for production of
 XX PT recombinant protein and transgenic plants resistant to attack by
 XX PT beetles

XX PS Claim 8; Pages 8-11; 12pp; German.

XX This sequence represents a novel bacterial crystal protein which can be
 CC used to control beetles of the family Scarabaeidae, especially
 CC Melolontha spp. (e.g. maybugs, cockchafers) which are pests of
 CC agriculture and forestry. The protein can inhibit eating, killing both
 CC adult beetles and larvae. It can be incorporated into eradication
 CC programmes involving Bacillus popilliae and Bacillus thuringiensis
 CC spores, fungal spores or cytolysing proteins in the form of a fusion
 CC protein. The DNA can also be used to produce transgenic plants that are
 CC resistant to attack by the beetles.

XX SQ Sequence 706 AA;

Query Match 100.0%; Score 29; DB 18; Length 706;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYVIT 5
 Db 506 dyvit 510
 |||||

RESULT 9

AAW71930

ID AAW71930 standard; Protein; 173 AA.

XX AC AAW71930;

XX DT 22-SEP-1995 (first entry)

XX DE Zag gene FAM binding domain.

XX KW ZAG; fast alpha-2-macroglobulin binding protein; FAM;
 XX KW plasma proteinase-inhibitor binding protein.

XX OS Streptococcus zooepidemicus strain V.

XX PN W09507296-A.

XX PD 16-MAR-1995.

XX PF 06-SEP-1994; 94WO-SE00826.

XX PR 06-SEP-1993; . 93SE-0002855.

XX PA (GUSS/) GUSS B.

XX PA (JONS/) JONSSON H.

XX PA (LIND/) LINDBERG M.

XX PA (MUEL/) MUELLER H.

XX PA (RANT/) RANTAMAKI L K.

XX PI Guss B, Jonsson H, Lindberg M, Mueller H, Rantamaki LK;

XX DR WPI; 1995-123382/16.

XX DR N-PSDB; AAQ89198.

XX PT DNA encoding fast alpha 2-macroglobulin-binding proteins - used
 XX PT to obtain prods. for sepn., detection or quantification or for
 XX PT binding inhibition

XX PS Claim 24; Page 37; 50pp; English.

XX A phage lambda EMBL3 library of S. equi subsp. zooepidemicus V
 CC was analyzed for fast-acting alpha-2-macroglobulin (FAM)- and
 CC IgG-binding activity. One clone, lambda SzGL, which expressed
 CC both activities, was analyzed to obtain DNA encoding the
 CC FAM-binding protein, ZAG. The FAM-binding domain (R71930) in
 CC ZAG was identified.

XX SQ Sequence 17; AA;

Query Match 96.6%; Score 28; DB 16; Length 173;
 Best Local Similarity 80.0%; Pred. No. 95;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYVIT 5

Db 156 dyvit 160

|||||

RESULT 10

Fri Jun 29 08:05:12 2001

us-09-724-406-4.rag

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AAB63700
ID AAB63700 standard; Protein; 200 AA.
XX
XX AAB63700;
AC
XX
XX 26-MAR-2001 (first entry)
DT
XX Human gastric cancer associated antigen protein sequence SEQ ID NO:1062.
DE
XX Human; breast cancer; gastric cancer; prostate cancer; diagnosis;
KW cancer associated antigen; cytostatic; cancer vaccine.
KW
XX Homo sapiens.
OS
XX WO200073801-A2.
PN
XX 07-DEC-2000.
PD
XX
XX 26-MAY-2000; 2000WO-US14749.
PF
XX
XX 28-MAY-1999; 99US-0136526.
PR
XX 10-SEP-1999; 99US-0133454.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
PA
XX
XX Obata Y;
PI
XX WPI; 2001-025274/03.
DR
XX
XX Nucleic acids encoding breast, gastric and prostate cancer associated
PT antigen precursors, useful for diagnosing and treating a condition
PT characterized by expression of an abnormal amount of a protein, e.g.
PT cancer -
XX
XX Example 1; Page 675; 799pp; English.
PS
XX AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014
CC represent nucleotide sequences encoding human breast, gastric and
CC prostate cancer associated antigen precursors (CAAP), respectively.
CC AAB63232 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970
CC represent human breast, gastric and prostate CAAP protein sequence
CC respectively. CAAPs have cytostatic activity and can be used in the
CC production of cancer vaccines. The human CAAP proteins, peptides, nucleic
CC acids or anti-CAAP antibodies are useful for diagnosing and treating a
CC condition characterised by expression of an abnormal amount of a protein,
CC e.g. cancer.
XX
XX Sequence 200 AA;
SQ

Query Match 96.6%; Score 28; DB 22; Length 200;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5
Db 99 dyyvt 103
|||:|

RESULT 11
AAG42791
ID AAG42791 standard; Protein; 254 AA.
XX
XX AAG42791;
AC
XX
XX 18-OCT-2000 (first entry)
DT
XX Arabidopsis thaliana protein fragment SEQ ID NO: 53407.
DE
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
XX

```

OS Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

XX 05-MAR-1999; 99US-0123180.

XX 09-MAR-1999; 99US-0123548.

XX 23-MAR-1999; 99US-0125788.

XX 25-MAR-1999; 99US-0126264.

XX 29-MAR-1999; 99US-0126785.

XX 01-APR-1999; 99US-0127462.

XX 06-APR-1999; 99US-0128234.

XX 08-APR-1999; 99US-0128714.

XX 16-APR-1999; 99US-0129845.

XX 19-APR-1999; 99US-0130077.

XX 21-APR-1999; 99US-0130449.

XX 23-APR-1999; 99US-0130510.

XX 28-APR-1999; 99US-0130891.

XX 30-APR-1999; 99US-0131449.

XX 30-APR-1999; 99US-0132048.

XX 30-APR-1999; 99US-0132407.

XX 04-MAY-1999; 99US-0132484.

XX 05-MAY-1999; 99US-0132485.

XX 06-MAY-1999; 99US-0132486.

XX 06-MAY-1999; 99US-0132487.

XX 07-MAY-1999; 99US-0132863.

XX 11-MAY-1999; 99US-0134256.

XX 14-MAY-1999; 99US-0134218.

XX 14-MAY-1999; 99US-0134219.

XX 14-MAY-1999; 99US-0134221.

XX 14-MAY-1999; 99US-0134370.

XX 18-MAY-1999; 99US-0134768.

XX 19-MAY-1999; 99US-0134941.

XX 20-MAY-1999; 99US-0135124.

XX 21-MAY-1999; 99US-0135353.

XX 24-MAY-1999; 99US-0135629.

XX 25-MAY-1999; 99US-0136021.

XX 27-MAY-1999; 99US-0136392.

XX 28-MAY-1999; 99US-0136782.

XX 01-JUN-1999; 99US-0137222.

XX 03-JUN-1999; 99US-0137528.

XX 04-JUN-1999; 99US-0137502.

XX 07-JUN-1999; 99US-0137724.

XX 08-JUN-1999; 99US-0138094.

XX 10-JUN-1999; 99US-0138540.

XX 10-JUN-1999; 99US-0138847.

XX 14-JUN-1999; 99US-0139119.

XX 16-JUN-1999; 99US-0139452.

XX 16-JUN-1999; 99US-0139453.

XX 17-JUN-1999; 99US-0139492.

XX 18-JUN-1999; 99US-0139454.

XX 18-JUN-1999; 99US-0139455.

XX 18-JUN-1999; 99US-0139456.

XX 18-JUN-1999; 99US-0139457.

XX 18-JUN-1999; 99US-0139458.

XX 18-JUN-1999; 99US-0139459.

XX 18-JUN-1999; 99US-0139460.

XX 18-JUN-1999; 99US-0139461.

XX 18-JUN-1999; 99US-0139462.

XX 18-JUN-1999; 99US-0139463.

XX 18-JUN-1999; 99US-0139750.

XX 18-JUN-1999; 99US-0139763.

XX 21-JUN-1999; 99US-0139817.

XX 22-JUN-1999; 99US-0139899.

XX 23-JUN-1999; 99US-0140353.

XX 23-JUN-1999; 99US-0140354.

XX 24-JUN-1999; 99US-0140695.

XX 28-JUN-1999; 99US-0140823.

XX 29-JUN-1999; 99US-0140991.

PR 30-JUN-1999; 99US-0141287.
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 PR 02-JUL-1999; 99US-0142055.
 PR 06-JUL-1999; 99US-0142230.
 PR 08-JUL-1999; 99US-0142803.
 PR 09-JUL-1999; 99US-0142920.
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 PR 13-JUL-1999; 99US-0143542.
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 PR 21-JUL-1999; 99US-0144814.
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 PR 31-AUG-1999; 99US-0151438.
 PR 01-SEP-1999; 99US-0151930.
 PR 07-SEP-1999; 99US-0152363.
 PR 10-SEP-1999; 99US-0153070.
 PR 13-SEP-1999; 99US-0153758.

PR 15-SEP-1999; 99US-0154018.
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 PR 28-OCT-1999; 99US-0161920.
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 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 96.68; Score 28; DB 21; Length 254;
 Best Local Similarity 80.0%; Pred. No. 1.4e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYIIT 5
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 Db 249 dyvvt 253

RESULT 12

AAG42790
 ID AAG42790 standard; Protein; 255 AA.

XX
 AC AAG42790;

XX
 DT 18-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 53406.

DE Protein identification; signal transduction pathway; metabolic pathway;
 XX hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX	25-FEB-1999;	99US-0121825.	PR	12-JUL-1999;	99US-0142977.
PR	05-MAR-1999;	99US-0123380.	PR	13-JUL-1999;	99US-0143542.
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PR	11-MAY-1999;	99US-0134256.	PR	23-JUL-1999;	99US-0145218.
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PR	08-JUN-1999;	99US-0138094.	PR	09-AUG-1999;	99US-0147493.
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PR	10-JUN-1999;	99US-0138847.	PR	10-AUG-1999;	99US-0148171.
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PR	18-JUN-1999;	99US-0139456.	PR	18-AUG-1999;	99US-0149426.
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PR	18-JUN-1999;	99US-0139458.	PR	20-AUG-1999;	99US-0149723.
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PR	18-JUN-1999;	99US-0139461.	PR	23-AUG-1999;	99US-0149930.
PR	18-JUN-1999;	99US-0139462.	PR	25-AUG-1999;</	

PT and for recombinant production of new nucleic acid sequencing reagents.

PT and for recombinant production of new nucleic acid sequencing reagents.

XX Claim 21; Page 108-110; 163pp; German.
 XX This invention describes a novel nucleic acid (I) containing a sequence
 CC that encodes hemocyanin (II), a domain of (I) or its fragment with the
 CC immunological properties of at least one domain of (II). The products of
 CC the invention have cytostatic, virucide, antibacterial, antiparasitic,
 CC immunomodulatory and antihypertensive activity. (I), and constructs
 CC additionally containing antigen-encoding sequences, are useful in gene
 CC therapy of tumors. Polypeptides encoded by (I) are useful for treating
 CC parasitic or viral infections and tumors, particularly schistosomiasis
 CC and carcinoma (of bladder, epithelium, ovary, breast, bronchi or
 CC colon-rectum), also hypertension, as vaccines, for treating cocaine
 CC misuse and very generally as carriers for pharmaceuticals, e.g.
 CC cytostatics. They may also be used to generate antibodies (Ab). Probes
 CC based on (I) and Ab are useful for detecting tumor-specific DNA in a cell
 CC (by detecting specific binding to cellular DNA or proteins), particularly
 CC where associated with the types of carcinoma listed above. Hemocyanins
 CC can be produced recombinantly, relatively inexpensively and in adequate
 CC amounts, eliminating the need to culture gastropods. When used as a
 CC carrier, (II) significantly increases the half-life of the attached
 CC pharmaceutical, by inhibiting ultrafiltration in the kidneys.
 XX SQ Sequence 515 AA;

Query Match 96.6%; Score 28; DB 21; Length 515;
 Best Local Similarity 80.0%; Pred. No. 3.1e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5
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 Db 490 dyvvt 494

RESULT 15
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 ID AAY93885 standard; Protein; 101 AA.
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 AC AAY93885;
 XX
 DT 03-OCT-2000 (first entry)
 XX
 DE Amino acid sequence of a protein encoded by Hepatitis Y virus genome.
 XX
 KW Hepatitis virus; Hepatitis Y virus; HYV; cell line ECACC 9110711;
 RW vaccine.
 XX
 OS Hepatitis Y virus.
 XX
 PN WO200037650-A1.
 XX
 PD 29-JUN-2000.
 XX
 PF 16-DEC-1999; 99WO-EP10179.
 XX
 PR 18-DEC-1998; 98EP-0204313.
 PR 20-JAN-1999; 99EP-0200167.
 XX
 PA (ALKU) AKZO NOBEL NV.
 XX
 PI Yap SH, Verslype CJC, Boender PJ, Hellings JA;
 XX
 DR WPI; 2000-442677/38.
 XX

PT Detecting non- A-G hepatitis virus, especially hepatitis Y virus, in a
 sample, comprising contacting the cell with antibodies specific for
 PT sequences in the virus genome -
 XX
 PS Disclosure; Page 17; 124pp; English.
 XX
 CC The present sequence represents a protein which is encoded by the
 CC genome of the Hepatitis Y virus. The specification describes a novel

CC Hepatitis virus, Hepatitis Y virus (HYV), and a method for detecting
 CC this virus in a hepatitis C negative sample. The method comprises
 CC contacting the sample with antibodies from the cell line ECACC 9110711,
 CC or monoclonal antibodies with the same immunoreactivity, and detecting
 CC immunocomplexes formed. The methods are used to detect non A-G hepatitis
 CC virus, especially hepatitis Y virus (HYV), in a sample. Proteins derived
 CC from HYV can be used in vaccines, which are used to protect against HYV.
 XX SQ Sequence 101 AA;
 Query Match 93.1%; Score 27; DB 21; Length 101;
 Best Local Similarity 80.0%; Pred. No. 86;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYYIT 5
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 Db 94 dyvlt 98
 Search completed: June 28, 2001, 16:14:33
 Job time: 1321 sec

us-09-724-406-4.ra1

Fri Jun 29 08:05:13 2001

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; SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/213,403
; FILING DATE: 15-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,693
; FILING DATE: 13-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2807-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 346 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-213-403-2

Query Match 100.0%; Score 29; DB 1; Length 346;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 131 DYYIT 135

RESULT 4
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; Sequence 2, Application US/08460741
; Patent No. 5670625
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; APPLICANT: Baum, Peter R.
; APPLICANT: Carpenter, Melissa
; TITLE OF INVENTION: No. 5670625el Cytokine Designated elk Ligand
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Apple Macintosh
; SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,741
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/213,403
; FILING DATE: 15-MAR-1994
; APPLICATION NUMBER: US 07/977,693
; FILING DATE: 13-NOV-1992
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2807-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 346 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-460-741-2

Query Match 100.0%; Score 29; DB 1; Length 346;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5
DB 131 DYYIT 135

RESULT 3
US-08-458-077-2
; Sequence 2, Application US/08458077
; Patent No. 5627267
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; APPLICANT: Baum, Peter R.
; APPLICANT: Carpenter, Melissa
; TITLE OF INVENTION: No. 5627267el Cytokine Designated elk Ligand
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Apple Macintosh
; SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,077
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/213,403
; FILING DATE: 15-MAR-1994
; APPLICATION NUMBER: US 07/977,693
; FILING DATE: 13-NOV-1992
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; QUERY MATCH
; BEST LOCAL SIMILARITY 100.0%;
; PRED. NO. 1E+02;
; SCORE 29; DB 1; LENGTH 346;
; INDELS 0; GAPS 0; MISMATCHES 0; CONSERVATIVE 5;
; MATCHES 5;
; MOLECULE TYPE: protein
; US-08-458-077-2
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5
|||||

Db 131 DYYIT 135

RESULT 5

US-08-747-240-2
; Sequence 2, Application US/08747240
; Patent No. 5728813
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; APPLICANT: Baum, Peter R.
; APPLICANT: Carpenter, Melissa
; TITLE OF INVENTION: No. 5728813el Cytokine Designated elk Ligand
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; OPERATING SYSTEM: Apple System 7.1
; SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/747.240
; FILING DATE: 12-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/213.403
; FILING DATE: 15-MAR-1994
; APPLICATION NUMBER: US 07/977.693
; FILING DATE: 13-NOV-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2807-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 346 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-747-240-2

Query Match 100.0%; Score 29; DB 1; Length 346;
Best Local Similarity 100.0%; Pred. No. le+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5
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Db 131 DYYIT 135

RESULT 6

US-08-299-567-6
; Sequence 6, Application US/08299567
; Patent No. 5747033
; GENERAL INFORMATION:
; APPLICANT: Davis, et al.
; TITLE OF INVENTION: METHOD OF ENHANCING THE BIOLOGICAL
; ACTIVITY OF EPH FAMILY LIGANDS

; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill River Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-6707
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/299,567
; FILING DATE: 01-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kempner, Gail M.
; REGISTRATION NUMBER: 32,143
; REFERENCE/DOCKET NUMBER: REG 290
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 914-345-7400
; TELEFAX: 914-345-7721
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 346 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-299-567-6

Query Match 100.0%; Score 29; DB 1; Length 346;
Best Local Similarity 100.0%; Pred. No. le+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5
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Db 131 DYYIT 135

RESULT 7

US-09-408-820-2
; Sequence 2, Application US/09408820
; Patent No. 6204057
; GENERAL INFORMATION:
; APPLICANT: Schaeffer, Wolfgang
; APPLICANT: Krieger, Lutz
; APPLICANT: Zhang, Jiaming
; TITLE OF INVENTION: Polynucleotides And The Proteins Encoded Thereby,
; FILE OF INVENTION: Suitable For Controlling Lamellicorn Beetles
; FILE REFERENCE: S-30403/A/UHD/GSC1996/PCT
; CURRENT APPLICATION NUMBER: US/09/408,820
; CURRENT FILING DATE: 1999-09-29
; EARLIER APPLICATION NUMBER: 09/051,454
; EARLIER FILING DATE: 1998-04-07
; EARLIER APPLICATION NUMBER: DE 195 40 223.5
; EARLIER FILING DATE: 1995-10-18
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 706
; TYPE: PRT
; ORGANISM: Bacillus popilliae
; FEATURE:
; OTHER INFORMATION: strain subspecies: melolonthae H1; stage of
; OTHER INFORMATION: development: spore stage; cell type: sporangium
; FEATURE:
; OTHER INFORMATION: immediate origin: isolate from the haemolymph of
; OTHER INFORMATION: Melolontha melolontha individuals captured on open
; OTHER INFORMATION: ground

Fri Jun 29 08:05:13 2001

us-09-724-406-4.ra1

FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(706)
; OTHER INFORMATION: mature protein crystal peptide determined by
; OTHER INFORMATION: experiment
US-09-408-820-2

Query Match 100.0%; Score 29; DB 4; Length 706;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYIIT 5
| | | | |
Db 506 DYIIT 510

RESULT 8
US-08-669-408B-8
; Sequence 8, Application US/08669408B
; Patent No. 6100055
; GENERAL INFORMATION:
; APPLICANT: GUSS, Bengt
; APPLICANT: JONSSON, Hans
; APPLICANT: LINDBERG, Martin
; APPLICANT: MUELLER, Hans-Peter
; APPLICANT: RANTAMAKI, Liisa K.
; TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING
; TITLE OF INVENTION: PLASMAPROTEINASE INHIBITOR-BINDING PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/669,408B
; FILING DATE: 03-JUL-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/SE94/00826
; FILING DATE: 06-SEP-1994
; PRIOR APPLICATION DATA: SE 9302855-3
; FILING DATE: 06-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 61743/102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 173 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-669-408B-8

Query Match 96.6%; Score 28; DB 3; Length 173;
Best Local Similarity 80.0%; Pred. No. 77;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYIIT 5
| | | | |
Db 156 DYIIT 160

RESULT 9
US-08-976-255-18
; Sequence 18, Application US/08976255
; Patent No. 6136581
; GENERAL INFORMATION:
; APPLICANT: Jono, Keith E.
; APPLICANT: Plowman, Gregory
; TITLE OF INVENTION: KINASE GENES AND USES
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; OPERATING SYSTEM: IBM Compatible
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,255
; FILING DATE: No. 6136581ember 21, 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031,675
; FILING DATE: No. 6136581ember 22, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 229/182
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 178 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-08-976-255-18

Query Match 93.1%; Score 27; DB 4; Length 170;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYIIT 5
| | | | |
Db 132 DYIIT 136

RESULT 10
US-08-976-255-16
; Sequence 16, Application US/08976255
; Patent No. 6136581
; GENERAL INFORMATION:
; APPLICANT: Jono, Keith E.
; APPLICANT: Plowman, Gregory
; TITLE OF INVENTION: KINASE GENES AND USES
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon

```

; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: California
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,255
; FILING DATE: No. 6136581ember 21, 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031,675
; FILING DATE: No. 6136581ember 22, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 229/182
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 275 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; US-08-976-255-16

```

```

Query Match 93.1%; Score 27; DB 4; Length 275;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 DXYIT 5
```

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Db 230 DYILT 234
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RESULT 11
US-08-976-255-17
; Sequence 17, Application US/08976255
; Patent No. 6136581
; GENERAL INFORMATION:
; APPLICANT: Jono, Keith E.
; APPLICANT: Plowman, Gregory
; TITLE OF INVENTION: KINASE GENES AND USES
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: California
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,255
; FILING DATE: No. 6136581ember 21, 1997
; CLASSIFICATION: 435

```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031,675
; FILING DATE: No. 6136581ember 22, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 229/182
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 472 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; US-08-976-255-17

```

```

Query Match 93.1%; Score 27; DB 4; Length 472;
Best Local Similarity 80.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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```
QY 1 DXYIT 5
```

```
Db 295 DYILT 299
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```

RESULT 12
US-08-647-144-2
; Sequence 2, Application US/08647144
; Patent No. 5858728
; GENERAL INFORMATION:
; APPLICANT: Gram, Hermann
; APPLICANT: Di Padova, Franco
; APPLICANT: Barclay, George R.
; APPLICANT: Foxton, Ian R.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST LPS CORE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: No. 5858728th Carolina
; COUNTRY: U.S.A.
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/647,144
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/119,046
; FILING DATE: 10-SEP-1993
; APPLICATION NUMBER: EP 92/00380
; FILING DATE: 22-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 1749-114
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 881-3140
; TELEFAX: (919) 881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids

```

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-647-144-2

Query Match      89.7%; Score 26; DB 2; Length 120;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5
Db 31 DYYMT 35

RESULT 13
US-08-647-144-4
; Sequence 4, Application US/08647144
; Patent No. 5858728
; GENERAL INFORMATION:
; APPLICANT: Gram, Hermann
; APPLICANT: Di Padova, Franco
; APPLICANT: Barclay, George R.
; APPLICANT: Poxton, Ian R.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST LPS CORE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: No. 5858728th Carolina
; COUNTRY: U.S.A.
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/647,144
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/119,046
; FILING DATE: 10-SEP-1993
; APPLICATION NUMBER: EP 92/00380
; FILING DATE: 22-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 1749-114
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 881-3140
; TELEFAX: (919) 881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-647-144-4

Query Match      89.7%; Score 26; DB 2; Length 120;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5
Db 31 DYYMT 35

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-647-144-2

Query Match      89.7%; Score 26; DB 2; Length 120;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5
Db 31 DYYMT 35

RESULT 14
US-08-442-542-6
; Sequence 6, Application US/08442542
; Patent No. 5686600
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine B.
; APPLICANT: Koziel, Michael G.
; TITLE OF INVENTION: Antibodies which Bind to Insect Gut
; TITLE OF INVENTION: Proteins and their Use
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,542
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/267,641
; FILING DATE: 28-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: CGC 1750
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8615
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-442-542-6

Query Match      89.7%; Score 26; DB 1; Length 124;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5
Db 31 DYYMT 35

RESULT 15
US-08-765-469-6
; Sequence 6, Application US/08765469
; Patent No. 6069301
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine B.
; APPLICANT: Koziel, Michael G.
; TITLE OF INVENTION: Antibodies which Bind to Insect Gut
; TITLE OF INVENTION: Proteins and their Use
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
US-08-765-469-6
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,469
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/267,641
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: CGC 1750
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8615
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-765-469-6

Query Match 89.7%; Score 26; DB 3; Length 124;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DYYIT 5
Db 31 DYYMT 35

Search completed: June 28, 2001, 16:01:13
Job time: 521 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2001, 15:52:32 ; Search time 234.85 Seconds
(without alignments)
1.622 Million cell updates/sec

Title: US-09-724-406-4
Perfect score: 29
Sequence: 1 DYIIT 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_68: *
1: piri: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	231	184422	cytochrome-c oxida
2	29	100.0	338	G71128	hypothetical prote
3	29	100.0	345	I48780	Stral/Eplg2 protei
4	29	100.0	345	I58406	LERK-2 - rat
5	29	100.0	346	S46993	elk ligand - human
6	29	100.0	358	H71088	hypothetical prote
7	29	100.0	360	T34510	hypothetical prote
8	29	100.0	365	D69092	conserved hypothet
9	29	100.0	369	ESBPC	3',5'-cyclic-nucle
10	29	100.0	473	D81322	outer membrane pro
11	29	100.0	527	A84050	acetate-CoA ligase
12	29	100.0	537	T50099	probable protein-t
13	29	100.0	736	C69307	conserved hypothet
14	29	100.0	1050	S54640	KCS1 protein - yea
15	29	100.0	1348	B23496	TyB protein - yea
16	29	100.0	1598	S69967	TyB protein - yea
17	29	100.0	1633	JC5056	polybromo 1 - chic
18	29	100.0	1770	S45842	TyB protein - yea
19	29	100.0	1770	S69953	TyB protein - yea
20	29	100.0	1770	S69948	TyB protein - yea
21	29	100.0	1770	S70233	TyB protein - yea
22	29	100.0	1770	S70230	TyB protein - yea
23	29	100.0	1770	S69966	TyB protein - yea
24	29	100.0	1770	S69950	TyB protein - yea
25	29	100.0	1770	S58651	TyB protein - yea
26	29	100.0	1771	S53592	TyB protein - yea
27	29	100.0	1810	S69973	TyB protein - yea
28	29	100.0	2338	T25810	hypothetical prote
29	29	100.0	3147	T18674	hypothetical prote

30	28	96.6	181	2	S75415	probable ribosomal
31	28	96.6	297	2	E71425	hypothetical prote
32	28	96.6	301	2	S52013	H+-transporting AT
33	28	96.6	328	2	C86351	hypothetical prote
34	28	96.6	367	2	B75597	first mannose tra
35	28	96.6	381	2	F64354	hypothetical prote
36	28	96.6	389	2	D64337	16S rRNA 5'-region
37	28	96.6	405	2	S42371	ATP-dependent Clp
38	28	96.6	467	2	E69601	hypothetical prote
39	28	96.6	536	2	H85176	probable epoxide h
40	28	96.6	594	2	T33686	hypothetical prote
41	28	96.6	699	2	H82030	cysteine-tRNA lig
42	28	96.6	755	2	T32971	hypothetical prote
43	28	96.6	818	2	T33689	hypothetical prote
44	28	96.6	818	2	T33687	hypothetical prote
45	28	96.6	998	1	Q0BBB1	B1 protein - black

ALIGNMENTS

RESULT 1

I84422
cytochrome-c oxidase (EC 1.9.3.1) chain II - common woolly monkey mitochondrion
C:Species: mitochondrion Lagotrix lagotricha (common woolly monkey)
C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 07-Dec-1999
C:Accession: I84422
R:Adkins, R.M.; Honeycutt, R.L.
J. Mol. Evol. 38, 215-231, 1994
A:Title: Evolution of the primate cytochrome c oxidase subunit II gene.
A:Reference number: I36906; MUID:94275866
A:Accession: I84422
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-231 <ADK>
A:Cross-references: GB:L22779; NID:g438681; PIDN:AAA20565.1; PID:g438682
C:Genetics:
A:Genome: mitochondrion
A:Genetic code: SGC1
C:Superfamily: cytochrome-c oxidase chain II; cytochrome-c oxidase chain II homology
F:9-214/Domain: cytochrome-c oxidase chain II homology <CO2>
F:161.196,200,207/Binding site: copper 1 (His, Cys, Cys, Met) #status predicted
F:196.196,200,204/Binding site: copper 2 (Cys, Glu, Cys, His) #status predicted
F:198/Binding site: magnesium (Glu) (shared with chain I) #status predicted

Query Match 100.0% Score 29; DB 2; Length 231;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYIIT 5

Db 119 DYIIT 123

RESULT 2

G71128
hypothetical protein PH0796 - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 28-Jul-2000
C:Accession: G71128
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Hino, Y.; Yamamoto, S.; Se
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogu
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
A:Reference number: A71000; MUID:98344137
A:Accession: G71128
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-338 <KAW>
A:Cross-references: GB:AF000003; NID:g3236130; PIDN:BAA29889.1; PID:g3257206
A:Experimental source: strain OT3

A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
 C:Genetics:
 A:Gene: PH0796
 C:Superfamily: Pyrococcus horikoshii hypothetical protein PH0973

Query Match 100.0%; Score 29; DB 2; Length 338;
 Best Local Similarity 100.0%; Pred. No. 72;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5
 |||||
 Db 85 DYYIT 89

RESULT 3

Stral/Eplg2 protein - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
 C:Accession: I48780; A5507; A55062; S52670
 R:Bouillet, P.; Oulad-Abdelghani, M.; Vicaire, S.; Garnier, J.M.; Schuhbauer, B.; Dolle, Dev. Biol. 170, 420-433, 1995
 A:Title: Efficient cloning of cDNAs of retinoic acid-responsive genes in P19 embryonal carcinoma cells
 A:Reference number: I48780; MUID:95377533
 A:Accession: I48780
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-345 <RES>
 A:Cross-references: EMBL:Z48781; NID:g747858; PIDN:CAA8695.1; PID:g747859
 R:Fletcher, F.A.; Renshaw, B.; Hollingsworth, T.; Baum, P.; Lyman, S.D.; Jenkins, N.A.; Genomics 24, 127-132, 1994
 A:Title: Genomic organization and chromosomal localization of mouse Eplg2, a gene encoding a protein tyrosine kinase
 A:Reference number: A5507; MUID:95203867
 A:Accession: A5507
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-345 <FLE>
 A:Cross-references: GB:U07598
 R:Shao, H.; Lou, L.; Pandey, A.; Pasquale, E.B.; Dixit, V.M. J. Biol. Chem. 269, 26606-26609, 1994
 A:Title: cDNA cloning and characterization of a ligand for the Cek5 receptor protein-tyrosine kinase
 A:Reference number: A55062; MUID:95014510
 A:Accession: A55062
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-89, T', 91-345 <SHA>
 A:Cross-references: GB:U12983; NID:g575928; PIDN:AAA53231.1; PID:g575929
 C:Genetics:
 A:Gene: EPLG2

Query Match 100.0%; Score 29; DB 2; Length 345;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5
 |||||
 Db 131 DYYIT 135

RESULT 4

LERK-2 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
 C:Accession: I58406
 R:Fletcher, F.A.; Carpenter, M.; Shilling, H.; Baum, P.; Ziegler, S.; Gimpel, S.; Hollin
 Oncogene 9, 3241-3248, 1994
 A:Title: LERK-2, a ligand for the receptor tyrosine kinase ELK, is evolutionarily conserved
 A:Reference number: I58406; MUID:95022634
 A:Accession: I58406
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
 A:Residues: 1-345 <RES>
 A:Cross-references: EMBL:U07560; NID:g563118; PIDN:AAA53092.1; PID:g563119
 C:Genetics:
 A:Gene: Eplg2

Query Match 100.0%; Score 29; DB 2; Length 345;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5
 |||||
 Db 131 DYYIT 135

RESULT 5

S46993
 elk ligand - human
 C:Species: Homo sapiens (man)
 C:Date: 15-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 28-May-1999
 C:Accession: S46993
 R:Beckmann, M.P.; Cerretti, D.P.; Baum, P.; vanden Bos, T.; James, L.; Farrah, T.; Ko
 EMO J. 13, 3757-3762, 1994
 A:Title: Molecular characterization of a family of ligands for eph-related tyrosine k
 A:Reference number: S46993; MUID:94349923
 A:Accession: S46993
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-346 <BEC>
 A:Cross-references: GB:U09304; NID:g538366; PIDN:AAA53093.1; PID:g538367

Query Match 100.0%; Score 29; DB 2; Length 346;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5
 |||||
 Db 131 DYYIT 135

RESULT 6

H71088
 hypothetical protein PH0973 - Pyrococcus horikoshii
 C:Species: Pyrococcus horikoshii
 C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 28-Jul-2000
 C:Accession: H71088
 R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yanamoto, S.; Se
 M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogu
 DNA Res. 5, 55-76, 1998
 A:Title: Complete sequence and gene organization of the genome of a hyper-thermophil
 A:Reference number: A71000; MUID:98344137
 A:Accession: H71088
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-358 <KAW>
 A:Cross-references: GB:AP000004; NID:g3236131; PIDN:BAA30070.1; PID:g3257387
 A:Experimental source: strain OT3
 A:Note: this accession replaces an interim accession for a sequence replaced by GenBa
 C:Genetics:
 A:Gene: PH0973
 C:Superfamily: Pyrococcus horikoshii hypothetical protein PH0973

Query Match 100.0%; Score 29; DB 2; Length 358;
 Best Local Similarity 100.0%; Pred. No. 77;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5
 |||||
 Db 85 DYYIT 89

RESULT 7

T34510
 hypothetical protein ZK1290.10 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jun-2000
 A:Accession: T34510
 R:Taich, A.
 submitted to the EMBL Data Library, July 1995
 A:Description: The sequence of C. elegans cosmid ZK1290.
 A:Reference number: Z21535
 A:Accession: T34510
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-360 <TAI>
 A:Cross-references: EMBL:U21308; PIDN:AAB93316.1; GSPDB:GN00020; CESP:ZK1290.10
 A:Experimental source: strain Bristol N2; clone ZK1290
 C:Genetics:
 A:Gene: CESP:ZK1290.10
 A:Map position: 2
 A:Introns: 23/1; 48/1; 158/3; 216/1; 264/1; 312/1; 331/3
 C:Superfamily: Caenorhabditis elegans hypothetical protein ZK1290.10

Query Match 100.0%; Score 29; DB 2; Length 360;
 Best Local Similarity 100.0%; Pred. No. 77;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5
 |||||
 Db 207 DYYIT 211

RESULT 8

D69092
 conserved hypothetical protein MTH1686 - Methanobacterium thermoautotrophicum (strain De
 C:Species: Methanobacterium thermoautotrophicum
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
 A:Accession: D69092
 R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
 Qiu, D.; Spadafora, R.; Vicalire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiواني, N.
 K.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
 J. Bacteriol. 179, 7135-7155, 1997
 A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func
 A:Reference number: A69000; MUID:98037514
 A:Accession: D69092
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-365 <MTH>
 A:Cross-references: GB:AE000926; GB:AE000666; NID:g2622806; PIDN:AAB86158.1; PID:g262280
 A:Experimental source: strain Delta H
 C:Genetics:
 A:Gene: MTH1686
 C:Superfamily: Pyrococcus horikoshii hypothetical protein PH0759

Query Match 100.0%; Score 29; DB 2; Length 365;
 Best Local Similarity 100.0%; Pred. No. 78;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5
 |||||
 Db 44 DYYIT 48

RESULT 9

ESBYPC
 3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), low-affinity - yeast (Saccharom
 N:Alternate names: protein G0574; protein NRB369; protein YGL248w
 C:Species: Saccharomyces cerevisiae
 C:Date: 31-Mar-1991 #sequence_revision 12-Apr-1996 #text_change 16-Jun-2000
 C:Accession: S61613; S05879; S64274
 R:Colisac, E.; Maillier, E.; Robineau, S.; Netter, P.

submitted to the EMBL Data Library, December 1995
 A:Reference number: S61598
 A:Accession: S61613
 A:Molecule type: DNA

A:Residues: 1-369 <COI>
 A:Cross-references: EMBL:X94357; NID:g1150575; PIDN:CAA64139.1; PID:g1150591
 Mol. Cell. Biol. 7, 3629-3636, 1987
 R:Nikawa, J.; Sass, P.; Wigler, M.
 A:Title: Cloning and characterization of the low-affinity cyclic AMP phosphodiesteras
 A:Reference number: S05879; MUID:88065501
 A:Accession: S05879

A:Molecule type: DNA
 A:Residues: 1-93, F', 95-369 <NIK>
 A:Cross-references: EMBL:M17781; NID:g172228; PIDN:AAA34896.1; PID:g172229
 A:Experimental source: strain PSI-2
 R:Colisac, E.; Maillier, E.; Netter, P.
 submitted to the Protein Sequence Database, May 1996
 A:Reference number: S64271
 A:Accession: S64274
 A:Molecule type: DNA
 A:Residues: 1-369 <COV>
 A:Cross-references: EMBL:Z72770; NID:g1322920; PIDN:CAA96968.1; PID:g1322921; GSPDB:G
 A:Experimental source: strain S288C
 C:Genetics:

A:Gene: SGD:PDE1; MIPS:YGL248w
 A:Cross-references: SGD:S0003217; MIPS:YGL248w
 A:Map position: 71.
 C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase
 C:Keywords: phosphoric diester hydrolase

Query Match 100.0%; Score 29; DB 1; Length 369;
 Best Local Similarity 100.0%; Pred. No. 79;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5
 |||||
 Db 123 DYYIT 127

RESULT 10

D81322
 outer membrane protein Cj1170c [imported] - Campylobacter jejuni (strain NCTC 11168)
 C:Species: Campylobacter jejuni
 C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 20-Apr-2000
 C:Accession: D81322
 R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chil
 C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Ba
 Nature 403, 665-668, 2000
 A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals
 A:Reference number: A81250; MUID:20150912
 A:Accession: D81322
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-473 <PAR>
 A:Cross-references: GB:AL135077; GB:AL111168; NID:g96968444; PIDN:CAB73424.1; PID:g9696
 A:Experimental source: serotype O2, strain NCTC 11168
 C:Genetics:
 A:Gene: Cj1170c
 C:Superfamily: Campylobacter jejuni outer membrane protein Cj1170c

Query Match 100.0%; Score 29; DB 2; Length 473;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5
 |||||
 Db 170 DYYIT 174

RESULT 11

A84050

Fri Jun 29 08:05:14 2001

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
 A:Residues: 1-736 <MLE>
 A:Cross-references: GB:AE000782; NID:g2689396; PIDN:AAB90778.1; PID:g265
 C:Superfamily: Archaeoglobus conserved hypothetical protein AF0459

Query Match 100.0%; Score 29; DB 1; Length 736;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5
 |||||
 DB 552 DYYIT 556

RESULT 14

S54640
 KCS1 protein - yeast (*Saccharomyces cerevisiae*)
 N:Alternate names: protein D328; protein PZF1050; protein YD9335.03c; protein YDR017
 C:Species: *Saccharomyces cerevisiae*
 C:Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jul-2000
 C:Accession: S54640; S63423; S67830; S60373; S72114
 R:Dedman, K.; Brown, D.; Hamlyn, N.; Bowman, S.
 submitted to the EMBL Data Library, May 1995
 A:Reference number: S54638
 A:Accession: S54640
 A:Molecule type: DNA
 A:Residues: 1-1050 <DED>
 A:Cross-references: EMBL:Z49770; NID:g840867; PID:g840870
 A:Experimental source: strain AB972
 R:Eide, L.G.; Sander, C.; Prydz, H.
 submitted to the EMBL Data Library, February 1996
 A:Description: Sequencing and analysis of a 35.4 kb region on the left arm of chromos
 A:Reference number: S63416
 A:Accession: S63423
 A:Molecule type: DNA
 A:Residues: 1-1050 <EID>
 A:Cross-references: EMBL:X95966; NID:g1216215; PID:e225526; PID:g1216223
 R:Prydz, H.; Eide, L.G.
 submitted to the Protein Sequence Database, July 1996
 A:Reference number: S67822
 A:Accession: S67830
 A:Molecule type: DNA
 A:Residues: 1-1050 <PRY>
 A:Cross-references: EMBL:Z74313; NID:g1431441; PID:e253292; PID:g1431442; MIPS:YDR017
 A:Experimental source: strain S288C
 R:Huang, K.N.; Symington, L.S.
 Genetics 141, 1275-1285, 1995
 A:Title: Suppressors of a *Saccharomyces cerevisiae* pkc1 mutation identify alleles of
 A:Reference number: S60373; MUID:96170769
 A:Accession: S60373
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-688, 'M', 690-1050 <HUA>
 R:Eide, L.G.; Sander, C.; Prydz, H.
 Yeast 12, 1085-1090, 1996
 A:Title: Sequencing and analysis of a 35.4 kb region on the left arm of chromosome IV
 A:Reference number: S72107; MUID:97051598
 A:Accession: S72114
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-1050 <ETW>
 A:Cross-references: EMBL:X95966; NID:g1216215; PID:CAA65208.1; PID:g1216223
 C:Genetics:
 A:Gene: SGD:KCS1
 A:Cross-references: MIPS:YDR017c; SGD:S0002424
 A:Map position: 4R

Query Match 100.0%; Score 29; DB 2; Length 1050;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;

acetate-CoA ligase BH3201 [imported] - *Bacillus halodurans* (strain C-125)

C:Species: *Bacillus halodurans*
 C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000
 C:Accession: A84050
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira

Nucleic Acids Res. 28, 4317-4331, 2000
 A:Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
 A:Reference number: A83650; MUID:20263314
 A:Accession: A84050
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-527 <STO>
 A:Cross-references: GB:AP001518; GB:BA000004; NID:g10175792; PIDN:BA06920.1; GSPDB:GN00

A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: BH3201
 C:Superfamily: human SA protein; acetate--CoA ligase homology

Query Match 100.0%; Score 29; DB 2; Length 527;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5
 |||||
 DB 396 DYYIT 400

RESULT 12

T50099
 probable protein-tyrosine phosphatase CDC14 homolog [imported] - fission yeast (*Schizos*
 C:Species: *Schizosaccharomyces pombe*
 C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000
 C:Accession: T50099
 R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Brown, S.; Harris, D.
 submitted to the EMBL Data Library, February 2000
 A:Reference number: Z25037
 A:Accession: T50099
 A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA
 A:Residues: 1-537 <WOO>
 A:Cross-references: EMBL:AL158056; PIDN:CA876271.1; GSPDB:GN00066; SPDB:SPAC1782.09c
 A:Experimental source: strain 972h(-); cosmid c1782
 C:Genetics:
 A:Gene: SPDB:SPAC1782.09c
 A:Map position: 1
 A:Introns: 17/1

Query Match 100.0%; Score 29; DB 2; Length 537;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5
 |||||
 DB 141 DYYIT 145

RESULT 13

C69307
 conserved hypothetical protein AF0459 - *Archaeoglobus fulgidus*
 C:Species: *Archaeoglobus fulgidus*
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000

C:Accession: C69307
 R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
 ; Flieduschmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
 Nature 390, 364-370, 1997
 A:Authors: Uffertback, T.; Cotton, M.D.; Spriggs, T.; Artlich, P.; Kaine, B.P.; Sykes, S.
 Smith, H.O.; Woese, C.R.; Venter, J.C.
 A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae
 A:Reference number: A69250; MUID:98049343
 A:Accession: C69307

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5

|||||

Db 821 DYYIT 825

RESULT 15

B23496

TyB protein - yeast (Saccharomyces cerevisiae) retrotransposon Ty1-17
 C:Species: Saccharomyces cerevisiae
 C:Date: 20-Aug-1987 #sequence_revision 20-Aug-1987 #text_change 25-Apr-1997
 C:Accession: B23496
 R:Warrington, J.R.; Waring, R.B.; Newlon, C.S.; Indge, K.J.; Oliver, S.G.
 Nucleic Acids Res. 13, 6679-6693, 1985
 A:Title: Nucleotide sequence characterization of Ty 1-17, a class II transposon from yeast
 A:Reference number: A93591; MUID:86041864
 A:Accession: B23496
 A:Molecule type: DNA
 A:Residues: 1-1348 <WAP>
 A:Cross-references: EMBL:X03840; EMBL:J01333; EMBL:X00633; EMBL:X02991
 C:Genetics:
 A:Mobile element: retrotransposon Ty1-17
 C:Superfamily: TyB protein

Query Match

Best Local Similarity 100.0%; Score 29; DB 2; Length 1348;

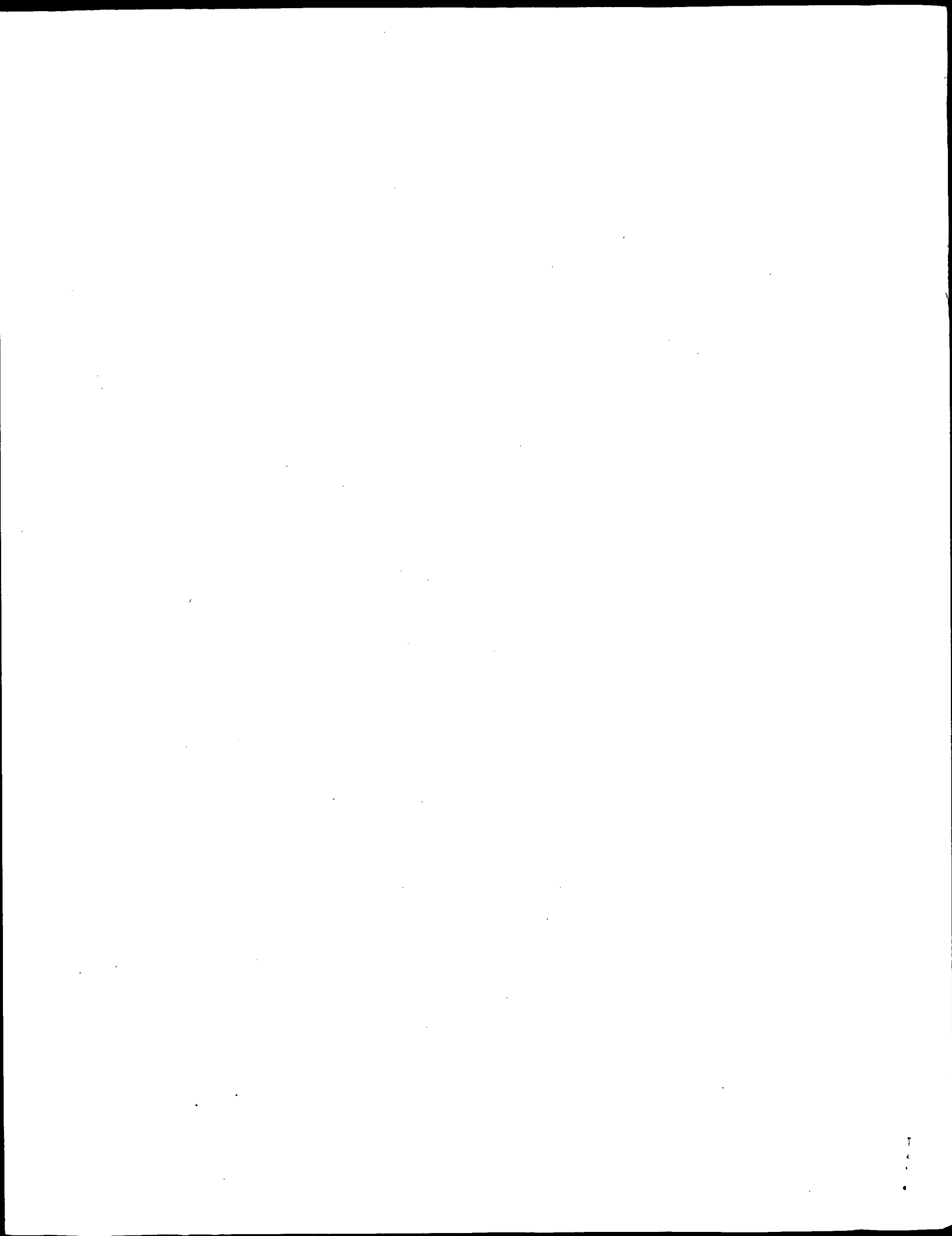
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5

|||||

Db 932 DYYIT 936

Search completed: June 28, 2001, 15:58:42
 Job time: 370 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2001, 15:52:32 ; Search time 105.36 Seconds
(without alignments)
1.626 Million cell updates/sec

Title: US-09-724-406-4
Perfect score: 29
Sequence: 1 DYIT 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	231	1	COX2_LAGLA
2	29	100.0	327	1	EFBI_XENIA
3	29	100.0	345	1	EFBI_MOUSE
4	29	100.0	345	1	EFBI_RAT
5	29	100.0	346	1	EFBI_HUMAN
6	29	100.0	360	1	YOFI_CAEEL
7	29	100.0	369	1	CNAL_YEAST
8	29	100.0	675	1	CIBA_PAEPP
9	29	100.0	695	1	CICA_PAEPP
10	29	100.0	706	1	CIAA_PAEPP
11	29	100.0	1347	1	YCB9_YEAST
12	28	96.6	181	1	RS4_SULSO
13	28	96.6	381	1	Y438_METJA
14	28	96.6	389	1	Y299_METJA
15	28	96.6	405	1	YNX4_CAEEL
16	28	96.6	467	1	HSLU_BACSU
17	28	96.6	1444	1	RRPL_RDVA
18	28	96.6	1444	1	RRPL_RDVF
19	27	93.1	174	1	HDCB_LACS3
20	27	93.1	206	1	T2D8_YEAST
21	27	93.1	233	1	PIC1_AGRTU
22	27	93.1	861	1	RFCL_YEAST
23	27	93.1	1037	1	YHIV_ECOLI
24	27	93.1	1125	1	YED_BORBU
25	27	93.1	1696	1	PKK5_BRACL
26	26	89.7	371	1	YMI8_PSEAE
27	25	86.2	235	1	SPEC_STRPY
28	25	86.2	235	1	Y037_METJA
29	25	86.2	239	1	ST14_YEAST
30	25	86.2	331	1	Y203_HUMAN
31	25	86.2	334	1	EFBI_CHICK
32	25	86.2	353	1	REC2_YEAST
33	25	86.2	377	1	DF3B_STAUA

34	25	86.2	377	1	PAT1_SOLTU	P15476 solanum tub
35	25	86.2	383	1	Y4GN_RHISN	P55470 rhizobium s
36	25	86.2	386	1	PAT0_SOLTU	P07745 solanum tub
37	25	86.2	386	1	PAT2_SOLTU	P15477 solanum tub
38	25	86.2	386	1	PAT3_SOLTU	P11768 solanum tub
39	25	86.2	429	1	CBPX_ORYSA	P52712 oryza sativ
40	25	86.2	432	1	AMIE_HAEIN	P44493 haemophilus
41	25	86.2	456	1	GLMU_ECOLI	P17114 escherichia
42	25	86.2	539	1	CBPX_ARATH	P32826 arabidopsis
43	25	86.2	553	1	IAGA_SALTI	P43016 salmoneilla
44	25	86.2	553	1	IAGA_SALTY	P43015 salmoneilla
45	25	86.2	567	1	ACHL_DROME	P09478 drosophila

ALIGNMENTS

```

RESULT 1
COX2_LAGLA
ID COX2_LAGLA STANDARD; PRT; 231 AA.
AC P98036;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1).
GN MTCO2 OR COII.
OS Lagotrix lagotricha (Common woolly monkey).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Ateleinae;
OC Lagotrix.
OX NCBI_TaxID=9519;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94275366; PubMed=8006990;
RA Adkins R.M., Honeycutt R.L.;
RT "Evolution of the primate cytochrome c oxidase subunit II gene.";
RL J. Mol. Evol. 38:215-231(1994).
CC -!- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CC CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-
CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. SUBUNIT 2
CC TRANSFERS THE ELECTRONS FROM CYTOCHROME C VIA ITS BINUCLEAR COPPER
CC A CENTER TO THE BINUCLEAR COPPER CENTER OF THE CATALYTIC SUBUNIT 1.
CC -!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O +
CC 4 FERRICYTOCHROME C.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC INNER MEMBRANE.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE SUBUNIT 2 FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L22779; AAA20565.1; -
CC HSP; P00404; IOCC.
CC InterPro; IPR001505; -
CC InterPro; IPR002429; -
CC Pfam; PF00116; COX2; 1.
CC PRINTS; PR01166; CYCOXIDASEII.
CC PROSITE; PS00078; COX2; 1.
CC Oxidoreductase; Copper; Mitochondrion; Transmembrane; Inner membrane;
CC Electron transport; Respiratory chain.
CC DOMAIN 1 26 MITOCHONDRIAL INTERMEMBRANE (POTENTIAL).
CC TRANSMEM 27 48 POTENTIAL.
CC FT DOMAIN 49 62 MITOCHONDRIAL MATRIX (POTENTIAL).
CC TRANSMEM 63 82 POTENTIAL.
CC FT DOMAIN 83 231 MITOCHONDRIAL INTERMEMBRANE (POTENTIAL).
CC METAL 161 196 COPPER A (PROBABLE).
CC METAL 196 196 COPPER A (PROBABLE).

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us-09-724-406-4.rsp

FT METAL 200 200 COPPER A (PROBABLE).
 FT METAL 204 204 COPPER A (PROBABLE).
 SQ SEQUENCE 231 AA; 26557 MW; 315E9B1B61CDED80 CRC64;

Query Match 100.0%; Score 29; DB 1; Length 231;

Best Local Similarity 100.0%; Pred. No. 17;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYIIT 5
 |||||
 Db 119 DYIIT 123

RESULT 2
 ID EFB1_XENLA STANDARD; PRT; 327 AA.
 AC 013097;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE EPHRIN-B1 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 2)
 DE (LERK-2) (ELK LIGAND) (ELK-L) (XLERK).
 GN EFB1 OR EPLG2 OR LERK2.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 [1]

SEQUENCE FROM N.A.
 RX MEDLINE=97316777; PubMed=9174051;
 RA Jones T.L., Karavanova I., Chong L., Zhou R.P., Daar I.O.;
 RT "Identification of Xlerk, an Eph family ligand regulated during
 RT mesoderm induction and neurogenesis in Xenopus laevis.";
 RL Oncogene 14:2159-2166(1997).
 CC -1- FUNCTION: MAY HAVE A ROLE IN THE DEVELOPING MESENCHYMAL AND
 CC NERVOUS TISSUE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: IN THE ADULT, EXPRESSED AT LOW LEVELS IN MOST
 CC ADULT TISSUES WITH INCREASED LEVELS OBSERVED IN THE KIDNEY,
 CC OOCYTES, OVARY AND TESTIS.
 CC -1- PTM: INDUCIBLE PHOSPHORYLATION OF TYROSINE RESIDUES IN THE
 CC CYTOPLASMIC DOMAIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC

EMBL; U31427; AAC35995.1; -
 DR InterPro: IPR001799; -
 DR Pfam: PF00812; Ephrin; 1.
 DR PROSITE: PS01299; EPHRIN; 1.
 KW Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 327 EPHRIN-B1.
 FT DOMAIN 21 225 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 226 246 POTENTIAL.
 FT DOMAIN 247 327 POTENTIAL.
 FT DOMAIN 325 327 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 327 327 PDZ RECOGNITION MOTIF (POTENTIAL).
 FT CARBOHYD 131 131 N-LINKED (GLNAC...) (POTENTIAL).
 FT CARBOHYD 202 202 N-LINKED (GLNAC...) (POTENTIAL).
 SQ SEQUENCE 327 AA; 36621 MW; 71230CE/F6BE5974 CRC64;

Query Match 100.0%; Score 29; DB 1; Length 327;
 Best Local Similarity 100.0%; Pred. No. 25;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYIIT 5
 |||||
 Db 123 DYIIT 127

RESULT 3
 ID EFB1_MOUSE STANDARD; PRT; 345 AA.
 AC P52795;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE EPHRIN-B1 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 2)
 DE (LERK-2) (ELK LIGAND) (ELK-L) (STRA1 PROTEIN) (CEK5 RECEPTOR LIGAND)
 DE (CEK5-L).
 GN EFB1 OR EPLG2 OR LERK2 OR STRA1 OR EPL2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV;
 RX MEDLINE=95203867; PubMed=7896266;
 RA Fletcher F.A., Renshaw B., Hollingsworth T., Baum P., Lyman S.D.,
 RA Jenkins N.A., Gilbert D.J., Copeland N.G., Davidson B.L.;
 RA "Genomic organization and chromosomal localization of mouse Eplg2, a
 RT gene encoding a binding protein for the receptor tyrosine kinase
 RT elk.";
 RT Genomics 24:127-132(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95377533; PubMed=7649373;
 RA Bouillet P., Oulad-Abdelghani M., Vicaire S., Garnier J.M.,
 RA Schuhbauer B., Dollé P., Chambon P.;
 RT "Efficient cloning of cDNAs of retinoic acid-responsive genes in P19
 RT embryonal carcinoma cells and characterization of a novel mouse gene,
 RT Stral (mouse LERK-2/Eplg2).";
 RT Dev. Biol. 170:420-433(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=95014510; PubMed=7929389;
 RA Shao H., Lou L., Pandey A., Pasquale E.B., Dixit V.M.;
 RT "cDNA cloning and characterization of a ligand for the Cek5 receptor
 RT protein-tyrosine kinase.";
 RL J. Biol. Chem. 269:26606-26609(1994).
 RN [4]
 RP FUNCTION.
 RX MEDLINE=20171264; PubMed=10704386;
 RA Mondl R., Wideman C., Kaprielian Z.;
 RT "Complementary expression of transmembrane ephrins and their receptors
 RT in the mouse spinal cord: a possible role in constraining the
 RT orientation of longitudinally projecting axons.";
 RL Development 127:1397-1410(2000).
 CC -1- FUNCTION: BINDS TO, AND INDUCE THE COLLAPSE OF, COMMISSURAL
 CC AXONS/GROWTH CONES IN VITRO. MAY PLAY A ROLE IN CONSTRAINING THE
 CC ORIENTATION OF LONGITUDINALLY PROJECTING AXONS.
 CC -1- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHB1 AND EPHAL.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: EXPRESSED ON LATERAL FLOOR PLATE CELLS,
 CC SPECIFICALLY ON COMMISSURAL AXON SEGMENTS THAT HAVE PASSED THROUGH
 CC THE FLOOR PLATE. EXPRESSED IN CELLS OF THE RETINAL GANGLION CELL
 CC LAYER DURING RETINAL AXON GUIDANCE TO THE OPTIC DISC.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN THE FLOOR PLATE THROUGHOUT THE
 CC PERIOD OF COMMISSURAL AXON PATHFINDING.
 CC -1- PTM: INDUCIBLE PHOSPHORYLATION OF TYROSINE RESIDUES IN THE
 CC CYTOPLASMIC DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
 CC

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P98172; *Crinoid*, PRI; 346 AA.

01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
EPHRI-B1 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 2) (LERK-2) (ELK LIGAND) (ELK-L)
EFNB1 OR EPLG2 OR LERK2 OR EFL-3.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
TISSUE=Placenta;
BEDLINE=94349523; PubMed=8070404;
Beckmann M.P., Cerretti D.P., Baum P., Vandenbos T., James L., Farrah T., Kozlosky C., Hollingsworth T., Shilling H., Maraskovsky E., Fletcher F.A., Lhotak V., Pawson T., Lyman S.D.;
"Molecular characterization of a family of ligands for eph-related tyrosine kinase receptors.";
EMBO J. 13:3757-3762(1994).
[2]
SEQUENCE FROM N.A.
Davis S., Gale N.W., Aldrich T.H., Maisonpierre P.C., Lhotak V., Pawson T., Goldfarb M., Vancopoulos G.D.;
Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A.
Fletcher F.A., Huebner K., Shaffer L.G., Monaco A., Mueller U., Kozlosky C., Druck T., Simoneau D.K., Fairweather N., Cerretti D.P., Belmont J.W., Beckmann M.P., Lyman S.D.;
Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
[4]
SEQUENCE FROM H.A.
Howden P.;
Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

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EMBL; U21308; AAB93316.1; -
WormPep; ZK1290.10; CR02080.
Hypothetical protein; Signal.
FT SIGNAL 1 21
CHAIN 22 360
SEQUENCE 360 AA; 39669 MW; 18751B6BC062D4F7 CRC64;

Query Match 100.0%; Score 29; DB 1; Length 360;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5
Db 207 DYYIT 211

RESULT 7
CNAL_YEAST STANDARD; PRT; 369 AA.
AC P22434;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 3', 5'-CYCLIC-NUCLEOTIDE PHOSPHODIESTERASE 1 (EC 3.1.4.17) (PDEASE 1)
DE (LOW-AFFINITY CAMP PHOSPHODIESTERASE) (3'; 5'-CNP).
GN PDE1 OR YGL248W OR NRB369.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;

SEQUENCE FROM N.A.
RX MEDLINE=88065501; PubMed=2824992;
RA Nikawa J.-I., Sass P., Wiegler M.;
RT "Cloning and characterization of the low-affinity cyclic AMP
phosphodiesterase gene of Saccharomyces cerevisiae.";
RL Mol. Cell. Biol. 7:3629-3636(1987).
RN [2]
RP SEQUENCE FROM N.A.
RP STRAIN=S28C / EV1679;
RX MEDLINE=97127827; PubMed=8972578;
RA Coissac E., Maillet E., Robineau S., Netter P.;
RT "Sequence of a 39,411 bp DNA fragment covering the left end of
chromosome VII of Saccharomyces cerevisiae.";
RL Yeast 12:1555-1562(1996).
CC -1- FUNCTION: CONTROLS THE LEVEL OF CAMP IN YEAST CELLS, TOGETHER WITH
THE HIGH-AFFINITY CAMP PHOSPHODIESTERASE (PDE2).
CC -1- CATALYTIC ACTIVITY: NUCLEOSIDE 3',5'-CYCLIC PHOSPHATE + H(2)O -
NUCLEOSIDE 5'-PHOSPHATE.
CC -1- SIMILARITY: BELONGS TO THE CAMP PHOSPHODIESTERASE CLASS-II FAMILY.

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EMBL; M17781; AAA34896.1; -
EMBL; X94357; CAA64139.1; -
EMBL; Z72770; CAA96968.1; -
DR PIR; S05879; ESEVPC.
DR SGD; S0003217; PDEL.
DR InterPro; IPR000396;
DR Pfam; PF02112; PDEase_II; 1.
DR PRINTS; PR00388; PDIESTERASE2.
DR PROSITE; PS00607; PDEASE-II; 1.

-1- FUNCTION: BINDS TO, AND INDUCE THE COLLAPSE OF, COMMISSURAL AXONS/GROWTH CONES IN VITRO. MAY PLAY A ROLE IN CONSTRAINING THE ORIENTATION OF LONGITUDINALLY PROJECTING AXONS (BY SIMILARITY).
-1- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPB1 AND EPB1.
-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-1- TISSUE SPECIFICITY: HEART, PLACENTA, LUNG, LIVER, SKELETAL MUSCLE, KIDNEY, PANCREAS.
-1- INDUCTION: BY TNF-ALPHA.
-1- PTM: INDUCIBLE PHOSPHORYLATION OF TYROSINE RESIDUES IN THE CYTOPLASMIC DOMAIN (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.

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EMBL; U09304; AAA53093.1; -
EMBL; L37361; AAA52369.1; -
EMBL; U09303; AAB41127.1; -
EMBL; AL136092; CAB86409.1; -
MIM; 300035; -
InterPro; IPR001799; -
Pfam; PF00812; Ephrin; 1.
PROSITE; PS01299; Ephrin; 1.
Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;
Signal; Phosphorylation.
FT SIGNAL 1 24
FT CHAIN 25 346
FT DOMAIN 25 237
FT TRANSMEM 238 258
FT DOMAIN 259 346
FT DOMAIN 344 346
FT CARBOHYD 139 139
SEQUENCE 346 AA; 38006 MW; 473DD2F1A5BF89DE CRC64;

Query Match 100.0%; Score 29; DB 1; Length 346;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5
Db 131 DYYIT 135

RESULT 6
YOFACAEEL STANDARD; PRT; 360 AA.
ID YOFACAEEL
AC Q09337;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHETICAL 39.7 KDA PROTEIN ZK1290.10 IN CHROMOSOME II PRECURSOR.
GN ZK1290.10.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Taich A.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.

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KW Hydrolase; CAMP.
FT CONFLICT 94
SQ SEQUENCE 369 AA; 42016 MW; 47B752477E99BA88 CRC64;

L -> F (IN REF. 1).

Query Match 100.0%; Score 29; DB 1; Length 369;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYVIT 5

DB 123 DYVIT 127

RESULT 8

ID CIBA_PAEPP STANDARD; PRT; 675 AA.
AC P57091;

DT 01-OCT-2000 (Rel. 40, Created)

DT 01-OCT-2000 (Rel. 40, Last sequence update)

DE PARASPORAL CRYSTAL PROTEIN CRY18BA (PARASPORAL DELTA-ENDOTOXIN
DE CRYXVIIIB(A)) (CRYSTALLINE PARASPORAL PROTOXIN) (76 KDA CRYSTAL
DE PROTEIN).

GN CRY18BA OR CRYXVIIIB(A).

OS Paenibacillus popilliae (Bacillus popilliae).

OC Bacteria; Firmicutes; Bacillus/Clostridium group;

OX NCBI_TaxID=78057;

[1]

RP SEQUENCE FROM N.A.

RC STRAIN=BP3;

RA Patel R., Yousten A.A., Rippere K.;

RT "Detection of two new cry genes in Paenibacillus popilliae.";
Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: BINDS TO THE BRUSH BORDER MEMBRANE VESICLES OF SCARAB
CC LARVAE AND DAMAGES THE GUT WALL SOMEHOW TO ALLOW THE VEGETATIVE
CC CELLS OF P. POPILLIAE TO ENTER THE HEMOLYMPH (BY SIMILARITY).

CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPORE FORMATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART

CC OF THE SPORE COAT (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO THE DELTA-ENDOTOXIN FAMILY.

CC -----

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CC -----

DR EMBL; AF169250; AAF89667.1;

KW Toxin; Sporulation.

FT DOMAIN 101 104 POLY-LEU.

FT DOMAIN 199 204 POLY-LEU.

SQ SEQUENCE 675 AA; 75848 MW; 823B588B4AE81DF5 CRC64;

Query Match 100.0%; Score 29; DB 1; Length 675;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYVIT 5

DB 469 DYVIT 473

RESULT 9

ID CIBA_PAEPP

AC P57092; STANDARD; PRT; 695 AA.

DT 01-OCT-2000 (Rel. 40, Created)

DT 01-OCT-2000 (Rel. 40, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PARASPORAL CRYSTAL PROTEIN CRY18CA (PARASPORAL DELTA-ENDOTOXIN
DE CRYXVIIIC(A)) (CRYSTALLINE PARASPORAL PROTOXIN) (78 KDA CRYSTAL
DE PROTEIN).

GN CRY18CA OR CRYXVIIIC(A).

OS Paenibacillus popilliae (Bacillus popilliae).

OC Bacteria; Firmicutes; Bacillus/Clostridium group;

OX NCBI_TaxID=78057;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 14706;

RA Patel R., Yousten A.A., Rippere K.;

RT "Detection of two new cry genes in Paenibacillus popilliae.";
Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: BINDS TO THE BRUSH BORDER MEMBRANE VESICLES OF SCARAB
CC LARVAE AND DAMAGES THE GUT WALL SOMEHOW TO ALLOW THE VEGETATIVE
CC CELLS OF P. POPILLIAE TO ENTER THE HEMOLYMPH (BY SIMILARITY).

CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPORE FORMATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART

CC OF THE SPORE COAT (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO THE DELTA-ENDOTOXIN FAMILY.

CC -----

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CC -----

DR EMBL; AF169251; AAF89668.1;

KW Toxin; Sporulation.

SQ SEQUENCE 695 AA; 78259 MW; 406AC9154D75E070 CRC64;

Query Match 100.0%; Score 29; DB 1; Length 695;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYVIT 5

DB 485 DYVIT 489

RESULT 10

ID CIBA_PAEPP

AC Q45358; STANDARD; PRT; 706 AA.

DT 01-OCT-2000 (Rel. 40, Created)

DT 01-OCT-2000 (Rel. 40, Last sequence update)

DE PARASPORAL CRYSTAL PROTEIN CRY18AA (PARASPORAL DELTA-ENDOTOXIN
DE CRYXVIIIA(A)) (CRYSTALLINE PARASPORAL PROTOXIN) (79 KDA CRYSTAL
DE PROTEIN).

GN CRY18AA OR CRYXVIIIA(A) OR CRYBP1.

OS Paenibacillus popilliae (Bacillus popilliae).

OC Bacteria; Firmicutes; Bacillus/Clostridium group;

OX NCBI_TaxID=78057;

RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC STRAIN=H1 / SUBSP. MELOLONTHAE;

RX MEDLINE=97352693; PubMed=9209052;

RA Zhang J., Hodgman T.C., Krieger L., Schnetter W., Schairer H.U.;

RT "Cloning and analysis of the first cry gene from Bacillus popilliae.";

RL J. Bacteriol. 179:4336-4341(1997).

CC -!- FUNCTION: BINDS TO THE BRUSH BORDER MEMBRANE VESICLES OF SCARAB
CC LARVAE AND DAMAGES THE GUT WALL SOMEHOW TO ALLOW THE VEGETATIVE
CC CELLS OF P. POPILLIAE TO ENTER THE HEMOLYMPH. ACTIVE ON

CC M. MELOLONTHAE.

CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPORE FORMATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART

Fri Jun 29 08:05:14 2001

CC OF THE SPORE COAT (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X99049; CAA67506.1; -
CC InterPro: IPR001178; -
CC Pfam: PF00555; endotoxin; 1.
CC Toxin; Sporulation.
FT CONFLICT 670 670 T -> F (IN AA SEQUENCE).
SQ SEQUENCE 706 AA; 79034 MW; 9172B949BE499C1D CRC64;

Query Match 100.0%; Score 29; DB 1; Length 706;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5
DB 506 DYYIT 510
|||||

RESULT 11
YCB9_YEAST STANDARD; PRT; 1347 AA.
ID YCB9_YEAST
AC P25384;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE TRANSPOSIN TY1-17 PROTEIN B.
GN TY1B OR YCLO19W OR YCLO19W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8620524; PubMed=3010239;
RA Warrington J.R., Anwar R., Newlon C.S., Waring R.B., Davies R.W.,
RA Indge K.J., Oliver S.G.;
RT "A 'hot-spot' for Ty transposition on the left arm of yeast
RT chromosome III.",
RL Nucleic Acids Res. 14:3475-3485(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041864; PubMed=2997719;
RA Warrington J.R., Waring R.B., Newlon C.S., Indge K.J., Oliver S.G.;
RA "Nucleotide sequence characterization of Ty 1-17, a class II
RT transposon from yeast.",
RL Nucleic Acids Res. 13:6679-6693(1985).
RN [3]
RP SEQUENCE FROM N.A.
RA Oliver S.G., Anwar R., Brown A., Gent M.E., Indge K.J., James C.M.,
RA Staveva L.I.;
RA Submitted (MAR-1992) to the EMBL/GenBank/DBJ databases.
RL -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A11.
CC -----
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CC -----
CC EMBL; X03840; CAA27458.1; -
CC EMBL; X59720; E264443; -

DR PIR; B23496; B23496.
DR PIR; S19345; S19345.
DR MEROPS; A11.003; -
DR SGD; S000524; YCLO19W.
KW Transposable element; Hypothetical protein; Hydrolase;
KW Aspartyl protease; ATP-binding.
FT NP_BIND 1223 1230 ATP (POTENTIAL).
SQ SEQUENCE 1347 AA; 154069 MW; AD3660C5E7B282FF CRC64;

Query Match 100.0%; Score 29; DB 1; Length 1347;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5
DB 931 DYYIT 935
|||||

RESULT 12
RS4_SULSO STANDARD; PRT; 181 AA.
ID RS4_SULSO
AC P95987;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE 30S RIBOSOMAL PROTEIN S4P.
DE RPS4P OR RPS4 OR C04049.
GN Sulfolobus solfataricus.
OS Sulfolobus solfataricus.
OC Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.
OX NCBI_TaxID=2287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 1617 / P2;
RX MEDLINE=97055432; PubMed=8899719;
RA Sensen C.W., Klenk H.-P., Singh R.K., Allard G., Chan C.C.-Y.,
RA Liu Q.-Y., Penny S.L., Young F., Schenk M.E., Gaasterland T.,
RA Doolittle W.F., Ragan M.A., Charlebois R.L.;
RA "Organizational characteristics and information content of an
RT archaeal genome: 156 kb of sequence from Sulfolobus solfataricus
RT P2.",
RL Mol. Microbiol. 22:175-191(1996).
RN [1]
RP -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA
RP (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 S4 RNA-BINDING DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE S4P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC -----
CC EMBL; Y08257; CAA69529.1; -
CC InterPro: IPR001912; -
CC InterPro: IPR002942; -
CC Pfam: PF01479; S4; 1.
DR PROSITE; PS00632; RIBOSOMAL_S4; 1.
KW Ribosomal protein; rRNA-binding.
FT DOMAIN 104 151 RNA-BINDING (S4 TYPE).
SQ SEQUENCE 181 AA; 20748 MW; E48B4C85CD98C522 CRC64;

Query Match 96.6%; Score 28; DB 1; Length 181;
Best Local Similarity 80.0%; Pred. No. 22;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5
DB 154 DYYIT 158
|||||

```

RESULT 13
Y438_METJA
ID Y438_METJA STANDARD; PRT; 381 AA.
AC Q57880;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHETICAL PROTEIN MJ0438.
GN MJ0438.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE-96337999; PubMed-8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kervilave A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii."
RL Science 273:1058-1073(1996).
CC -----
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CC -----
CC EMBL; U67495; AAB98426.1; -
CC TIGR; MJ0438; -
CC InterPro; IPR000241; -
CC Pfam; PF01170; UPF0020.1.
CC PROSITE; PS01261; UPF0020.1.
CC PROSITE; PS00092; NC_MTASE; UNKNOWN_1.
CC Hypothetical protein.
CC SEQUENCE 381 AA; 43738 MW; 9BB972D94479444D CRC64;
DR EMBL; U67495; AAB98426.1; -
DR TIGR; MJ0438; -
DR InterPro; IPR000241; -
DR InterPro; IPR002052; -
DR Pfam; PF01170; UPF0020.1.
DR PROSITE; PS01261; UPF0020.1.
DR PROSITE; PS00092; NC_MTASE; UNKNOWN_1.
DR Hypothetical protein.
DR SEQUENCE 381 AA; 43738 MW; 9BB972D94479444D CRC64;

Query Match 96.6%; Score 28; DB 1; Length 381;
Best Local Similarity 80.0%; Pred. No. 50;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5
DB 2 DYYVT 6

RESULT 14
Y299_METJA
ID Y299_METJA STANDARD; PRT; 389 AA.
AC Q57747;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHETICAL PROTEIN MJ0299.
GN MJ0299.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Berks M., Smith A.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE BESTROPHIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z30423; CAA83005.1; -
CC PIR; S42371; S42371.
CC WormPep; T2065.4; CE00481.
CC InterPro; IPR000615; -
CC Pfam; PF01062; Worm_family_8; 1.

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RP SEQUENCE FROM N.A.
RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE-96337999; PubMed-8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kervilave A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii."
RL Science 273:1058-1073(1996).
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CC -----
CC EMBL; U67485; AAB98286.1; -
CC TIGR; MJ0299; -
CC InterPro; IPR002803; -
CC Pfam; PF01950; DUF100; 1.
CC Hypothetical protein.
CC SEQUENCE 389 AA; 43245 MW; 1BB8D890F931CE73 CRC64;

Query Match 96.6%; Score 28; DB 1; Length 389;
Best Local Similarity 80.0%; Pred. No. 51;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5
DB 49 DYYVT 53

RESULT 15
YNN4_CAEEL
ID YNN4_CAEEL STANDARD; PRT; 405 AA.
AC P34577;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE HYPOTHETICAL 47.7 KDA PROTEIN T2065.4 IN CHROMOSOME III.
GN T2065.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Berks M., Smith A.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE BESTROPHIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z30423; CAA83005.1; -
CC PIR; S42371; S42371.
CC WormPep; T2065.4; CE00481.
CC InterPro; IPR000615; -
CC Pfam; PF01062; Worm_family_8; 1.

```

us-09-724-406-4.rsp

Fri Jun 29 08:05:14 2001

KW Hypothetical protein.
SQ SEQUENCE 405 AA; 47718 MW; 0374DEF2334B0380 CRC64;

Query Match 96.6%; Score 28; DB 1; Length 405;
Best Local Similarity 80.0%; Pred. No. 53;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5
| | | |
Db 204 DYYIT 208

Search completed: June 28, 2001, 15:54:34
Job time: 122 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 28, 2001, 15:52:32 ; Search time 411.58 Seconds
(without alignments)
1.607 Million cell updates/sec

Title: us-09-724-406-4
Perfect score: 29
Sequence: 1 DYYIT 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues
Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_unclassified.*
- 13: sp_vertebrate.*
- 14: sp_virus.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	104	14	Q9J583
2	29	100.0	208	8	Q21565
3	29	100.0	338	1	O58526
4	29	100.0	358	1	O58692
5	29	100.0	365	1	O27721
6	29	100.0	472	14	Q9EML2
7	29	100.0	473	2	Q9PNC5
8	29	100.0	527	2	Q9K806
9	29	100.0	537	3	Q9P7H1
10	29	100.0	613	5	Q9VBJ6
11	29	100.0	736	1	O29790
12	29	100.0	767	3	Q12357
13	29	100.0	1050	3	Q12494
14	29	100.0	1285	3	Q03934
15	29	100.0	1346	3	Q04345
16	29	100.0	1346	3	Q05679
17	29	100.0	1346	3	Q05369
18	29	100.0	1347	3	Q03494
19	29	100.0	1633	13	Q90941

20	29	100.0	1770	3	Q12113
21	29	100.0	1770	3	Q12501
22	29	100.0	1770	3	Q12503
23	29	100.0	1770	3	Q07791
24	29	100.0	1770	3	Q12472
25	29	100.0	1770	3	Q12491
26	29	100.0	1771	3	P87006
27	29	100.0	1810	3	Q12022
28	29	100.0	2338	5	O94269
29	29	100.0	3147	5	Q17464
30	28	96.6	107	3	O9HEB0
31	28	96.6	184	11	O9JK38
32	28	96.6	301	8	Q36376
33	28	96.6	328	10	O9XI00
34	28	96.6	353	14	O9PYZ0
35	28	96.6	367	2	O9RZB4
36	28	96.6	429	2	O56212
37	28	96.6	443	5	O9VLC1
38	28	96.6	536	10	O23444
39	28	96.6	586	10	O9SNT3
40	28	96.6	594	5	O9TZ18
41	28	96.6	699	2	O9JWJ3
42	28	96.6	755	5	O45093
43	28	96.6	791	1	O9HM29
44	28	96.6	818	5	O9TZ17
45	28	96.6	818	5	O9TW90

ALIGNMENTS

RESULT 1

Q9J583 PRELIMINARY; PRT; 104 AA.
AC Q9J583;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE ORF FPV147 HT MOTIF GENE FAMILY PROTEIN.
GN FPV147.
OS Fowlpox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OX Avipoxvirus.
OX NCBI_TaxID=10361;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20193820; PubMed=10729156;
RA Afonso C.L., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
RT "The genome of fowlpox virus."
RL J. Virol. 74:3815-3831(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Afonso C.L., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF198100; AAF4491.1;
SQ SEQUENCE 104 AA; 12685 MW; AB7468F313419D94 CRC64;

Query Match 100.0%; Score 29; DB 14; Length 104;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYYIT 5
|
|
|
|
|
Db 44 DYYIT 48

RESULT 2

O21565 PRELIMINARY; PRT; 208 AA.
ID O21565
AC O21565;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)

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DR      ProDom; PD014260; -; 1.
DR      5890F6CB9ECFED24 CRC64;

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Query Match 100.0%; Score 29; DB 1; Length 365;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5
Db 44 DYYIT 48

RESULT 6
Q9EML2
ID Q9EML2 PRELIMINARY; PRT; 472 AA.
AC Q9EML2;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE AMV194.
GN AMV194.
OS Amsacta moorei entomopoxvirus (AnEPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
OC Entomopoxvirus B.
OX NCBI_TaxID=28321;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20396580; PubMed=10936094;
RA Bowden A.L., Glassberg K.J., Diggins J., Shaw R., Farmerie W.,
Moyer R.W.;
RA "Complete Genomic Sequence of the Amsacta moorei Entomopoxvirus:
RT Analysis and Comparison with Other Poxviruses.";
RL Virology 274:120-139(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Bowden A.L., Glassberg K.J., Diggins J., Shaw R., Farmerie W.,
Moyer R.W.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF250284; AAG02900.1; -;
SQ SEQUENCE 472 AA; 57680 MW; 532DF441C6009AFE CRC64;

Query Match 100.0%; Score 29; DB 14; Length 472;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5
Db 200 DYYIT 204

RESULT 7
Q9PNC5
ID Q9PNC5 PRELIMINARY; PRT; 473 AA.
AC Q9PNC5;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN.
GN CJI170C.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
OC Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=NCTC 111168;
RC MEDLINE=20150912; PubMed=10688204;
RA Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
BAHAM D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., Van Vliet A.H.M.,
Whitehead S., Barrall B.G.;
RA "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT reveals hypervariable sequences.";
RL Nature 403:665-668(2000).

DR EMBL: AL139077; CAB73424.1; -;
SQ SEQUENCE 473 AA; 53339 MW; AE6597673B356785 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 473;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5
Db 170 DYYIT 174

RESULT 8
Q9K806
ID Q9K806 PRELIMINARY; PRT; 527 AA.
AC Q9K806;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE ACETATE-COA LIGASE.
GN BH3201.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=86565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RA Takami H., Nakasone K., Takaki Y.;
RL Submitted (MA3-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP001513; BAB06920.1; -;
DR InterPro; IPR000873; -;
DR Pfam; PF00501; AMP-binding; 1.
DR PRINTS; PRO0154; AMPBINDING.
DR PROSITE; PS00455; AMP_BINDING; 1.
KW Ligase.
SQ SEQUENCE 527 AA; 59359 MW; 6E67E1DCFBA45B8D CRC64;

Query Match 100.0%; Score 29; DB 2; Length 527;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5
Db 396 DYYIT 400

RESULT 9
Q9P7H1
ID Q9P7H1 PRELIMINARY; PRT; 537 AA.
AC Q9P7H1;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE PROBABLE PROTEIN-TYROSINE PHOSPHATASE CDC14 HOMOLOG.
GN SPAC1782.09C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972H-;
RA Wood V., Rajandream M.A., Barrell B.G., Brown S., Harris D.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL158056; CAB76271.1; -;
DR InterPro; IPR000242; -;
DR InterPro; IPR000340; -;
DR InterPro; IPR000387; -;
DR Pfam; PF00782; DSPC; 1.

DR PRINTS: PR00700; PRTYPHPTASE.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE; PS00556; TYR_PHOSPHATASE_2; 1.
 KW Hydrolase.
 SQ SEQUENCE 537 AA; 60253 MW; F5E50A8C0924C7EA CRC64;

Query Match 100.0%; Score 29; DB 3; Length 537;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXYIT 5
 Db 141 DXYIT 145

RESULT 10
 Q9VBJ6 PRELIMINARY; PRT; 613 AA.

AC Q9VBJ6;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE CG14540 PROTEIN.
 GN CG14540.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballwey L.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laske P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weisscock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 DR EMBL; AF003754; AAF56538.1; -.

DR FlyBase; FBgn0039398; CG14540.
 SQ SEQUENCE 613 AA; 68546 MW; FE292B04E8E82FC CRC64;

Query Match 100.0%; Score 29; DB 5; Length 613;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXYIT 5
 Db 76 DXYIT 80

RESULT 11
 O29790 PRELIMINARY; PRT; 736 AA.

AC O29790;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE CONSERVED HYPOTHETICAL PROTEIN.
 GN AF0459.
 OS Archaeoglobus fulgidus.
 OC Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
 OC Archaeoglobus.
 OX NCBI_TaxID=2234;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
 RX MEDLINE=98049343; PubMed=9389475;
 RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
 RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
 RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyriades N.C.,
 RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
 RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
 RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
 RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
 RA Cotton P.W., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
 RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
 RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
 RA Venter J.C.;
 RT "The complete genome sequence of the hyperthermophilic, sulphate-
 reducing Archaeon Archaeoglobus fulgidus."
 RL Nature 390:364-370(1997).
 DR EMBL; AE001073; AAB90778.1; -.
 DR TIGR; AF0459; -.
 DR InterPro; IPR000731; -.
 DR InterPro; IPR001395; -.
 DR PROSITE; PS00063; ALDO-KETO-REDUCTASE_3; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 736 AA; 81942 MW; 1234B6CCA1995011 CRC64;

Query Match 100.0%; Score 29; DB 1; Length 736;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXYIT 5
 Db 552 DXYIT 556

RESULT 12
 Q12357 PRELIMINARY; PRT; 767 AA.

AC Q12357;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE FRAME-SHIFT IN TYB PROBABLY NOT FUNCTIONAL.
 GN TV1B.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rieger M., Mueller-Auer S., Brueckner M., Schaefer M.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MIPS;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z72824; CAA97037.1; -;
 DR EMBL; Z72823; CAA97029.1; -;
 DR InterPro; IPR000194; -;
 DR PROSITE; PS00152; ATPASE_ALPHA_BETA; UNKNOWN_1.
 SQ SEQUENCE 767 AA; 87951 MW; 5F69264A58605BA5 CRC64;

Query Match 100.0%; Score 29; DB 3; Length 767;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYYIT 5
 |||||
 Db 351 DYYIT 355

RESULT 13

Q12494 PRELIMINARY; PRT; 1050 AA.
 AC Q12494; P89899;
 DT 01-NOV-1996 (TREMELrel. 01, Created)
 DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
 DT 01-MAR-2001 (TREMELrel. 16, Last annotation update)
 DE CHROMOSOME IV READING FRAME ORF YDR017C.
 GN KCS1.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Prydz H., Eide L.G.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MIPS;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96170769; PubMed=8601473;
 RA Huang K.N., Symington L.S.;
 RT "Suppressors of a Saccharomyces cerevisiae pkc1 mutation identify
 alleles of the phosphatase gene PTC1 and of a novel gene encoding a
 putative basic leucine zipper protein.";
 RT Genetics 141:1275-1285(1995).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Eide L.G., Sander C., Prydz H.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB972;
 RA Dedman K., Brown D., Hamlyn N., Bowman S.;
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB572;
 RA Barrell B., Rajandream M.A.;

RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z74313; CAA98837.1; -;
 DR EMBL; S81651; AAB36234.1; -;
 DR EMBL; X95966; CAA65208.1; -;
 DR EMBL; Z49770; CAA98942.1; -;

DR EMBL; Z74314; CAA98839.1; -;
 DR SGD; S0002424; KCS1.
 KW Hypothetical protein.
 SQ SEQUENCE 1050 AA; 119549 MW; 9C7507CA5F4B0FC7 CRC64;

Query Match 100.0%; Score 29; DB 3; Length 1050;
 Best Local Similarity 100.0%; Pred. No. 6.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYYIT 5
 |||||
 Db 821 DYYIT 825

RESULT 14

Q03934 PRELIMINARY; PRT; 1285 AA.
 AC Q03934;
 DT 01-NOV-1996 (TREMELrel. 01, Created)
 DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
 DT 01-MAR-2001 (TREMELrel. 16, Last annotation update)
 DE HYPOTHETICAL PROTEIN (FRAGMENT).
 GN TYB OR YDR261W-B.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB972;
 RA Murphy L., Harris D.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB972;
 RA Barrell B., Rajandream M.A., Walsh S.V.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY. THE PROTEASE BELONGS TO THE PEPTIDASE FAMILY A1; ALSO
 CC KNOWN AS THE EUKARYOTIC ASPARTYL PROTEASES FAMILY.

DR EMBL; Z68329; CAA92721.1; -;
 DR SGD; S0007397; YDR261W-B.
 DR InterPro; IPR000194; -;
 DR InterPro; IPR001584; -;
 DR InterPro; IPR001969; -;
 DR Pfam; PF00665; rve; 1.
 DR PROSITE; PS00141; ASP_PROTEASE; 1.
 DR PROSITE; PS00152; ATPASE_ALPHA_BETA; UNKNOWN_1.
 KW Aspartyl protease; Hydrolase; Hypothetical protein.
 FT NON_TER 1285 1285
 SQ SEQUENCE 1285 AA; 146556 MW; 7E29F748800E52D2 CRC64;

Query Match 100.0%; Score 29; DB 3; Length 1285;
 Best Local Similarity 100.0%; Pred. No. 7.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYYIT 5
 |||||
 Db 930 DYYIT 934

RESULT 15

Q04345 PRELIMINARY; PRT; 1346 AA.
 AC Q04345;
 DT 01-NOV-1996 (TREMELrel. 01, Created)
 DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
 DT 01-MAR-2001 (TREMELrel. 16, Last annotation update)
 DE HYPOTHETICAL 153.9 KDA PROTEIN.
 GN TYB, YDR673.05C OR YDR034C-D.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-AB972;
 RA Connor R., Churcher C.M.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-AB972;
 RA Barrell B., Rajandream M.A., Walsh S.V.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: THE PROTEASE BELONGS TO THE PEPTIDASE FAMILY A1; ALSO
 CC -2- KNOWN AS THE EUKARYOTIC ASPARTYL PROTEASES FAMILY.
 DR EMBL; Z68196; CAA92372.1; -.
 DR SGD; S0007345; YDR034C-D.
 DR InterPro; IPR001194; -.
 DR InterPro; IPR001584; -.
 DR InterPro; IPR001969; -.
 DR Pfam; PF00665; rve; 1.
 DR PROSITE; PS00141; ASP_PROTEASE; 1.
 DR PROSITE; PS00152; ATPASE_ALPHA_BETA; UNKNOWN_1.
 KW Aspartyl protease; Hydrolase; Hypothetical protein.
 SQ SEQUENCE 1346 AA; 153889 MW; 53B74F9E55C03ADF CRC64;

Query Match 100.0%; Score 29; DB 3; Length 1346;
 Best Local Similarity 100.0%; Pred. No. 8.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYIT 5

Db 930 DYYIT 934

Search completed: June 28, 2001, 16:08:18
 Job time: 946 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2001, 16:14:33 ; Search time 362.28 seconds
(without alignments)
2.845 Million cell updates/sec

Title: US-09-724-406-6
Perfect score: 101
Sequence: 1 WYPGSGNTKYNKFKG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_0601.*

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- 12: /SID58/gcgdata/geneseq/geneseq/AA1991.DAT.*
- 13: /SID58/gcgdata/geneseq/geneseq/AA1992.DAT.*
- 14: /SID58/gcgdata/geneseq/geneseq/AA1993.DAT.*
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- 19: /SID58/gcgdata/geneseq/geneseq/AA1998.DAT.*
- 20: /SID58/gcgdata/geneseq/geneseq/AA1999.DAT.*
- 21: /SID58/gcgdata/geneseq/geneseq/AA2000.DAT.*
- 22: /SID58/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	93	92.1	117	9 AAP80148	Biosynthetic antib
2	93	92.1	117	9 AAP80149	Biosynthetic antib
3	93	92.1	249	9 AAP80154	Biosynthetic antib
4	92	91.1	116	16 AAR79241	Heavy chain variab
5	91	90.1	138	21 AAY56873	MAB CT-M-01 heavy
6	91	90.1	139	14 AAR33950	CTMO1 VH. Synthet
7	91	90.1	139	14 AAR33953	gH1 variable domai
8	91	90.1	139	18 AAR29750	Anti-HMFG MAB CTMO
9	91	90.1	139	18 AAW29753	CDR-grafted humani
10	91	90.1	139	21 AAY56877	gH1 variable domai
11	91	90.1	382	18 AAW26651	Chimeric receptor

12	91	90.1	403	18 AAW26648	Chimeric receptor
13	91	90.1	473	18 AAW26646	Chimeric receptor
14	91	90.1	514	18 AAW26647	Chimeric receptor
15	91	90.1	651	18 AAW26649	Chimeric receptor
16	91	90.1	692	18 AAW26650	Chimeric receptor
17	90	89.1	17	21 AAY78323	Anti-zeta-chain an
18	90	89.1	123	21 AAY78325	Monoclonal antibod
19	90	89.1	469	14 AAR40384	Bispecific anti-ze
20	90	89.1	532	21 AAY78328	Activating polypep
21	88	87.1	555	22 AAB19871	Activating polypep
22	88	87.1	565	22 AAB19873	Activating polypep
23	88	87.1	577	22 AAB19872	Activating polypep
24	88	87.1	704	22 AAB19888	MLV envelope glyco
25	86	85.1	15	20 AAY40700	A3 derivative #21,
26	86	85.1	15	21 AAB30039	Scaffold protein S
27	84	83.2	112	22 AAB74000	Anti-chrysantheic
28	83	82.2	121	18 AAW07437	Anti-DNA antibody
29	82	81.7	122	9 AAP81365	Heavy chain variab
30	82	81.2	116	17 AAW03742	Murine monoclonal
31	82	81.2	132	22 AAB62049	Mouse monoclonal a
32	82	81.2	274	14 AAR44228	Chimeric Ig superf
33	80	79.2	122	18 AAW01577	Lead binding MAb 1
34	79	78.2	119	19 AAW49813	Amino acid sequenc
35	79	78.2	119	19 AAW49814	Amino acid sequenc
36	79	78.2	138	14 AAR32666	Variable region of
37	79	78.2	138	19 AAW49810	Humanised C4G1 Ig
38	79	78.2	222	14 AAR39267	Fragment of humani
39	79	78.2	222	19 AAW49817	Humanised C4G1 Ig
40	79	78.2	235	14 AAR39268	Humanised C4G1 Ig
41	79	78.2	235	19 AAW49818	Amino acid sequenc
42	79	78.2	449	14 AAR43339	Completely humanis
43	79	78.2	449	19 AAW49816	Amino acid sequenc
44	78	77.2	17	18 AAW27348	CDR2 from murine a
45	78	77.2	118	16 AAR79159	Human IgE receptor

ALIGNMENTS

RESULT 1
AAP80148
ID AAP80148 standard; peptide; 117 AA.
XX
AC AAP80148;
XX
DT 13-OCT-1990 (first entry)
XX
DE Biosynthetic antibody binding site.
XX
KW Biosynthetic antibody binding site; complementarity determining region;
KW framework region.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Region 28..38
FT /label=CDR1
FT Region 46...66
FT /label=CDR2
FT Region 98..104
FT /label=CDR3

XX WO8809344-A.
XX
PD 01-DEC-1988.
XX
PF Heavy chain variab
XX MAB CT-M-01 heavy
XX CTMO1 VH. Synthet
XX gH1 variable domai
XX Anti-HMFG MAB CTMO
XX CDR-grafted humani
XX gH1 variable domai
XX Chimeric receptor
PI Huston JS, Oppermann H;

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XX DR WPI; 1988-353928/49.
XX PF Recombinant multifunctional protein - having antibody binding site and a
XX PT sequence for biological activity, ion sequestering or binding to a solid
XX PT support.
XX PS
XX PA Disclosure; : 5pp; English.
XX PI
XX PI The biosynthetic antibody binding site forms part of a single chain
XX CC multi-functional biosynthetic protein. The protein also comprises
XX CC an effector molecule with biological activity (eg an enzyme, toxin,
XX CC receptor binding site, growth factor, lymphokine, cytokine or
XX CC antimetabolite), an amino acid sequence capable of sequestering an
XX CC ion (eg calmodulin or metallothionein), or an amino acid sequence
XX CC capable of selective binding to a solid support (eg streptavidin or
XX CC a fragment of protein A). The BABS contains at least one domain
XX CC homologous to part/all of the variable region of an immunoglobulin
XX CC capable of binding the preselected antigenic determinant. The protein
XX CC can be used for specific binding assays, affinity purification, biocatalysts,
XX CC drug targeting, imaging and immunological treatment of oncogenic and
XX CC infectious diseases. It offers fewer cleavage sites to circulating
XX CC proteolytic enzymes, and has improved stability. It reaches target
XX CC tissues rapidly and is quickly cleared from the body. It also has
XX CC reduced immunogenicity and its design facilitates binding to other
XX CC moieties in drug targeting and imaging applications. The BABS
XX CC is a 26-10/g-loop hybrid - it comprises framework region from 26-10 VH
XX CC and the CDRs from glp-4 VH.
XX CC
XX CC Sequence 117 AA;

Query Match 92.1%; Score 93; DB 9; Length 117;
Best Local Similarity 88.2%; Pred. No. 2.3e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WYPGSGNTKYNEKFGK 17
Db 50 wyppgngntkynenfk 66
||||:||||||| |||

RESULT 2
AAP80149 ID AAP80149 standard; protein; 117 AA.
AC AAP80149;
XX
XX 13-OCT-1990 (first entry)
XX
XX Biosynthetic antibody binding site.
XX
XX Biosynthetic antibody binding site; complementarity determining region;
XX framework region.
XX
XX Mus musculus/Homo sapiens.
XX
XX Key Location/Qualifiers
XX FH Region 10..27
XX FT /label-newm1 framework region
XX FT Region 28..38
XX FT /label-CDR
XX FT Region 39..45
XX FT /label-newm2 framework region
XX FT Region 46..66
XX FT /label-CDR
XX FT Region 67..97
XX FT /label-newm3 framework region
XX FT Region 98..104
XX FT /label-CDR
XX FT Region 105..117
XX FT /label-newm4 framework region
XX PN WO8809344-A.

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XX PD 01-DEC-1988.
XX PF 19-MAY-1988; 88WO-US01737.
XX PR 21-MAY-1987; 87US-0052800.
XX PA (CREA-) CREATIVE BIOMOLECULES INC.
XX PI
XX PI Huston JS, Oppermann H;
XX WPI; 1988-353928/49.
XX Recombinant multifunctional protein - having antibody binding site and
XX PT sequence for biological activity, ion sequestering or binding to a solid
XX PT support.
XX PS
XX PA Disclosure; : 5pp; English.
XX PI
XX PI The biosynthetic antibody binding site forms part of a single chain
XX CC multi-functional biosynthetic protein. The protein also comprises
XX CC an effector molecule with biological activity (eg an enzyme, toxin,
XX CC receptor binding site, growth factor, lymphokine, cytokine or
XX CC antimetabolite), an amino acid sequence capable of sequestering an
XX CC ion (eg calmodulin or metallothionein), or an amino acid sequence
XX CC capable of selective binding to a solid support (eg streptavidin or
XX CC a fragment of protein A). The BABS contains at least one domain
XX CC homologous to part/all of the variable region of an immunoglobulin
XX CC capable of binding the preselected antigenic determinant. The protein
XX CC can be used for specific binding assays, affinity purification, biocatalysts,
XX CC drug targeting, imaging and immunological treatment of oncogenic and
XX CC infectious diseases. It offers fewer cleavage sites to circulating
XX CC proteolytic enzymes, and has improved stability. It reaches target
XX CC tissues rapidly and is quickly cleared from the body. It also has
XX CC reduced immunogenicity and its design facilitates binding to other
XX CC moieties in drug targeting and imaging applications. The BABS
XX CC is a newm/g-loop hybrid - it comprises framework regions from human
XX CC myeloma antibody NEWM VH and the complementarity determining regions
XX CC from glp-4 VH, ie illustrates a 'humanised' binding site having a
XX CC human framework but an affinity for lysozyme similar to murine glp-4.
XX CC
XX CC Sequence 117 AA;

Query Match 92.1%; Score 93; DB 9; Length 117;
Best Local Similarity 88.2%; Pred. No. 2.3e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WYPGSGNTKYNEKFGK 17
Db 50 wyppgngntkynenfk 66
||||:||||||| |||

RESULT 3
AAP80154 ID AAP80154 standard; protein; 249 AA.
AC AAP80154;
XX
XX 01-JAN-1980 (first entry)
XX
XX Biosynthetic antibody binding site.
XX
XX Biosynthetic antibody binding site; framework region; assay; imaging;
XX multifunctional protein.
XX
XX WO8809344-A.
XX
XX 01-DEC-1988.
XX PR 19-MAY-1988; 88WO-US01737.
XX PF
XX PT 21-MAY-1987; 87US-0052800.
XX PN

```

XX PA (CREA-) CREATIVE BIOMOLECULES INC.
XX PI Huston JS, Oppermann H;
XX DR WPI; 1988-353928/49.
XX DR N-PSDB; AAN80180.
XX
XX Recombinant multifunctional protein - having antibody binding site and a
XX PT sequence for biological activity, ion sequestering or binding to a
XX PT solid support.
XX PS
XX PS Disclosure; 15pp; English.
XX
XX The biosynthetic antibody binding site forms part of a recombinant
XX CC multifunctional protein which also comprises an effector protein, an AA
XX CC acid sequence capable of sequestering an ion, or a sequence capable of
XX CC binding to a solid support. The BABS comprises the framework region from
XX CC murine anti-digoxin monoclonal antibody 26-10 heavy chain variable region
XX CC and the complementarity determining region from G-loop-4 heavy chain
XX CC variable region and has lysozyme specificity. The effector protein is an
XX CC enzyme, toxin, receptor, binding site, growth factor, cytokine
XX CC or antimetabolite. The sequence capable of sequestering an ion is
XX CC calmodulin or metallothionein. The sequence capable of binding to solid
XX CC support is streptavidin or a protein A fragment. The protein may be used
XX CC for, eg specific binding assays, affinity purification, biocatalysts, drug
XX CC targeting, imaging and immunological treatment of oncogenic etc.
XX CC diseases. The protein offers fewer cleavage sites to circulating
XX CC proteolytic enzymes and have improved stability. They reach target organs
XX CC rapidly and are cleared quickly from the body. They also have reduced
XX CC immunogenicity.
XX SQ Sequence 249 AA;

Query Match 92.1%; Score 93; DB 9; Length 249;
Best Local Similarity 88.2%; Pred. No. 5.3e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WYPCSGNTRYNEKFKG 17
| | | | | : | | | | |
DB 52 WYPCSGNTRYNEKFKG 68

RESULT 4
AAR79241
ID AAR79241 standard; Protein; 116 AA.
XX
XX AAR79241;
XX
XX 21-DEC-1995 (first entry)
XX
XX Heavy chain variable region for monoclonal antibody 4A10.
XX
XX Monoclonal antibody; heavy metal; mercury; variable region;
XX KW heavy chain.
XX
XX Synthetic.
XX OS
XX WO9520607-A.
XX PN
XX 03-AUG-1995.
XX PD
XX 27-JAN-1995; 95WO-US01199.
XX PF
XX 27-JAN-1994; 94US-0187407.
XX PR
XX (BION-) BIONEERASKA INC.
XX PA
XX Lopez O, Wagner FW, Wylie DE;
XX PI
XX WPI; 1995-275415/36.
XX DR N-PSDB; AAR79498.

XX
XX PT New polypeptide(s) which bind heavy metals, esp. mercury - derived from
XX PT monoclonal antibodies, used for detecting, removing, adding or
XX PT neutralising heavy metals
XX PS
XX PS Claim 13; Page 54; 106pp; English.
XX
XX Hybridoma antibodies have been produced with the spleen cells of
XX CC BALB/c mouse that had received multiple injections of mercuric ions
XX CC reacted with glutathione to produce a mercuric ion coordinate
XX CC covalent compound which was covalently bound to keyhole limpet
XX CC hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23F8, 2D5,
XX CC 5B6 and 3E8) were producing MABs that were strongly positive
XX CC against glutathione-mercuric ions but negative against glutathione
XX CC without mercuric ions. RNA was isolated from hybridoma cells with
XX CC guanidine isothiocyanate. First strand cDNA synthesis was catalysed
XX CC by M-MLV reverse transcriptase. The primers used for cDNA synthesis
XX CC were complementary to the 5' end of the CH1 domain of the heavy
XX CC chain expressed by the hybridoma of interest, or to the 5' and of
XX CC the C kappa domain. Some of the primers used for cDNA synthesis are
XX CC shown in AAR797311-097518. The primer used for cDNA synthesis of the
XX CC variable region of a particular antibody polypeptide was also used
XX CC for PCR amplification of that variable region, in conjunction with
XX CC an appropriate V-region primer. In addition, the VH primer AAR797518
XX CC was used to amplify the mab 2D5 and 5B6 heavy chains. The sequences
XX CC of the PCR amplified nucleotides were determined. These are given
XX CC in AAR79498-097510 and the deduced AA sequences in AAR79241-R79250 &
XX CC AAR79970-R79971. The descriptions of the SEQ ID nos given on pp 44-45
XX CC and in the claims are different from the descriptions in the
XX CC sequence listings. The descriptions in the sequence listings are
XX CC used here.
XX SQ Sequence 116 AA;

Query Match 91.1%; Score 92; DB 16; Length 116;
Best Local Similarity 88.2%; Pred. No. 3.3e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WYPCSGNTRYNEKFKG 17
| | | | | : | | | | |
DB 50 WYPCSGNTRYNEKFKG 66

RESULT 5
AAY56873
ID AAY56873 standard; Protein; 138 AA.
XX
XX AAY56873;
XX
XX 14-APR-2000 (first entry)
XX
XX MAB CT-M-01 heavy chain VH domain.
XX
XX Cytotoxic; drug conjugate; humanized; monoclonal antibody; CT-M-01;
XX KW human milk fat globule; growth inhibition.
XX
XX Homo sapiens.
XX OS
XX US6015562-A.
XX PN
XX 18-JAN-2000.
XX PD
XX 16-FEB-1996; 96US-0603024.
XX PF
XX 31-OCT-1994; 94US-0332025.
XX PR
XX 22-SEP-1992; 92US-0948277.
XX PR
XX 06-OCT-1993; 93US-0132725.
XX
XX (AMCY) AMERICAN CYANAMID CO.
XX PA
XX Hamann PR, Hinman LM;
XX PI
XX

DR WPI: 2000-126309/11.
 DR N-PSDB; AAZ46912.

XX New cytotoxic drug conjugates are useful for inhibiting the growth of
 PT unwanted cells -

XX Disclosure; Columns 21-22; 37pp; English.

XX The invention relates to cytotoxic drug conjugates of a specified
 CC formula. The conjugate comprise a humanized monoclonal antibody (MAB)
 CC hu:CT-M-01 reactive to human milk fat globule, its antigen-recognizing
 CC fragments, or chemically manipulated counterparts. The cytotoxic drug
 CC conjugates are useful for inhibiting the growth of unwanted cells.
 CC The present sequence represents the MAB CT-M-01 heavy chain VH domain.

XX Sequence 138 AA;

Query Match 90.1%; Score 91; DB 21; Length 138;
 Best Local Similarity 94.1%; Pred. No. 5.8e-07;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WYPGSGNTKYNKFKG 17
 DB 69 widpgsgntkynkfkfg 85

RESULT 6

AAR33950
 ID AAR33950 standard; Protein; 139 AA.

XX AC AAR33950;

XX 16-JUL-1993 (first entry)

XX CTM01 VH.

XX Heavy; light; chain; variable; domain; CTM01; PCR; primer; carcinoma;
 KW immunoglobulin; murine; monoclonal; antibody; MAB; IgG-kappa; ovary;
 KW humanised; diagnosis; therapy; breast; uterus; lung.

XX Synthetic.

XX Key Location/Qualifiers
 FH Peptide 1..19
 FT /note= "Signal peptide"
 FT Protein 20..139
 FT /note= "Mature protein"

XX EP534742-A.

XX 31-MAR-1993.

XX 24-SEP-1992; 92EP-0308680.

XX 26-SEP-1991; 91GB-0020467.

XX (CLLT) CELLTech LTD.

XX Adair JR, Baker TS, Hamann PR, Hinman LM, Lyons AH;
 PI Menendez AT, Owens RJ;

XX WPI: 1993-102837/13.
 DR N-PSDB; AAQ38877.

XX Anti-human milk fat globule humanised antibodies - useful as
 PT conjugate for in-vivo diagnosis and therapy of e.g. ovarian or
 PT breast cancer

XX Disclosure; Page 17-18; 57pp; English.

XX The sequences given in AAR33950-51 represent the heavy and light chain
 CC variable domains of CTM01 respectively. The DNA encoding these

CC peptides was isolated by PCR using the primer sequences given in
 CC AAQ38879-80. Examination of these amino acid sequences revealed
 CC considerable homology with other characterised immunoglobulin genes.
 CC The murine monoclonal antibody (MAB), CTM01, was confirmed to be an
 CC IgG-kappa antibody. CTM01 was used in the production of a humanised
 CC antibody for in vivo diagnosis and therapy of carcinomas of ovary,
 CC breast, uterus and lung.

XX Sequence 139 AA;

Query Match 90.1%; Score 91; DB 14; Length 139;
 Best Local Similarity 94.1%; Pred. No. 5.8e-07;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WYPGSGNTKYNKFKG 17

DB 69 widpgsgntkynkfkfg 85

RESULT 7

AAR33953
 ID AAR33953 standard; Protein; 139 AA.

XX AC AAR33953;

XX 16-JUL-1993 (first entry)

XX gH1 variable domain.

XX Heavy; light; chain; variable; domain; carcinoma; monoclonal; HAM;
 KW immunoglobulin; murine; antibody; MAB; ovary; humanised; diagnosis;
 KW therapy; breast; uterus; lung; CDR-grafted; gH1; CTM01.

XX Synthetic.

XX Key Location/Qualifiers
 FH Region 45..54
 FT /label= CDR1
 FT Region 69..85
 FT /label= CDR2
 FT Region 118..128
 FT /label= CDR3

XX EP534742-A.

XX 31-MAR-1993.

XX 24-SEP-1992; 92EP-0308680.

XX 26-SEP-1991; 91GB-0020467.

XX (CLLT) CELLTech LTD.

XX Adair JR, Baker TS, Hamann PR, Hinman LM, Lyons AH;
 PI Menendez AT, Owens RJ;

XX WPI: 1993-102837/13.
 DR N-PSDB; AAQ38882-89.

XX Anti-human milk fat globule humanised antibodies - useful as
 PT conjugate for in-vivo diagnosis and therapy of e.g. ovarian or
 PT breast cancer

XX Disclosure; Page 27; 57pp; English.

XX This sequence represents the CDR-grafted heavy chain, gH1. This
 CC protein is encoded by the DNA constructed using the oligonucleotides
 CC given in AAQ38882-89. This heavy chain was used in conjunction with a
 CC light chain (see also AAR33954) in the production of a humanised
 CC antibody molecule (HAM). At least one of the complementarity
 CC determining regions (CDR's) of the variable domain is derived from
 CC the mouse monoclonal antibody (MAB) CTM01 and the remaining immuno-

xx CC This protein comprises a chimeric receptor consisting of an scFv
CC engineered from anti-CD3 human antibody CTMO1 linked to an
CC

AA
PT
AA
PT
PT

PD 03-JUL-1997.
XX
PF 23-DEC-1996; 96WO-GB03209.
XX
PR 21-DEC-1995; 95GB-0026131.
XX
PA (CLIT) CELLTech THERAPEUTICS LTD.
XX
PI Bebbington CR, Finney HM, Lawson ADG, Weir ANC;
XX
DR WPI; 1997-351052/32.
DR N-PSDB; AAT90512.
XX
PT New DNA systems for activating cells - comprising DNA coding for a
PT chimeric receptor comprising 2 or more different cytoplasmic
PT signalling components.
XX
PS Disclosure: Fig 7; 90pp: English.
XX
CC This protein comprises a chimeric receptor consisting of an scfv
CC engineered from anti-CD3 human antibody CTMO1 linked to an
CC extracellular spacer comprising the human IgG1 hinge, CH2 and CH3,
CC linked to transmembrane and intracellular regions of the human T
CC cell receptor zeta chain. It can be expressed in host cells (e.g.
CC Jurkat) using a chimeric receptor gene (see AAT90512) constructed
CC from DNA cassettes encoding each receptor component. In a claimed
CC cell activation process an effector cell is transformed with DNA
CC encoding a chimeric receptor containing 2 or more different
CC cytoplasmic signalling components. Also claimed is use of DNA
CC encoding a recombinant chimeric receptor in a DNA delivery system.
CC The DNA delivery systems can be used for the activation of cells to
CC provide e.g. an increase in cell proliferation, expression of
CC cytokines with e.g. pro- or anti-inflammatory responses, stimulation
CC of cytolytic activity, differentiation or other effector functions,
CC antibody secretion, phagocytosis, tumour infiltration and/or
CC increased adhesion. They can be used in the treatment of e.g.
CC infectious disease, inflammatory disease, cancer, allergic/atopic
CC disease, congenital disease, dermatologic disease, neurologic
CC disease, transplant and metabolic/idiopathic disease (claimed).
CC In particular, they can be used in the treatment of rheumatoid
CC arthritis, osteoarthritis, inflammatory bowel disease, asthma,
CC eczema, cystic fibrosis, sickle cell anaemia, psoriasis, multiple
CC sclerosis, organ or tissue transplant rejection, graft-versus-host
CC disease or diabetes (claimed).
XX
SQ Sequence 651 AA:

Query Match 90.1%; Score 91; DB 18; Length 651;
Best Local Similarity 94.1%; Pred. No. 3.2e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIYPGSGNTKYNEKFKG 17
|||
Db 209 widpgsgntkynefkfg 225

Search completed: June 28, 2001, 16:14:34
Job time: 1322 sec

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OM protein - protein search, using sw model

Run on: June 28, 2001, 16:01:13 ; Search time 138.34 Seconds
(without alignments)
2.475 Million cell updates/sec

Title: US-09-724-406-6
Perfect score: 101
Sequence: 1 WYPGSGNTKYNEKFG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	92	91.1	116	2	US-08-888-366-2
2	91	90.1	138	3	US-08-603-024-2
3	91	90.1	139	1	US-08-253-877C-8
4	91	90.1	139	1	US-08-253-877C-19
5	91	90.1	139	2	US-08-452-164A-8
6	91	90.1	139	2	US-08-452-164A-19
7	91	90.1	139	3	US-08-603-024-18
8	83	82.2	98	3	US-08-881-037-64
9	80	79.2	122	4	US-08-767-128-4
10	79	78.2	119	1	US-08-458-516-10
11	79	78.2	119	1	US-08-458-516-11
12	79	78.2	138	1	US-08-458-516-7
13	79	78.2	222	1	US-08-458-516-22
14	79	78.2	235	1	US-08-458-516-23
15	79	78.2	449	1	US-08-458-516-13
16	76	75.2	355	3	US-08-875-811-57
17	75	74.3	113	3	US-08-881-037-18
18	75	74.3	121	3	US-08-881-037-65
19	74	73.3	140	1	US-08-476-275-6
20	74	73.3	249	2	US-08-797-689-18
21	72	71.3	17	1	US-08-318-970B-7
22	72	71.3	119	4	US-08-767-128-20
23	70	69.3	91	2	US-08-713-939A-70
24	70	69.3	91	2	US-08-713-939A-78
25	70	69.3	92	2	US-08-713-939A-79
26	70	69.3	92	2	US-08-713-939A-85
27	70	69.3	95	2	US-08-713-939A-86

28	70	69.3	101	2	US-08-713-939A-82
29	70	69.3	103	2	US-08-713-939A-84
30	70	69.3	108	2	US-08-713-939A-83
31	70	69.3	114	2	US-08-713-939A-68
32	70	69.3	114	2	US-08-713-939A-76
33	70	69.3	114	2	US-08-713-939A-77
34	70	69.3	119	4	US-08-767-128-10
35	69	68.3	17	4	US-07-987-264-2
36	69	68.3	117	2	US-08-822-028-2
37	69	68.3	117	4	US-08-479-285-2
38	69	68.3	118	2	US-08-428-257A-74
39	69	68.3	118	2	US-08-428-257A-78
40	69	68.3	118	4	US-09-199-149-2
41	69	68.3	118	4	US-09-199-149-5
42	69	68.3	118	4	US-07-987-264-14
43	69	68.3	118	4	US-07-987-264-60
44	69	68.3	119	2	US-08-561-521-10
45	69	68.3	119	2	US-08-561-521-12

ALIGNMENTS

RESULT 1
US-08-888-366-2
; Sequence 2, Application US/08888366
; Patent No. 5972656
; GENERAL INFORMATION:
; APPLICANT: Lopez, Osvaldo
; APPLICANT: Wylie, Dwane E.
; APPLICANT: Wagner, Fred W.
; TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefo
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.
; CITY: Minneapolis
; STATE: MN
; COUNTRY: US
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/888,366
; FILING DATE: 03-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/187,407
; FILING DATE: 27-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,542
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/493,299
; FILING DATE: 14-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/324,392
; FILING DATE: 14-MAR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.39USC1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: protein
US-08-888-366-2

Query Match 91.1%; Score 92; DB 2; Length 116;
Best Local Similarity 88.2%; Pred. No. 8.2e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WIYPGSGNTKYNEKFKG 17

Db 50 WIYPGSGNTKYNEKFKG 66

RESULT 2

US-08-603-024-2

; Sequence 2, Application US/08603024

; Patent No. 6015562

; GENERAL INFORMATION:

; APPLICANT: Hinman, Lois M.

; APPLICANT: Menendez, Ana T.

; APPLICANT: Hamann, Phillip R.

; TITLE OF INVENTION: TARGETED FORMS OF METHYLTRITHIO

; TITLE OF INVENTION: ANTITUMOR AGENTS

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: American Home Products Corporation

; STREET: One Campus Drive

; CITY: Parsippany

; STATE: NJ

; COUNTRY: USA

; ZIP: 07054

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/603,024

; FILING DATE: 16-FEB-1996

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Barnhard, Elizabeth M.

; REGISTRATION NUMBER: 31,088

; REFERENCE/DOCKET NUMBER: 31,932-03

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 973-683-2158

; TELEFAX: 973-683-4117

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 138 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-603-024-2

Query Match 90.1%; Score 91; DB 3; Length 138;
Best Local Similarity 94.1%; Pred. No. 1.4e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WIYPGSGNTKYNEKFKG 17

Db 69 WIDPGSGNTKYNEKFKG 85

RESULT 3

US-08-253-877C-8

; Sequence 8, Application US/08253877C

; Patent No. 5773001

; GENERAL INFORMATION:

; APPLICANT: Hamann, Phillip R.

; APPLICANT: Hinman, Lois

; APPLICANT: Hollander, Irwin

; APPLICANT: Holcomb, Ryan
; APPLICANT: Hallett, William
; APPLICANT: Tsou, Hwei-Ru
; APPLICANT: Weiss, Martin J.
; TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor
; TITLE OF INVENTION: Agents and Intermediates for Their Synthesis
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: American Cyanamid Company

; STREET: One Cyanamid Plaza

; CITY: Wayne

; STATE: New Jersey

; COUNTRY: U.S.A.

; ZIP: 07470-8426

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/253,877C

; FILING DATE: 03-JUN-1994

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Barnhard, Elizabeth M.

; REGISTRATION NUMBER: 31,088

; REFERENCE/DOCKET NUMBER: 32,368

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-831-3246

; TELEFAX: 201-831-3305

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 139 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-253-877C-8

Query Match 90.1%; Score 91; DB 1; Length 139;
Best Local Similarity 94.1%; Pred. No. 1.4e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WIYPGSGNTKYNEKFKG 17

Db 69 WIDPGSGNTKYNEKFKG 85

RESULT 4

US-08-253-877C-19

; Sequence 19, Application US/08253877C

; Patent No. 5773001

; GENERAL INFORMATION:

; APPLICANT: Hamann, Phillip R.

; APPLICANT: Hinman, Lois

; APPLICANT: Hollander, Irwin

; APPLICANT: Holcomb, Ryan

; APPLICANT: Hallett, William

; APPLICANT: Tsou, Hwei-Ru

; APPLICANT: Weiss, Martin J.

; TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor

; TITLE OF INVENTION: Agents and Intermediates for Their Synthesis

; NUMBER OF SEQUENCES: 73

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: American Cyanamid Company

; STREET: One Cyanamid Plaza

; CITY: Wayne

; STATE: New Jersey

; COUNTRY: U.S.A.

; ZIP: 07470-8426

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/253,877C
FILING DATE: 03-JUN-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 32,368
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-683-3246
TELEFAX: 201-683-3305
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-253-877C-19

Query Match 90.1%; Score 91; DB 1; Length 139;
Best Local Similarity 94.1%; Pred. No. 1.4e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WYPGSGNTKYNEKFKG 17
|| |||||
DB 69 WIDPGSGNTKYNEKFKG 85

RESULT 5
US-08-452-164A-8
Sequence 8, Application US/08452164A
Patent No. 5877296
GENERAL INFORMATION:
APPLICANT: Hamann, Philip R.
APPLICANT: Hinman, Lois
APPLICANT: Hollander, Irwin
APPLICANT: Holcomb, Ryan
APPLICANT: Hallett, William
APPLICANT: Tsou, Hwei-Ru
APPLICANT: Weiss, Martin J.
TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor
Agents and Intermediates for Their Synthesis
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Home Products Corporation
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,164A
FILING DATE: 26-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 32,368-04
TELEPHONE: 201-683-2158
TELEFAX: 201-683-4117
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,164A
FILING DATE: 26-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 32,368-04
TELEPHONE: 201-683-2158
TELEFAX: 201-683-4117
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids

Query Match 90.1%; Score 91; DB 2; Length 139;
Best Local Similarity 94.1%; Pred. No. 1.4e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WYPGSGNTKYNEKFKG 17
|| |||||
DB 69 WIDPGSGNTKYNEKFKG 85

RESULT 7

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-452-164A-8

Query Match 90.1%; Score 91; DB 2; Length 139;
Best Local Similarity 94.1%; Pred. No. 1.4e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WYPGSGNTKYNEKFKG 17
|| |||||
DB 69 WIDPGSGNTKYNEKFKG 85

RESULT 6
US-08-452-164A-19
Sequence 19, Application US/08452164A
Patent No. 5877296
GENERAL INFORMATION:
APPLICANT: Hamann, Philip R.
APPLICANT: Hinman, Lois
APPLICANT: Hollander, Irwin
APPLICANT: Holcomb, Ryan
APPLICANT: Hallett, William
APPLICANT: Tsou, Hwei-Ru
APPLICANT: Weiss, Martin J.
TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor
Agents and Intermediates for Their Synthesis
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Home Products Corporation
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,164A
FILING DATE: 26-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 32,368-04
TELEPHONE: 201-683-2158
TELEFAX: 201-683-4117
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-452-164A-19

Query Match 90.1%; Score 91; DB 2; Length 139;
Best Local Similarity 94.1%; Pred. No. 1.4e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WYPGSGNTKYNEKFKG 17
|| |||||
DB 69 WIDPGSGNTKYNEKFKG 85

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RESULT      8
US-08-881-037-64
; Sequence 64, Application US/08881037
; Patent No. 6080588
; GENERAL INFORMATION:
; APPLICANT:  Glick, Gary D.
; APPLICANT:  Swanson, Patrick C.
; TITLE OF INVENTION:  DNA BINDING ANTIBODIES
; NUMBER OF SEQUENCES:  113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  Morrison & Foerster
; STREET:     755 Page Mill Road
; CITY:       Palo Alto
; STATE:      CA
; COUNTRY:    USA
; ZIP:        94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE:  Floppy disk
; COMPUTER:     IBM PC compatible
; OPERATING SYSTEM:  PC-DOS/MS-DOS
; SOFTWARE:     Patent In Release #1.0.
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RESULT          9
US-08-767-128-4
; Sequence 4, Application US/08767128
; Patent No. 611079
;
; GENERAL INFORMATION:
;
; APPLICANT: WYLIE, DWANE E.
; APPLICANT: LOPEZ, OSVALDO
; APPLICANT: MURRAY, PETER JOSEPH
; APPLICANT: GOEBEL, PETER
;
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; NUCLEOTIDES CODING THEREFORE
;
; NUMBER OF SEQUENCES: 46
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 611079west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ version 1.5
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,128
; FILING DATE:
;
; CLASSIFICATION: 424
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 04-DEC-1996
;
; CLASSIFICATION: 424
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09258
; FILING DATE: 05-JUN-1996
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/541,373
; FILING DATE: 10-OCT-1995
;
; PRIOR APPLICATION DATA:

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APPLICATION NUMBER: 08/462,798
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.49USF1
TELEPHONE: 612/371-5278
TELEFAX: 612/332-9081
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-767-128-4

Query Match 79.2%; Score 80; DB 4; Length 122;
Best Local Similarity 81.2%; Pred. No. 5.2e-05;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYPGSGNTKYNEKFK 16
| | | | |
DB 50 WYPGSGSIKYNEKFK 65

RESULT 10
US-08-458-516-10
; Sequence 10, Application US/08458516
; Patent No. 5777085
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIB/IIIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: N-terminal fragment
US-08-458-516-10

Query Match 78.2%; Score 79; DB 1; Length 119;
Best Local Similarity 87.5%; Pred. No. 7.1e-05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 IYPGSGNTKYNEKFKG 17
| | | | | | | | | |
DB 51 IYPGSGGTNYNEKFKG 66

RESULT 11
US-08-458-516-11
; Sequence 11, Application US/08458516
; Patent No. 5777085
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIB/IIIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: N-terminal fragment
; US-08-458-516-11

Query Match 78.2%; Score 79; DB 1; Length 119;
Best Local Similarity 87.5%; Pred. No. 7.1e-05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 IYPGSGNTKYNEKFKG 17
| | | | | | | | | |
DB 51 IYPGSGGTNYNEKFKG 66

RESULT 12
US-08-458-516-7
; Sequence 7, Application US/08458516

Patent No. 5777085
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIB/IIIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; LENGTH: 138 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-458-516-7

Query Match 78.2%; Score 79; DB 1; Length 138;
Best Local Similarity 87.5%; Pred. No. 8.3e-05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 IYPGSGNTYNEKFKG 17
||||| | |||||
Db 70 IYPGSGGTYNEKFKG 85

RESULT 13
US-08-458-516-22
; Sequence 22, Application US/08458516
; Patent No. 5777085
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIB/IIIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; LENGTH: 222 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-458-516-22

Query Match 78.2%; Score 79; DB 1; Length 222;
Best Local Similarity 87.5%; Pred. No. 0.00014;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 IYPGSGNTYNEKFKG 17
||||| | |||||
Db 51 IYPGSGGTYNEKFKG 66

RESULT 14
US-08-458-516-23
; Sequence 23, Application US/08458516
; Patent No. 5777085
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIB/IIIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run On: June 28, 2001, 15:58:42 ; Search time 234.85 Seconds
(without alignments)
5.514 Million cell updates/sec

Title: US-09-724-406-6

Perfect score: 101
Sequence: 1 WIYPGSGNTYNEKFKG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68.*
1: piri.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	101	100.0	67	2 H28833	Ig kappa chain V r
2	101	100.0	107	2 PH0999	Ig heavy chain V r
3	101	100.0	109	2 PH0997	Ig heavy chain V r
4	101	100.0	111	2 PH0998	Ig heavy chain V r
5	101	100.0	246	2 S38950	Ig gamma chain - m
6	101	100.0	446	2 S40295	Ig gamma-2a chain
7	98	97.0	106	2 PH1002	Ig heavy chain V r
8	98	97.0	109	2 PH1001	Ig heavy chain V r
9	98	97.0	115	2 A54378	Ig heavy chain V r
10	92	91.1	104	2 S28466	Ig heavy chain V r
11	92	91.1	117	1 HVMSA1	Ig heavy chain V r
12	90	89.1	469	2 S37483	Ig gamma-2a chain
13	89	88.1	120	2 G28195	Ig heavy chain V r
14	89	88.1	138	2 S21810	Ig heavy chain V r
15	87	86.1	91	2 PH0242	Ig heavy chain V r
16	87	86.1	107	2 PH0240	Ig heavy chain V r
17	87	86.1	107	2 PH0243	Ig heavy chain V r
18	87	86.1	107	2 PH0241	Ig heavy chain V r
19	83	82.2	96	2 PH1165	Ig heavy chain V r
20	83	82.2	110	2 PH1000	Ig heavy chain V r
21	82	81.2	110	2 PH0244	Ig heavy chain V r
22	82	81.2	112	2 S26473	Ig heavy chain V r
23	82	81.2	112	2 PH0245	Ig heavy chain V r
24	82	81.2	120	2 F28195	Ig heavy chain V r
25	81	80.2	119	2 E30562	Ig heavy chain V r
26	79	78.2	112	2 PH0979	Ig heavy chain V r
27	77	76.2	115	2 PH0238	Ig heavy chain V r
28	75	74.3	94	2 G32513	Ig heavy chain V r
29	75	74.3	475	2 S01321	Ig gamma-2b chain

ALIGNMENTS

RESULT 1

H28833

Ig kappa chain V region (HP22.202.16) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-May-1997
C:Accession: H28833
R:Corbet, S.; Hirn, M.; Roth, C.; Theze, J.; Fougereau, M.; Schliff, C.
J. Immunol. 141, 779-784, 1988
A:Title: Allelic manipulation of the GAT idiotype cascade. Immunization of C57BL/
A:Reference number: A92827; MUID:88285674
A:Accession: H28833
A:Molecule type: mRNA
A:Residues: 1-67 <COR>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin

Query Match 100.0%; Score 101; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 4.1e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIYPGSGNTYNEKFKG 17

Db 19 WIYPGSGNTYNEKFKG 35

RESULT 2

PH0999

Ig heavy chain V region (clone 74-cl) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PH0999
R:Tillman, D.M.; Jon, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
A:Reference number: PH0999
A:Accession: PH0999
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-107 <VIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:14-97/Domain: immunoglobulin homology <IMW>

Query Match

Best Local Similarity 100.0%; Score 101; DB 2; Length 107;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIYPGSGNTYNEKFKG 17

|||||

Db 49 WIYPGSGNTKYNEKFKG 65

RESULT 3

PH0997

Ig heavy chain V region (clone 17s-c2) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PH0997

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marlon, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell, strain [NZB x NZW]F1

A:Reference number: PH0971; MUID:92381444

A:Accession: PH0997

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-109 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 101; DB 2; Length 109;

Best Local Similarity 100.0%; Pred. No. 6.8e-09;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIYPGSGNTKYNEKFKG 17

Db 50 WIYPGSGNTKYNEKFKG 66

RESULT 4

PH0998

Ig heavy chain V region (clone 165.3) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PH0998

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marlon, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell, strain [NZB x NZW]F1

A:Reference number: PH0971; MUID:92381444

A:Accession: PH0998

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-111 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 101; DB 2; Length 111;

Best Local Similarity 100.0%; Pred. No. 6.9e-09;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIYPGSGNTKYNEKFKG 17

Db 50 WIYPGSGNTKYNEKFKG 66

RESULT 5

S38950

Ig gamma chain - mouse

C:Species: Mus musculus (house mouse)

C:Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999

C:Accession: S38950

R:Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Biol. Chem. Hoppe-Seyler 374, 993-1000, 1993

A:Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alpha

A:Reference number: S38950; MUID:94128242

A:Accession: S38950

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-246 <KLE>

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: immunoglobulin

F:137-201/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 101; DB 2; Length 246;

Best Local Similarity 100.0%; Pred. No. 1.6e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIYPGSGNTKYNEKFKG 17

Db 50 WIYPGSGNTKYNEKFKG 66

RESULT 6

S40295

Ig gamma-2a chain (mAb735) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999

C:Accession: S40295

R:Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; submitted to the EMBL Data Library, January 1993

A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 again

A:Reference number: S40295

A:Accession: S40295

A:Molecule type: protein

A:Residues: 1-446 <KLE>

C:Genetics:

A:Map position: 12

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid

F:1-446/Product: Ig gamma-2a chain #status experimental <MAT>

F:1-117/Domain: V-D-J region <VDJ>

F:118-446/Domain: C region <CH1>

F:118-214/Domain: C1 region <CH1>

F:215-230/Region: hinge

F:231-340/Domain: C2 region <CH2>

F:341-446/Domain: C3 region <CH3>

F:360-427/Domain: immunoglobulin homology <IMM>

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted

F:132/Disulfide bonds: interchain (to light chain) #status predicted

F:224,227,229/Disulfide bonds: interchain #status predicted

F:297/Binding site: carbohydrate (Asn) #status experimental

Query Match 100.0%; Score 101; DB 2; Length 446;

Best Local Similarity 100.0%; Pred. No. 2.9e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIYPGSGNTKYNEKFKG 17

Db 50 WIYPGSGNTKYNEKFKG 66

RESULT 7

PH1002

Ig heavy chain V region (clone 165.45) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PH1002

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marlon, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective

A:Reference number: PH0971; MUID:92381444

A:Accession: PH1002

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-106 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

Db 49 WIYPGSGNTKYNEKFKG 65

RESULT 3

PH0997

Ig heavy chain V region (clone 17s-c2) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PH0997

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marlon, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell, strain [NZB x NZW]F1

A:Reference number: PH0971; MUID:92381444

A:Accession: PH0997

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-109 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 101; DB 2; Length 109;

Best Local Similarity 100.0%; Pred. No. 6.8e-09;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIYPGSGNTKYNEKFKG 17

Db 50 WIYPGSGNTKYNEKFKG 66

RESULT 4

PH0998

Ig heavy chain V region (clone 165.3) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PH0998

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marlon, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell, strain [NZB x NZW]F1

A:Reference number: PH0971; MUID:92381444

A:Accession: PH0998

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-111 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 101; DB 2; Length 111;

Best Local Similarity 100.0%; Pred. No. 6.9e-09;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIYPGSGNTKYNEKFKG 17

Db 50 WIYPGSGNTKYNEKFKG 66

RESULT 5

S38950

Ig gamma chain - mouse

C:Species: Mus musculus (house mouse)

C:Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999

C:Accession: S38950

R:Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Biol. Chem. Hoppe-Seyler 374, 993-1000, 1993

A:Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alpha

A:Reference number: S38950; MUID:94128242

A:Accession: S38950

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-246 <KLE>

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: immunoglobulin

F:137-201/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 101; DB 2; Length 246;

Best Local Similarity 100.0%; Pred. No. 1.6e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIYPGSGNTKYNEKFKG 17

Db 50 WIYPGSGNTKYNEKFKG 66

RESULT 6

S40295

Ig gamma-2a chain (mAb735) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999

C:Accession: S40295

R:Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; submitted to the EMBL Data Library, January 1993

A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 again

A:Reference number: S40295

A:Accession: S40295

A:Molecule type: protein

A:Residues: 1-446 <KLE>

C:Genetics:

A:Map position: 12

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid

F:1-446/Product: Ig gamma-2a chain #status experimental <MAT>

F:1-117/Domain: V-D-J region <VDJ>

F:118-446/Domain: C region <CH1>

F:118-214/Domain: C1 region <CH1>

F:215-230/Region: hinge

F:231-340/Domain: C2 region <CH2>

F:341-446/Domain: C3 region <CH3>

F:360-427/Domain: immunoglobulin homology <IMM>

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted

F:132/Disulfide bonds: interchain (to light chain) #status predicted

F:224,227,229/Disulfide bonds: interchain #status predicted

F:297/Binding site: carbohydrate (Asn) #status experimental

Query Match 100.0%; Score 101; DB 2; Length 446;

Best Local Similarity 100.0%; Pred. No. 2.9e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIYPGSGNTKYNEKFKG 17

Db 50 WIYPGSGNTKYNEKFKG 66

RESULT 7

PH1002

Ig heavy chain V region (clone 165.45) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PH1002

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marlon, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective

A:Reference number: PH0971; MUID:92381444

A:Accession: PH1002

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-106 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 97.0%; Score 98; DB 2; Length 106;
Best Local Similarity 94.1%; Pred. No. 2e-08;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIYPGSGNTKYNEKFKG 17
|||||:|||||:|||||

Db 49 WIYPGSGNTKYNDKFKG 65

RESULT 8

PH1001

Ig heavy chain V region (clone 111.68) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C;Accession: PH1001

R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marlon, T.N.

J. Exp. Med. 176, 761-779, 1992

A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell

A;Reference number: PH0971; MUID:92381444

A;Accession: PH1001

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-109 <TIL>

A;Experimental source: B cell, strain [NZB x NZW]F1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 97.0%; Score 98; DB 2; Length 109;

Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIYPGSGNTKYNEKFKG 17
|||||:|||||:|||||

Db 50 WIYPGSGNTKYNDKFKG 66

RESULT 9

A54378

Ig heavy chain V region anti-triplex DNA - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999

C;Accession: A54378

R;Agazie, Y.M.; Lee, J.S.; Burkholder, G.D.

J. Biol. Chem. 269, 7019-7023, 1994

A;Title: Characterization of a new monoclonal antibody to triplex DNA and immunofluoresc

A;Reference number: A54378; MUID:94165109

A;Accession: A54378

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-115 <AGA>

A;Cross-references: GB:S68981; NID:g545744; PIDN:AB30095.1; PID:g545745

A;Note: experimental source: spleen and myeloma cell line MOPC 315.43

A;Note: sequence inconsistent with nucleotide translation

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 97.0%; Score 98; DB 2; Length 115;

Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIYPGSGNTKYNEKFKG 17
|||||:|||||:|||||

Db 50 WIYPGSGNTKYNEKFKG 66

RESULT 10

S26466

Ig heavy chain V region - mouse

C;Species: Mus musculus (house mouse)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C;Accession: S26466

R;Kavaler, J.

submitted to the EMBL Data Library, April 1991

A;Reference number: S26459

A;Accession: S26466

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-104 <KAV>

A;Cross-references: EMBL:X59116; NID:g51933; PIDN:CAA1842.1; PID:g51934

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;3-86/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 91.1%; Score 92; DB 2; Length 104;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIYPGSGNTKYNEKFKG 17
|||||:|||||:|||||

Db 38 WIYPGSGSTKYNEKFKG 54

RESULT 11

HVMSA1

Ig heavy chain precursor V region (A1/A4) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 22-Jun-1999

C;Accession: A02029

R;Yancopoulos, G.D.; Alt, F.W.

Cell 40, 271-281, 1985

A;Title: Developmentally controlled and tissue-specific expression of unrearranged V-

A;Reference number: A90860; MUID:85099340

A;Accession: A02029

A;Molecule type: DNA

A;Residues: 1-117 <YAN>

A;Cross-references: GB:M13787; NID:g196006; PIDN:AAA38499.1; PID:g466291

A;Note: the sequence was determined from the germline gene

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-117/Product: Ig heavy chain V region (A1/A4) #status predicted <MAT>

F;20-49/Region: framework 1

F;34-117/Domain: immunoglobulin homology <IMM>

F;50-54/Region: complementarity-determining 1

F;55-68/Region: framework 2

F;69-85/Region: complementarity-determining 2

F;86-117/Region: framework 3

F;41-115/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 91.1%; Score 92; DB 1; Length 117;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIYPGSGNTKYNEKFKG 17
|||||:|||||:|||||

Db 69 WIYPGSGSTKYNEKFKG 85

RESULT 12

S37483

Ig gamma-2a chain - mouse

C;Species: Mus musculus (house mouse)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C;Accession: S37483

R;Ducancel, F.F.D.

submitted to the EMBL Data Library, February 1993

A:Reference number: S37483
A:Accession: S37483
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-469 <DUC>
A:Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:276-345/Domain: immunoglobulin homology <IMM>

Query Match 89.1%; Score 90; DB 2; Length 469;
Best Local Similarity 88.2%; Pred. No. 1.7e-06;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WIYPGSGNTKYNEKFKG 17
||||| ||||||| |||
DB 69 WIYPASGNTKYNEKFKG 85

RESULT 13

Ig heavy chain V region (anti-haloperidol antibody B) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 23-Jul-1999
C:Accession: G28195
R:Sherman, M.A.; Deans, R.J.; Bolger, M.B.
J. Biol. Chem. 263, 4059-4063, 1988
A:Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amino acid s
A:Reference number: A28195; MUID:88153717
A:Accession: G28195
A:Molecule type: mRNA
A:Residues: 1-120 <SHE>
A:Cross-references: GB:M19772; NID:g195520; PIDN:AAA38340.1; PID:g195521
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 88.1%; Score 89; DB 2; Length 120;
Best Local Similarity 88.2%; Pred. No. 6e-07;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIYPGSGNTKYNEKFKG 17
||||| ||||||| |||
DB 50 WIYPGNVNTKYNEKFKG 66

RESULT 14

Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S21810
R:Ostermeyer, M.; Brack, C.H.; Traunecker, A.; Koehler, G.
submitted to the EMBL Data Library, January 1991
A:Description: Nucleotide sequence of a rearranged VDJ-region of a mouse Ig mu heavy cha
A:Reference number: S21810
A:Accession: S21810
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-138 <OST>
A:Cross-references: EMBL:X56936; NID:g54163; PIDN:CAA40257.1; PID:g54164
C:Genetics:
A:introns: 15/3
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 88.1%; Score 89; DB 2; Length 138;
Best Local Similarity 88.2%; Pred. No. 7e-07;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIYPGSGNTKYNEKFKG 17
||||| ||||||| |||
DB 69 WIYPGNVNTKYNEKFKG 85

RESULT 15

Ig heavy chain V region (anti-DNA, S54VH) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
C:Accession: PL0242
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
A:Reference number: PL0231; MUID:90111618
A:Accession: PL0242
A:Molecule type: mRNA
A:Residues: 1-91 <SHL>

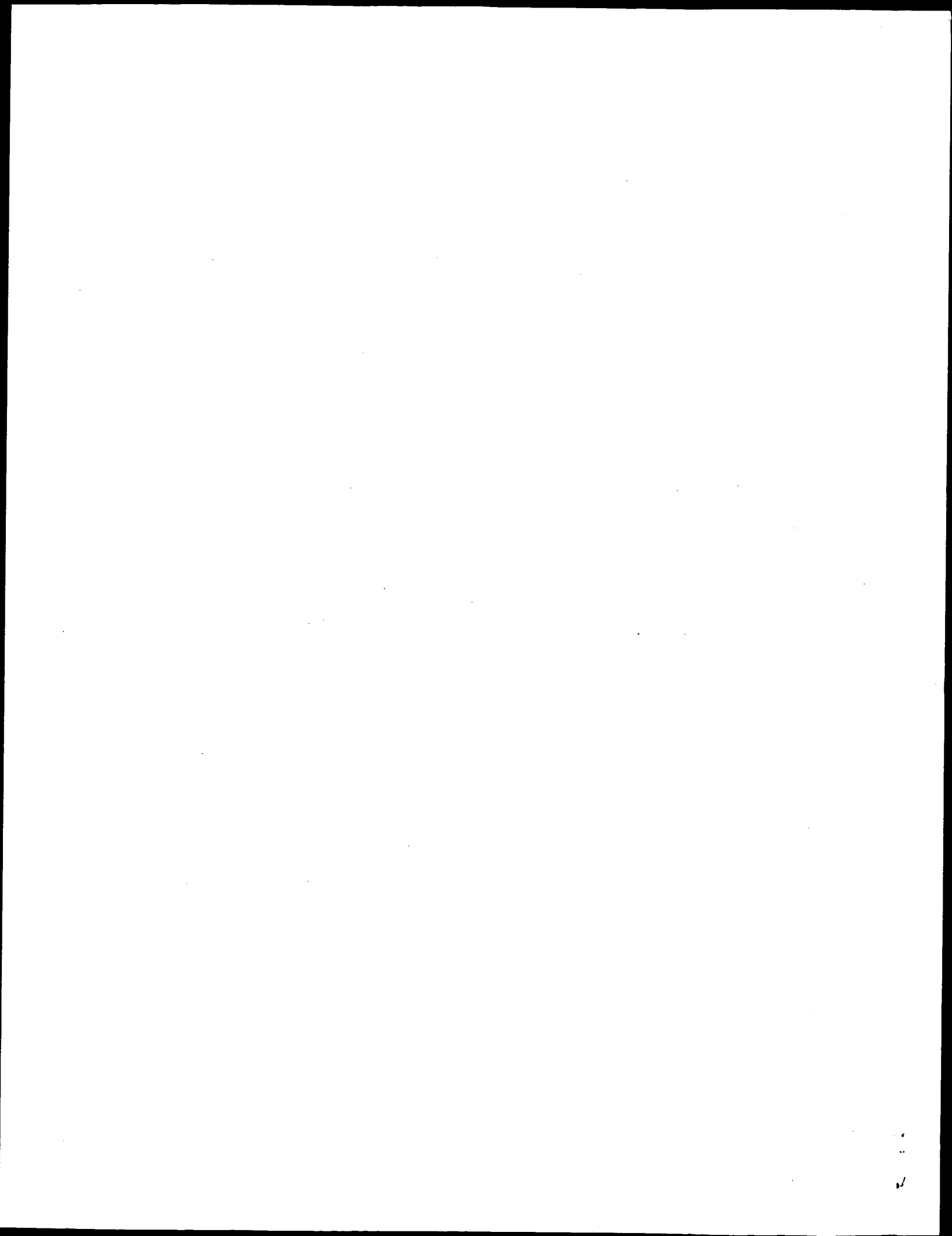
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-8/Region: framework 1
F:9-13/Region: complementarity-determining 1
F:14-27/Region: framework 2
F:28-44/Region: complementarity-determining 2
F:45-76/Region: framework 3
F:77-87/Region: complementarity-determining 3
F:88-91/Region: framework 4

Query Match 86.1%; Score 87; DB 2; Length 91;
Best Local Similarity 93.8%; Pred. No. 9.4e-07;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIYPGSGNTKYNEKFK 16
||| ||||||| |||
DB 28 WIYPGSGNTKYNEKFK 43

Search completed: June 28, 2001, 15:58:42
Job time: 370 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2001, 15:54:34 ; Search time 105.36 Seconds
(without alignments)
5.527 Million cell updates/sec

Title: US-09-724-406-6
Perfect score: 101
Sequence: 1 WIYPGSGNTKYNKFKG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues
Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	92	91.1	117	1 HV52_MOUSE	P06327 mus musculus
2	72	71.3	120	1 HV03_MOUSE	P01747 mus musculus
3	62	61.4	117	1 HV09_MOUSE	P01753 mus musculus
4	62	61.4	117	1 HV10_MOUSE	P01754 mus musculus
5	62	61.4	117	1 HV49_MOUSE	P06328 mus musculus
6	62	61.4	139	1 HV07_MOUSE	P01751 mus musculus
7	61	60.4	117	1 HV04_MOUSE	P01748 mus musculus
8	61	60.4	140	1 HV02_MOUSE	P01746 mus musculus
9	58	57.4	117	1 HV12_MOUSE	P01756 mus musculus
10	58	57.4	117	1 HV13_MOUSE	P01757 mus musculus
11	58	57.4	117	1 HV14_MOUSE	P01758 mus musculus
12	58	57.4	118	1 HV51_MOUSE	P06330 mus musculus
13	58	57.4	121	1 HV01_MOUSE	P01745 mus musculus
14	56	55.4	117	1 HV06_MOUSE	P01750 mus musculus
15	55	54.5	120	1 HV50_MOUSE	P06329 mus musculus
16	55	54.5	136	1 HV15_MOUSE	P01759 mus musculus
17	54	53.5	147	1 HV1C_HUMAN	P01744 homo sapien
18	53	52.5	117	1 HV05_MOUSE	P01749 mus musculus
19	50	49.5	138	1 HV48_MOUSE	P03980 mus musculus
20	49	48.5	117	1 HV1G_HUMAN	P23083 homo sapien
21	47	46.5	137	1 HV11_MOUSE	P01755 mus musculus
22	47	46.5	606	1 RP3A_MOUSE	P47708 mus musculus
23	47	46.5	684	1 RP3A_RAT	P47709 rattus norv
24	46.5	46.0	226	1 KAD3_BOVIN	P08760 bos taurus
25	46	45.5	117	1 HV1B_HUMAN	P01743 homo sapien
26	46	45.5	692	1 YK06_YEAST	P36062 saccharomyc
27	45.5	45.0	819	1 EFG2_YEAST	P39677 saccharomyc
28	43.5	43.1	509	1 VP64_NPVOP	P13625 oryza pseu
29	43	42.6	566	1 HEMA_TAZIN	P26140 influenza a
30	43	42.6	596	1 NUOL_CAMJTE	Q9Pma7 campylobact
31	42.5	42.1	116	1 HV61_MOUSE	P18532 mus musculus
32	42.5	42.1	241	1 KADA_ORYSA	Q08479 oryza sativ
33	42.5	42.1	243	1 KADB_ORYSA	Q08480 oryza sativ

34	42.5	42.1	246	1 KAD_ARATH	O82514 arabidopsis
35	42.5	42.1	509	1 VP67_NPVCF	P41717 choristoneu
36	42	41.6	183	1 RM32_YEAST	P25348 saccharomyc
37	42	41.6	376	1 ERG6_CANAL	O74198 candida alb
38	42	41.6	433	1 YBBY_ECOLI	P77328 escherichia
39	42	41.6	468	1 LIP2_RAT	P22503 phaseolus v
40	42	41.6	496	1 GUN_PHAVU	P54318 rattus norv
41	42	41.6	542	1 RESB_BACSU	P35161 bacillus a
42	42	41.6	566	1 HEMA_IJNZJ	P03455 influenza a
43	41	40.6	262	1 SPIB_HUMAN	O01892 homo sapien
44	41	40.6	304	1 STRL_STRGR	P29781 streptomyce
45	41	40.6	557	1 MAOX_ANAPL	P28227 anas platyr

ALIGNMENTS

```

RESULT 1
HV52_MOUSE
ID HV52_MOUSE STANDARD; PRT; 117 AA.
AC P06327;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION VH58 A1/A4 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85099340; PubMed=2578321;
RA Yancopoulos G.D.; Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of
  unrearranged VJ gene segments.";
RL Cell 40:271-281 (1985).
-----
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  -----
DR EMBL; M13787; AAA38499.1; -
DR PIR; A02029; HVMSA1.
DR InterPro; IPR003006; -
DR Pfam; PF00047; ig.1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH58 A1/A4.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 65 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12971 MW; 880BC138856DFC9D CRC64;

```

Query Match 91.1%; Score 92; DB 1; Length 117;
Best Local Similarity 88.2%; Pred. No. 6.3e-08;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WIYPGSGNTKYNKFKG 17

Db 69 WIYPGSGNTKYNKFKG 85

RESULT 2
HV03_MOUSE

```

ID HV03_MOUSE STANDARD; PRT; 120 AA.
AC P01747; 1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=83131846; PubMed=6186498;
RA Siekevitz M., Geffer M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsenate
RT idiotypic response of the strain A mouse.";
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -1- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE. THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
DR PIR: A02028; HVM5G7.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region; Antiarsonate antibody; Hybridoma.
FT NON_TER 120 120
FT SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;

Query Match 71.3%; Score 72; DB 1; Length 120;
Best Local Similarity 76.5%; Pred. No. 0.0001;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYPGSGNTKYNEKPKG 17
Db : ||: |||||
49 YINPGYTKYNEKPKG 65

RESULT 3
HV09_MOUSE STANDARD; PRT; 117 AA.
AC P01753; P11271;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 186-1 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RX STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Botwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the Npb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: J00533; AAA38602.1; -.
CC PIR: C02034; HVMS45.
CC InterPro: IPR003006; -.
CC Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 145.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT NON_TER 117 117
FT SEQUENCE 117 AA; 12921 MW; D37DE8A3F543E996 CRC64;

Query Match 61.4%; Score 62; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.004;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGSGNTKYNEKFK 16
Db : ||: |||||
70 IDPNSGGTKYNEKFK 84

RESULT 4
HV10_MOUSE STANDARD; PRT; 117 AA.
ID HV10_MOUSE
AC P01754; P11270;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 145 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RX STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Botwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the Npb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: J00533; AAA38602.1; -.
CC PIR: C02034; HVMS45.
CC InterPro: IPR003006; -.
CC Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 145.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT NON_TER 117 117
FT SEQUENCE 117 AA; 12921 MW; D37DE8A3F543E996 CRC64;

Query Match 61.4%; Score 62; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.004;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGSGNTKYNEKFK 16
Db : ||: |||||
70 IDPNSGGTKYNEKFK 84

RESULT 5
HV49_MOUSE

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FT DOMAIN 86 117 FRAMEWORK 3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12772 MW; C530F829C906F69B CRC64;

Query Match 60.4%; Score 61; DB 1; Length 117;
 Best Local Similarity 73.3%; Pred. No. 0.0058;
 Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGSGNTKYNKFKG 16
 | : : : : :
 DB 70 INPNGGTYNNEKFK 84

RESULT 8

HV02_MOUSE
 ID HV02_MOUSE STANDARD; PRT; 140 AA.
 AC P01746;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION 93G7 PRECURSOR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-A/J;
 RX MEDLINE=82152818; PubMed=6801765;
 RA Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
 RA Capra J.D.;
 RT "Somatic mutation in genes for the variable portion of the
 RT immunoglobulin heavy chain."
 RL Science 216:309-311(1982).
 CC -----

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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----

DR EMBL; J00493; AAA38128.1;
 DR PIR; A02028; HVM5G7
 DR InterPro; IP003006;
 DR Pfam; PF00047; ig; 1.
 KW Immunoglobulin v region; Antiarsonate antibody; Hybridoma; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.
 FT NON_TER 140 140
 SQ SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;

Query Match 60.4%; Score 61; DB 1; Length 140;
 Best Local Similarity 64.7%; Pred. No. 0.007;
 Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 WYPGSGNTKYNKFKG 17
 : : : : :
 DB 69 YINPGNGYINNEKFKG 85

RESULT 9

HV12_MOUSE
 ID HV12_MOUSE STANDARD; PRT; 117 AA.
 AC P01756;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION MOPC 104E.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=83075344; PubMed=6816276;
 RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
 RA Hood L.E.;
 RT "Complete amino acid sequence of a mouse mu chain: homology among
 RT heavy chain constant region domains."
 RL Biochemistry 21:5415-5424(1982).
 CC -I- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
 CC PROTEIN HAS ALSO BEEN DETERMINED.
 CC -I- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
 DR PIR; A02039; MHMS4E.
 DR InterPro; IP003006;
 DR Pfam; PF00047; ig; 1.
 KW Immunoglobulin v region; Glycoprotein.
 FT DISULFID 22 96 BY SIMILARITY.
 FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .).
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;

Query Match 57.4%; Score 58; DB 1; Length 117;
 Best Local Similarity 62.5%; Pred. No. 0.017;
 Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IYPGSGNTKYNKFKG 17
 | : : : : :
 DB 51 INPNNGGTSYNKFKG 66

RESULT 10

HV13_MOUSE
 ID HV13_MOUSE STANDARD; PRT; 117 AA.

AC P01757;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION J558.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=80078170; PubMed=6765983;
 RA Schilling J., Clevinger B., Davie J.M., Hood L.;
 RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
 RT rearrangements in heavy chain v-region gene segments."
 RL Nature 283:35-40(1980).
 CC -I- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
 CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
 CC WHICH OCCUR IN THE D AND J SEGMENTS.
 CC -I- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
 DR PIR; A26242; MHMSJ5.
 DR InterPro; IP003006;
 DR Pfam; PF00047; ig; 1.
 KW Immunoglobulin v region.
 FT DISULFID 22 96 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match 57.4%; Score 58; DB 1; Length 117;
 Best Local Similarity 62.5%; Pred. No. 0.017;
 Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IYPGSGNTKYNKFKG 17
 | : : : : :
 DB 51 INPNNGGTSYNKFKG 66

```

RESULT 11
HV14_MOUSE
ID HV14_MOUSE STANDARD; PRT; 117 AA.
AC P01758;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 108A PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81245215; PubMed=6789211;
RA Givol D., Zakut R., Efron K., Rechavi G., Ram D., Cohen J.B.;
RT "Diversity of germ-line immunoglobulin VH genes.";
RL Nature 292:426-430(1981).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00488; AAA38519.1; -.
DR PIR; A02041; HVMS8A.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; ig; 1.
KW Immunoglobulin V region; Signal.
FT CHAIN 1
FT SIGNAL 19
FT NON_TER 117 IG HEAVY CHAIN V REGION 108A.
FT SEQUENCE 117 AA; 12972 MW; 428CB44DF25D1BC2 CRC64;
SQ
Query Match 57.4%; Score 58; DB 1; Length 117;
Best Local Similarity 62.5%; Pred. No. 0.017;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 WYPGSGNKKYNEKFK 16
DB 69 YIYPNGGTGYNQKFK 84
:||||:|:|:|:|
:||||:|:|:|:|

RESULT 12
HV51_MOUSE
ID HV51_MOUSE STANDARD; PRT; 118 AA.
AC P06330;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION AC38 205.12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR; A02040; MHMS38.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; ig; 1.
FT CHAIN 1
FT NON_TER 98
FT SEQUENCE 117 AA; 12972 MW; 428CB44DF25D1BC2 CRC64;
SQ
Query Match 57.4%; Score 58; DB 1; Length 117;
Best Local Similarity 62.5%; Pred. No. 0.017;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 WYPGSGNKKYNEKFK 16
DB 69 YIYPNGGTGYNQKFK 84
:||||:|:|:|:|
:||||:|:|:|:|

RESULT 13
HV01_MOUSE
ID HV01_MOUSE STANDARD; PRT; 121 AA.
AC P01745;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION MPC 11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81053741; PubMed=6253904;
RA Zakut R., Cohen J., Givol D.;
RT "Cloning and sequence of the cDNA corresponding to the variable
RT region of immunoglobulin heavy chain MPC11.";
RL Nucleic Acids Res. 8:3591-3601(1980).
RN [2]
RP REVISIONS.
RA Zakut R., Cohen J., Givol D.;
RA Nucleic Acids Res. 8:4839-4840(1980).
CC -1- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
CC FROM A MYELOMA THAT SECRETES IGG2B.
DR PIR; A02027; GVM511.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; ig; 1.
DR Immunoglobulin V region.
KW Immunoglobulin V region.
FT CHAIN 1
FT NON_TER 121
FT SEQUENCE 121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;
SQ
Query Match 57.4%; Score 58; DB 1; Length 121;
Best Local Similarity 62.5%; Pred. No. 0.018;
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 2 IYPGSGNKKYNEKFKG 17
DB 51 IYPGGGFTYNDNLKG 66
|||||:|:|:|:|
|||||:|:|:|:|

RESULT 14
HV06_MOUSE
ID HV06_MOUSE STANDARD; PRT; 117 AA.
AC P01750;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 102 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CS7BL/6;

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FT DOMAIN 99 104 D SEGMENT.
FT DOMAIN 105 118 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 118 118
SQ SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;

Query Match 57.4%; Score 58; DB 1; Length 118;
Best Local Similarity 62.5%; Pred. No. 0.018;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 2 IYPGSGNKKYNEKFKG 17
DB 51 INPNNGGTSYNQKFKG 66
|:|:|:|:|:|:|
|:|:|:|:|:|:|

RESULT 13
HV01_MOUSE
ID HV01_MOUSE STANDARD; PRT; 121 AA.
AC P01745;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION MPC 11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81053741; PubMed=6253904;
RA Zakut R., Cohen J., Givol D.;
RT "Cloning and sequence of the cDNA corresponding to the variable
RT region of immunoglobulin heavy chain MPC11.";
RL Nucleic Acids Res. 8:3591-3601(1980).
RN [2]
RP REVISIONS.
RA Zakut R., Cohen J., Givol D.;
RA Nucleic Acids Res. 8:4839-4840(1980).
CC -1- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
CC FROM A MYELOMA THAT SECRETES IGG2B.
DR PIR; A02027; GVM511.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; ig; 1.
DR Immunoglobulin V region.
KW Immunoglobulin V region.
FT CHAIN 1
FT NON_TER 121
FT SEQUENCE 121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;
SQ
Query Match 57.4%; Score 58; DB 1; Length 121;
Best Local Similarity 62.5%; Pred. No. 0.018;
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 2 IYPGSGNKKYNEKFKG 17
DB 51 IYPGGGFTYNDNLKG 66
|||||:|:|:|:|
|||||:|:|:|:|

RESULT 14
HV06_MOUSE
ID HV06_MOUSE STANDARD; PRT; 117 AA.
AC P01750;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 102 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CS7BL/6;

```

RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
DR PIR: A02032; HVMS02.
DR InterPro: IPR003006; -
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 102.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 58 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12867 MW; 740A65DD851FC8C CRC64;

Query Match 55.4%; Score 56; DB 1; Length 117;
Best Local Similarity 56.2%; Pred. No. 0.036;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 IYPGSGNTKYNEKFKG 17

DB 70 IHPDSDTNYNQKFKG 85

RESULT 15
HV50_MOUSE
ID HV50_MOUSE STANDARD; PRT; 120 AA.
AC P06329;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION AC38 15.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR: A02037; MHMS15.
DR InterPro: IPR003006; -
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 105 D SEGMENT.
FT DOMAIN 106 120 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13311 MW; 914453F426F09834 CRC64;

Query Match 54.5%; Score 55; DB 1; Length 120;
Best Local Similarity 66.7%; Pred. No. 0.054;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 IYPGSGNTKYNEKFK 16

DB 51 INPSNGTNYNEKFK 65

Search completed: June 28, 2001, 15:54:34
Job time: 122 sec

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OM protein - protein search, using sw model

Run on: June 28, 2001, 16:08:18 ; Search time 411.58 Seconds
(without alignments)

Title: US-09-724-406-6
Perfect score: 101
Sequence: 1 WIYPGSGNTKYNEKFG 17

Scoring table: BLOSUM62

Searched: 425026 seqs, 132305027 residues
Total number of hits satisfying chosen parameters: 425026

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database :
SPTRMBL16.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_humani.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_unclassified.*
13: sp_vertebrate.*
14: sp_virus.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			ID	Description
		Match	Length	DB		
1	69	68.3	110	11	Q9JL77	Q9j177 mus musculus
2	64	63.4	118	11	Q9ZLCA	Q9z1c4 mus musculus
3	62	61.4	110	11	Q9JL83	Q9j183 mus musculus
4	58	57.4	109	11	Q9JL85	Q9j185 mus musculus
5	58	57.4	117	11	Q9QXF0	Q9qx10 mus musculus
6	58	57.4	117	11	Q9QXE9	Q9qx09 mus musculus
7	53	52.5	125	4	Q9UL95	Q9ul95 homo sapien
8	53	52.5	498	2	Q9KDO9	Q9kdg9 bacillus ba
9	52	51.5	119	4	Q9UL94	Q9ul94 homo sapien
10	50.5	50.0	691	5	Q9VZE7	Q9vze7 drosophila
11	50	49.5	119	5	Q9GZR2	Q9gyz2 schistosoma
12	49	48.5	172	5	Q17999	Q17999 caenorhabdi
13	47	46.5	109	11	Q9JL85	Q9j185 mus musculus
14	47	46.5	143	10	Q9SMU5	Q9smu5 arabidopsis
15	46	45.5	89	11	Q9J162	Q9j162 mus musculus
16	46	45.5	124	4	Q9UL92	Q9ul92 homo sapien
17	46	45.5	305	11	Q9JH69	Q9jh69 mus musculus
18	46	45.5	328	11	Q9J165	Q9j165 mus musculus
19	45	44.6	218	2	Q9Z505	Q9z505 streptomyce

ALIGNMENTS

RESULT 1

RESULT
09.JI.77

ID	Q9JL77	PRELIMINARY;	PRT;	110 AA.
----	--------	--------------	------	---------

AC Q9JL77;

DATE	DESCRIPTION	AMOUNT	CHECK NO.	BANK	INTEREST	TOTAL	DATE	DESCRIPTION	AMOUNT	CHECK NO.	BANK	INTEREST	TOTAL
01-OCT-2000	TRFMBLREL	15					01-OCT-2000	TRFMBLREL	15				
01-OCT-2000	TRFMBLREL	15					01-OCT-2000	TRFMBLREL	15				

01-OCT-2000	(TREMBlrel. 15,	Last sequence update)
01-MAR-2001	(TREMBlrel. 16,	Last annotation update)

DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION

Mus musculus (Mouse).

Lurayota, Metazoa; R
Mammalia; Eutheria; R
OC

NCBI_TaxID=10090;

[1] SEQUENCE FROM N. 2

RC : STRAIN=DBA/2:

RA Malkiel S., Liao L

RT "Characterization of

acetyl-glucosamine
Submitted (NOV-1999)

EMBL; AF206029; AAF69327.1; -;

DR InterPro; IPR003006; -.

UR InterPro; IPR003596; -.
OR Pfam: PF00047; ig. 1

DR SM00406; IGv; 1.

[illegible]

NON_TER	110	110
SEQUENCE	110	121

TO THE ATTORNEY GENERAL

Query Match	68
Best Local Similarity	75

Best local similarity 75
Matches 12; Conservativ

100

```

Query Match      68.3%; Score 69; DB 11; Length 110;
Best Local Similarity 75.0%; Pred. No. 0.00096;
Matches 12; Conservative 2; Mismatches 2; Indels

```

2 IYPGSGNTKYNEKFG 17

䷗

RESULT 2

Q9Z1C4

Q9Z1C4	PRELIMINARY;	PRT;	118 AA.
Q9Z1C4			

25214

DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE ANTI-PORCINE VCAM MAB 3F4 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALE/C;
 RA Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
 RA Matis L.M., Evans M.J.;
 FT "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
 RT IgG2/34 constant regions block human leukocyte binding to porcine
 RT endothelial cells."
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 CC EMBL: U7801; AAD00293.1; -.
 DR InterPro; IPR003006; -.
 DR InterPro; IPR003596; -.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR NON_TER 1
 FT NON_TER 118 118
 FT SEQUENCE 118 AA; 13036 MW; 90EEC559D31EC4FC CRC64;
 SQ SEQUENCE 118 AA; 13036 MW; 90EEC559D31EC4FC CRC64;

Query Match 63.4%; Score 64; DB 11; Length 118;
 Best Local Similarity 62.5%; Pred. No. 0.0067;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 2 IYPGSGNTKYNEKFKG 17
 DB 51 IYPGSGTSTYQKFKG 66

RESULT 3
 ID Q9JL83 PRELIMINARY; PRT; 110 AA.
 AC Q9JL83;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALE/C;
 RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
 RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
 RT acetyl-glucosamine antibodies from mice with autoimmune myocarditis."
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF206023; AAF69321.1; -.
 DR InterPro; IPR003006; -.
 DR InterPro; IPR003596; -.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR NON_TER 1
 FT NON_TER 110 110
 FT SEQUENCE 110 AA; 12052 MW; 84E6F2AD219AF95E CRC64;
 SQ SEQUENCE 110 AA; 12052 MW; 84E6F2AD219AF95E CRC64;

Query Match 61.4%; Score 62; DB 11; Length 110;
 Best Local Similarity 68.8%; Pred. No. 0.013;
 Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 2 IYPGSGNTKYNEKFKG 17
 DB 11 IYPSGNTKYNEKFKG 17

Db 43 IYPGSGDAYNGKFKG 58
 RESULT 4
 ID Q9JL75 PRELIMINARY; PRT; 109 AA.
 AC Q9JL75;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALE/C;
 RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
 RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
 RT acetyl-glucosamine antibodies from mice with autoimmune myocarditis."
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF206031; AAF69329.1; -.
 DR InterPro; IPR003006; -.
 DR InterPro; IPR003596; -.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR NON_TER 1
 FT NON_TER 109 109
 FT SEQUENCE 109 AA; 12118 MW; FF65E441BBF936A6 CRC64;
 SQ SEQUENCE 109 AA; 12118 MW; FF65E441BBF936A6 CRC64;

Query Match 57.4%; Score 58; DB 11; Length 109;
 Best Local Similarity 64.7%; Pred. No. 0.057;
 Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 WIYPGSGNTKYNEKFKG 17
 DB 41 YINPYNDGTKYNEKFKG 57

RESULT 5
 ID Q9QXF0 PRELIMINARY; PRT; 117 AA.
 AC Q9QXF0;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Clemens A., Rademakers A., Specht C., Koelsch E.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ225171; CAB65236.1; -.
 DR InterPro; IPR003006; -.
 DR InterPro; IPR003596; -.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR NON_TER 1
 FT NON_TER 117 117
 FT SEQUENCE 117 AA; 13060 MW; D816AD0858A47E4C CRC64;
 SQ SEQUENCE 117 AA; 13060 MW; D816AD0858A47E4C CRC64;

Query Match 57.4%; Score 58; DB 11; Length 117;
 Best Local Similarity 62.5%; Pred. No. 0.061;
 Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 2 IYPGSGNTKYNEKFKG 17
 DB 11 IYPSGNTKYNEKFKG 17

0.01 0.02 0.03 0.04 0.05 0.06 0.07 0.08 0.09 0.10 0.11 0.12 0.13 0.14 0.15 0.16 0.17 0.18 0.19 0.20 0.21 0.22 0.23 0.24 0.25 0.26 0.27 0.28 0.29 0.30 0.31 0.32 0.33 0.34 0.35 0.36 0.37 0.38 0.39 0.40 0.41 0.42 0.43 0.44 0.45 0.46 0.47 0.48 0.49 0.50 0.51 0.52 0.53 0.54 0.55 0.56 0.57 0.58 0.59 0.60 0.61 0.62 0.63 0.64 0.65 0.66 0.67 0.68 0.69 0.70 0.71 0.72 0.73 0.74 0.75 0.76 0.77 0.78 0.79 0.80 0.81 0.82 0.83 0.84 0.85 0.86 0.87 0.88 0.89 0.90 0.91 0.92 0.93 0.94 0.95 0.96 0.97 0.98 0.99 1.00

100

DR Pfam: PF01827; DUF38.1;
SQ SEQUENCE 172 AA; 13765 MW; 374F392DF599AE6E CRC64;

Query Match 48.5%; Score 49; DB 5; Length 172;
Best Local Similarity 37.5%; Pred. No. 2.7;
Matches 6; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 WIYPGSGNTKYNEFK 16
DB 128 WYYPKSGNMQFRVEYR 143

RESULT 13
Q9JL85 PRELIMINARY; PRT; 109 AA.
AC Q9JL85;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RT Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF206021; AAF69319.1;
DR InterPro: IPR003596;
DR InterPro: IPR003596;
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGv; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11944 MW; DFE615FE6CED4EDE CRC64;

Query Match 46.5%; Score 47; DB 11; Length 109;
Best Local Similarity 50.08; Pred. No. 3.4;
Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGSGNTKYNEFKG 17
DB 43 IDPATGHSKYDPKFGQ 58

RESULT 14
Q9SM05 PRELIMINARY; PRT; 143 AA.
AC Q9SM05;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 30S RIBOSOMAL PROTEIN S9-LIKE.
GN T2J13.80.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Rieger M., Gabel C., Mueller-Auer S., Schaefer M., Zipp M.,
RA Mewes H.W., Lemcke K., Mayer K.F.X., Quetier P., Salanoubat M.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;

RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL132967; CAB62002.1;
DR InterPro: IPR003754;
DR Pfam: PF00380; Ribosomal_S9; 2.
KW Ribosomal protein.
SQ SEQUENCE 143 AA; 16398 MW; 290B418BDB687FCA CRC64;

Query Match 46.5%; Score 47; DB 10; Length 143;
Best Local Similarity 57.1%; Pred. No. 4.6;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 WIYPGSGNTKYNEK 14
DB 33 WIQPGGKQVNEK 46

RESULT 15
Q9JI62 PRELIMINARY; PRT; 89 AA.
AC Q9JI62;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE PROTEOLIPID M6B ISOFORM ALPHA-BETA-GAMMA.
GN M6B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Werner H., Dimou L., Nave K.-A.;
RT "Multiple splice isoforms of M6B, a PLP/DM20-related tetraspan
RT membrane protein in neurons and oligodendrocytes.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF254879; AAF87997.1;
SQ SEQUENCE 89 AA; 10077 MW; 5AA429B3A5B80403 CRC64;

Query Match 45.5%; Score 46; DB 11; Length 89;
Best Local Similarity 63.6%; Pred. No. 3.9;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WIYPGSGNTKY 11
DB 34 WMYPGSKNHQY 44

Search completed: June 28, 2001, 16:08:19
Job time: 947 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 28, 2001, 16:14:34 ; Search time 362.28 seconds
(without alignments)
1.339 Million cell updates/sec

Title: US-09-724-406-8
Perfect score: 54
Sequence: 1 YGNWYFAY 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_0601.*
1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.*
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17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.*
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20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	50	92.6	140	12 AAR12234	Mouse Mab 2G12 H c
2	50	92.6	141	12 AAR12356	Heavy chain variab
3	44	81.5	369	22 AAR73388	Anti-VHSV single c
4	43.5	80.6	116	16 AAR79245	Heavy chain variab
5	43.5	80.6	116	16 AAR79246	Heavy chain variab
6	43	79.6	122	18 AAR01577	Lead binding Mab 1
7	43	79.6	129	21 AAY43866	Heavy chain (VH) 9
8	42.5	78.7	248	19 AAW58826	Human CD30 binding
9	42.5	78.7	273	22 AAB70763	Single chain Fv an
10	41	75.9	119	18 AAW01585	Lead binding Mab 1
11	37.5	69.4	116	18 AAW04592	Anti-DNA antibody

12	37	68.5	17	AAW05038	Synthetic peptide
13	37	68.5	158	21 AAB18127	Pinus radiata meth
14	37	68.5	210	21 AAB18064	Pinus radiata meth
15	37	68.5	234	20 AAY22171	Drosophila Acp29AB
16	36.5	67.6	119	19 AAW49813	Amino acid sequenc
17	36.5	67.6	119	19 AAW49814	Amino acid sequenc
18	36.5	67.6	138	14 AAR39266	Mouse C4G1 Ig heav
19	36.5	67.6	138	19 AAW49810	Variable region of
20	36.5	67.6	222	14 AAR39267	Humanised C4G1 Ig
21	36.5	67.6	222	19 AAW49817	Fragment of human
22	36.5	67.6	235	14 AAR39268	Humanised C4G1 Ig
23	36.5	67.6	235	19 AAW49818	Amino acid sequenc
24	36.5	67.6	449	14 AAR43339	Completely humanis
25	36.5	67.6	449	19 AAW49816	Amino acid sequenc
26	36	66.7	119	7 AAP60335	Immunoglobulin hea
27	36	66.7	119	9 AAP81025	V region of H chai
28	36	66.7	191	20 AAW73377	Human HPDV78 prot
29	36	66.7	267	21 AAB09776	TMV 30K movement p
30	36	66.7	270	21 AAG08976	Arabidopsis thalia
31	36	66.7	272	21 AAG08975	Arabidopsis thalia
32	36	66.7	470	7 AAP60351	Chimeric human-mou
33	36	66.7	470	8 AAP70547	Sequence of novel
34	36	66.7	573	19 AAW76315	Myceliophthora the
35	36	66.7	573	19 AAW76316	Myceliophthora the
36	36	66.7	573	19 AAW76317	Myceliophthora the
37	36	66.7	573	19 AAW79077	Myceliophthora the
38	36	66.7	573	19 AAW79078	Myceliophthora the
39	36	66.7	573	19 AAW79079	Myceliophthora the
40	36	66.7	573	19 AAW59913	Myceliophthora the
41	36	66.7	573	19 AAW62503	Myceliophthora the
42	36	66.7	573	19 AAW51782	Myceliophthora the
43	36	66.7	573	19 AAW63124	Myceliophthora the
44	36	66.7	573	21 AAY91085	Myceliophthora the
45	36	66.7	616	17 AAW07635	Rat brain derived

ALIGNMENTS

RESULT 1
AAR12234
ID AAR12234 standard; Protein; 140 AA.
XX
AC AAR12234;
XX
DT 19-AUG-1991 (first entry)
XX
DE Mouse Mab 2G12 H chain V region.
XX
KW HIV-1; chimera.
XX
OS Mus sp.
XX
PN WO9107494-A.
XX
PD 30-MAY-1991.
XX
PF 13-NOV-1990; 30WO-USO66627.
XX
PR 13-NOV-1989; 39US-0433703.
XX
PA (XOMA-) XOMA CORP.
XX
PI Better MD, Horwitz AH, Ghosh-Dastidar P, Robinson RP;
XX
DR WPI; 1991-178106/24.
XX
DR N-PSDB; AAQ12014.
XX
PT New chimeric mouse human antibodies - used in treatment, diagnosis
XX
PT and prophylaxis of HIV infections.
XX
PS Disclosure; Fig 7; 108pp; English.

Fri Jun 29 08:05:21 2001

us-09-724-406-8.rag

CC The mouse VH gene product may be used to produce chimeric mouse-
 CC human Abs against HIV-1 comprising human Ig constant regions and
 CC murine variable regions. These novel sequence are useful in
 CC treatment, diagnosis and prophylaxis of HIV infections, and may be
 CC produced by a bacterial, yeast or mammalian expression system.
 XX
 SQ Sequence 140 AA;

Query Match 92.6%; Score 50; DB 12; Length 140;
 Best Local Similarity 87.5%; Pred. No. 0.29;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGNWYFAY 8

Db 123 ygnwfay 130

RESULT 2

AA12356
 ID AAR12356 standard; Protein; 141 AA.

XX
 AC AAR12356;

XX 15-AUG-1991 (first entry)

XX Heavy chain variable region of murine 2G12 immunoglobulin.

DE Chimeric antibodies; immunoconjugates; HIV; AIDS.

KW Mus musculus.

OS WO9107493-A.

XX 30-MAY-1991.

XX 13-NOV-1990; 90WO-US06615.

XX 13-NOV-1989; 89US-0433730.

XX (XOMA-) XOMA CORP.

PA (GREG) GREEN CROSS CORP.

XX Better MD, Horwitz AH, Ghosh-Dastidar P, Robinson RR;

XX WPI; 1991-178044/24.

DR N-PSDB; AAQ12058.

XX New chimeric mouse-human antibodies - used to detect, kill and

XX remove HIV-1 antigen from sample

XX Disclosure; fig 7; 107pp; English.

XX This is the heavy-chain variable (V) region of a mouse monoclonal

XX antibody (MAB), 2G12, and is specific for an HIV-1 viral antigen.

XX It is used in the construction of a chimeric MAB comprising heavy

XX and light chains having murine V regions and human C regions.

XX The chimeric MABs are more effective than murine MAB 2G12 since

XX they have an increased compatibility in humans. The heavy and

XX light chain V-regions are joined by manipulating their respective

XX joining (J) regions, to generate restriction enzyme recognition

XX sites. The chimeric MABs can be used as immunoconjugates, in

XX association with e.g. toxins for HIV treatment. They can also be

XX used in diagnosis of HIV.

XX See also AAQ12056-57 and AAQ12059-63.

SQ Sequence 141 AA;

Query Match 92.6%; Score 50; DB 12; Length 141;

Best Local Similarity 87.5%; Pred. No. 0.29;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGNWYFAY 8

Db 123 ygnwfay 130

RESULT 3

AA12356
 ID AAB73388 standard; Protein; 369 AA.

XX
 AC AAB73388;

XX 05-JUN-2001 (first entry)

XX Anti-VHSV single chain antibody BUL.

XX Anti-VHSV; single chain antibody BUL; scAb; scFv;

XX monoclonal antibody 3F1H10; variable region; antiviral; anti-allergy;

XX human kappa light chain constant domain; vaccine; gene therapy;

XX rainbow trout TGF-beta signal peptide; transforming growth factor beta;

XX genetic prophylaxis.

XX Chimeric - Oncorhynchus mykiss.

OS Chimeric - Mus musculus.

OS Chimeric - Homo sapiens.

XX Synthetic.

XX WO200121800-A1.

XX 29-MAR-2001.

XX 20-SEP-2000; 2000WO-GB03605.

XX 20-SEP-1999; 99DK-0001329.

XX (UVAB-) UNIV ABERDEEN.

PA (STAT-) STATENS VETERINAERE SERUMLABORATORIUM.

XX Secombes CJ, Cunningham C, Lorenzen N;

XX WPI; 2001-257991/26.

XX N-PSDB; AAF73388.

XX New non-infectious nucleic acid construct encoding recombinant antibody

XX molecule, useful for conferring protective immunity to infectious

XX diseases, preventing allergic reactions or reactions caused by toxins

XX in animals

XX Example; Page -: 29pp; English.

XX The invention relates to a non-infectious nucleic acid construct

XX encoding a recombinant (e.g., single chain) antibody molecule. The

XX nucleic acid construct is adapted for in vivo establishment of protective

XX immunity to an infectious disease in an animal, or is formulated for in

XX vivo prevention of an allergic reaction to an allergen or a reaction

XX caused by the presence of a toxic substance in an animal. Constructs of

XX the invention are thus useful for treating infectious disease caused by

XX viral haemorrhagic septicaemia virus (VHSV) (fish), infectious

XX haematopoietic necrosis virus (fish), bovine viral diarrhoea virus,

XX pseudorabies virus (pigs), plasmocytosis virus (mink), feline leukaemia

XX virus, human immunodeficiency virus, and hepatitis A virus (human).

CC antibody, BUI. BUI is reactive to the fish pathogenic rhabdovirus, VHSV.
 CC BUI is derived from the variable regions of the VHSV-reactive murine
 CC monoclonal antibody 3F1H10, and also contains the rainbow trout
 CC transforming growth factor beta (TGF-beta) signal peptide at the N-
 CC terminus (to ensure secretion of the single chain antibody) and the
 CC human kappa light chain constant domain (used as a tag to facilitate
 CC detection) at the C-terminus.
 CC Note: The present sequence is not shown in the specification, but has
 CC been decoded from the corresponding nucleic acid sequence (AAF76338).
 CC
 XX
 SQ Sequence 369 AA;

Query Match 81.5%; Score 44; DB 22; Length 369;
 Best Local Similarity 87.5%; Pred. No. 7.3;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNYWFAY 8
 ||| ||||
 Db 123 ygndwfay 130

RESULT 4
 AAR79245
 ID AAR79245 standard; Protein: 116 AA.
 XX
 AC AAR79245;

XX 21-DEC-1995 (first entry)
 XX Heavy chain variable region for monoclonal antibody 2D5.
 XX
 DE Monoclonal antibody; heavy metal; mercury; variable region;
 KW heavy chain.
 XX
 OS Synthetic.
 XX
 PN W09520607-A.
 XX
 PD 03-AUG-1995.

XX 27-JAN-1995; 95WO-US01199.
 XX
 PF 27-JAN-1994; 94US-0187407.
 XX
 PR (BION-) BIONEBRASKA INC.
 XX
 PA Lopez O, Wagner FW, Wylie DE;
 XX
 PI WPI: 1995-275415/36.
 DR N-PSDB; AAQ97502.
 XX

PT New polypeptide(s) which bind heavy metals, esp. mercury - derived from
 PT monoclonal antibodies, used for detecting, removing, adding or
 PT neutralising heavy metals
 XX
 PS Claim 13; Page 59-60; 106pp; English.

XX Hybridoma antibodies have been produced with the spleen cells of
 CC BALB/c mouse that had received multiple injections of mercuric ions
 CC reacted with glutathione to produce a mercuric ion coordinate
 CC covalent compound which was covalently bound to keyhole limpet
 CC hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23F8, 2D5,
 CC 5B6 and 3B8) were producing MABs that were strongly positive
 CC against glutathione-mercuric ions but negative against glutathione
 CC without mercuric ions. RNA was isolated from hybridoma cells with
 CC guanidine isothiocyanate. First strand cDNA synthesis was catalysed
 CC by MuLV reverse transcriptase. The primers used for cDNA synthesis
 CC were complementary to the 5' end of the CHI domain of the heavy
 CC chain expressed by the hybridoma of interest, or to the 5' and of
 CC the C kappa domain. Some of the primers used for cDNA synthesis are
 CC shown in AAQ97511-097518. The primer used for cDNA synthesis of the
 CC variable region of a particular antibody polypeptide was also used

CC for PCR amplification of that variable region, in conjunction with
 CC an appropriate V-region primer. In addition, the VH primer AAQ97518
 CC was used to amplify the mAb 2D5 and 5B6 heavy chains. The sequences
 CC of the PCR amplified nucleotides were determined. These are given
 CC in AAQ97498-097510 and the deduced AA sequences in AAR79241-R79250 &
 CC AAR78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45
 CC and in the claims are different from the descriptions in the
 CC sequence listings. The descriptions in the sequence listings are
 CC used here.

XX
 SQ Sequence 116 AA;

Query Match 80.6%; Score 43.5; DB 16; Length 116;
 Best Local Similarity 88.9%; Pred. No. 2.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 YGNY-WFAY 8
 |||| ||||
 Db 97 ygnyvwfay 105

RESULT 5
 AAR79246
 ID AAR79246 standard; Protein: 116 AA.
 XX
 AC AAR79246;

XX 21-DEC-1995 (first entry)
 XX Heavy chain variable region for monoclonal antibody 5B6.
 XX
 DE Monoclonal antibody; heavy metal; mercury; variable region;
 KW heavy chain.
 XX
 OS Synthetic.
 XX
 PN W09520607-A.
 XX
 PD 03-AUG-1995.

XX 27-JAN-1995; 95WO-US01199.
 XX
 PF 27-JAN-1994; 94US-0187407.
 XX
 PR (BION-) BIONEBRASKA INC.
 XX
 PA Lopez O, Wagner FW, Wylie DE;
 XX
 PI WPI: 1995-275415/36.
 DR N-PSDB; AAQ97503.

PT New polypeptide(s) which bind heavy metals, esp. mercury - derived from
 PT monoclonal antibodies, used for detecting, removing, adding or
 PT neutralising heavy metals
 XX
 PS Claim 13; Page 61; 106pp; English.

XX Hybridoma antibodies have been produced with the spleen cells of
 CC BALB/c mouse that had received multiple injections of mercuric ions
 CC reacted with glutathione to produce a mercuric ion coordinate
 CC covalent compound which was covalently bound to keyhole limpet
 CC hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23F8, 2D5,
 CC 5B6 and 3B8) were producing MABs that were strongly positive
 CC against glutathione-mercuric ions but negative against glutathione
 CC without mercuric ions. RNA was isolated from hybridoma cells with
 CC guanidine isothiocyanate. First strand cDNA synthesis was catalysed
 CC by MuLV reverse transcriptase. The primers used for cDNA synthesis
 CC were complementary to the 5' end of the CHI domain of the heavy
 CC chain expressed by the hybridoma of interest, or to the 5' and of
 CC the C kappa domain. Some of the primers used for cDNA synthesis are
 CC shown in AAQ97511-097518. The primer used for cDNA synthesis of the
 CC variable region of a particular antibody polypeptide was also used

CC for PCR amplification of that variable region, in conjunction with
 CC an appropriate V-region primer. In addition, the VH primer AAQ97518
 CC was used to amplify the mAb 2D5 and 5B6 heavy chains. The sequences
 CC of the PCR amplified nucleotides were determined. These are given
 CC in AAQ97498-Q97510 and the deduced AA sequences in AAR79241-R79250 &
 CC AAR79970-R79971. The descriptions of the SEQ ID nos given on pp 44-45
 CC and in the claims are different from the descriptions in the
 CC sequence listings. The descriptions in the sequence listings are
 CC used here.

XX Sequence 116 AA;
 SQ

Query Match 80.8%; Score 43.5; DB 16; Length 116;
 Best Local Similarity 88.9%; Pred. No. 2.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 YGNY--WFAY 8
 |||| ||||
 Db 97 ygnvewfay 105

RESULT 6
 AAW01577
 ID AAW01577 standard; Protein; 122 AA.

XX AC AAW01577;

XX DT 22-AUG-1997 (first entry)

XX DE Lead binding MAB 1254 heavy chain variable region.

XX KW Monoclonal antibody; Fd fragment; lead cation; perfume; cosmetic;
 XX pharmaceutical; health care; skin treatment; pesticide; herbicide;
 XX heavy metal.

XX OS Mus musculus.

XX PN WO9639518-A1.

XX PD 12-DEC-1996.

XX PF 05-JUN-1996; 96WO-US09258.

XX PR 10-OCT-1995; 95US-0541373.

XX PR 05-JUN-1995; 95US-0462798.

XX PA (BION-) BIONEERASKA INC.

XX PI Lopez O, Murray PJ, Wyllie DB;

XX DR WPI; 1997-043140/04.

XX DR N-PSDB; AAT58251.

XX DNA encoding heavy metal binding polypeptide sequences - used for
 PT detecting, removing, adding or neutralising heavy metals, such as
 PT lead cations

XX Claim 12; Page 58; 125pp; English.

XX The present sequence represents the heavy chain variable region for
 XX monoclonal antibody (Mab) 1254, which immunoreacts with a lead cation.
 CC The sequence was derived from RNA isolated from mouse hybridoma cells.
 CC The protein can be used for binding heavy metals, such as lead cations.
 CC It can be used for detecting, removing, adding or neutralising the
 CC heavy metals in biological and inanimate systems. It can be used in
 CC e.g. aqueous liquid systems, in biological or environmental systems or
 CC in such compositions as perfumes, cosmetics, pharmaceuticals, health
 CC care products, skin treatment products, pesticides, herbicides,
 CC solvents used in the production of semi-conductor and integrated
 CC circuit components and production materials for electronic components.
 CC The products can provide for applications involving minute amounts of
 CC specific heavy metals.

XX Sequence 122 AA;
 SQ

Query Match 79.6%; Score 43; DB 18; Length 122;
 Best Local Similarity 80.0%; Pred. No. 3.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 YGNY--WFAY 8
 |||| ||||
 Db 102 ygnvawfay 111

RESULT 7
 AAY43866
 ID AAY43866 standard; Peptide; 129 AA.

XX AC AAY43866;

XX DT 11-FEB-2000 (first entry)

XX DE Heavy chain (VH) gene sequence of Bacillus anthracis antibody 7-1.

XX KW Heavy chain; VH; IgG; monoclonal antibody; spore; Bacillus;
 XX VH gene usage; anthrax.

XX OS Mus sp.

XX PN WO9955842-A1.

XX PD 04-NOV-1999.

XX PF 27-APR-1999; 99WO-US09122.

XX PR 29-APR-1998; 98US-0069628.

XX PA (UABR-) UAB RES FOUND.

XX PI Kearney JF;

XX DR WPI; 2000-013435/01.

XX Monoclonal antibody specific for Bacillus spores, used to detect
 PT anthrax -

XX Example 13; Page 53-54; 64pp; English.

XX CC AAY43862-75 represent the amino acid sequences of the heavy chain
 CC (VH) gene sequences from antibodies against Bacillus anthracis
 CC spores. The antibodies are produced by different hybridomas. The
 CC specification describes monoclonal antibodies (especially IgG
 CC antibodies) which are highly specific and can discriminate between the
 CC spores of the Bacillus family. The antibodies are produced by exposing
 CC mice to Bacillus spores. The humoral immune response to Bacillus spore.
 CC shows a conservation of VH gene usage which is distinct for each spore.
 CC Peptide fragments derived from the antibodies are also capable of
 CC binding spores. The monoclonal antibody, and peptide fragments of it, can
 CC be used to detect Bacillus spores in a field sample. It is particularly
 CC uses for detecting anthrax in a field sample.

XX Sequence 129 AA;

Query Match 79.6%; Score 43; DB 21; Length 129;
 Best Local Similarity 80.0%; Pred. No. 3.7;
 Matches 8; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 YGNY--WFAY 8
 |||| ||||
 Db 77 ygnvpawfay 86

RESULT 8

AAW58826
 ID AAW58826 standard; Protein; 248 AA.
 AC AAW58826;
 XX
 DT 18-AUG-1998 (first entry)
 XX
 DE Human CD30 binding protein.
 XX
 KW CD30 binding protein; human; suppressor; proliferation; metastasis;
 XX tumour formation; CD30 antigen.
 OS Homo sapiens.
 XX
 PN DE19640733-A1.
 XX
 PD 09-APR-1998.
 XX
 PF 02-OCT-1996; 96DE-1040733.
 XX
 PR 02-OCT-1996; 96DE-1040733.
 XX
 PA (ABKE/) ABKEN H.
 XX
 DR WPI; 1998-218120/20.
 XX
 DR N-PSDB; AAV11399.
 XX
 XX Polypeptide than binds to CD30 without cell activation - for
 PT inhibiting proliferation and metastasis of tumour cells, etc.
 XX
 PS Claim 3; Page 7-8; 8pp; German.
 XX
 CC This sequence represents a human CD30 binding protein which can be
 CC used in a method for suppressing unchecked proliferation, tumour
 CC formation and metastasis of cells expressing the CD30 antigen. This
 CC protein specifically binds to CD30 without inducing cell activation by
 CC CD30. The protein can also be used for probing, binding or enriching
 CC CD30-expressing cells in vivo or in body fluids, cell suspensions or
 CC tissues in vitro. A substance coupled to the protein accumulates in the
 CC vicinity of CD30-expressing cells in vivo or in vitro.
 XX
 SQ Sequence 248 AA;

Query Match 78.7%; Score 42.5; DB 19; Length 248;
 Best Local Similarity 72.7%; Pred. No. 8.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
 QY 1 YGNY---WFAV 8
 DB 104 ygnyeYtwfay 114

RESULT 9
 AAB70763
 ID AAB70763 standard; Protein; 273 AA.
 AC AAB70763;
 XX
 DT 18-MAY-2001 (first entry)
 XX
 DE Single chain Fv antibody construct anti-CD30 VL domain protein.
 XX
 KW Single chain Fv antibody; anti-CD16; anti-CD30; VH domain; VL domain;
 XX fusion construct; CD16 receptor; CD30 surface protein; cytostatic;
 KW tumor cell; natural killer cell activation; Hodgkin's disease;
 XX Read-Sternberg disease.
 OS Synthetic.
 XX
 PN DE19937264-A1.
 XX
 PD 15-FEB-2001.

XX 06-AUG-1999; 99DE-1037264.
 PF
 XX 06-AUG-1999; 99DE-1037264.
 PR
 XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 PA
 XX Arndt M, Little M, Kipriyanov S, Krauss J, Pfreundschuh M;
 PI WPI; 2001-184000/19.
 DR
 XX New Fv-antibody construct, useful for treating Hodgkin and
 PT Reed-Sternberg diseases, has binding sites for CD16 receptor and CD30
 PT surface protein
 XX
 PS Disclosure; Page 11; 18pp; German.
 XX
 CC This invention describes a novel Fv-antibody construct (I) having binding
 CC sites for a CD16 receptor and a CD30 surface protein. The invention also
 CC describes (1) expression vector encoding (I); (2) transformants
 CC containing the vector of (1); (3) preparation of (I) by culturing cells
 CC of (2); and (4) kit comprising (I) and/or the vector of (1), and
 CC auxiliaries such as buffers, solvents, carriers, controls and labels, or
 CC their replacements. The products of the invention have cytostatic
 CC activity. (I) causes lysis of CD30+, specifically tumor, cells. It
 CC activates natural killer cells, through the CD16 receptor, and directs
 CC them to CD30-expressing cells. (I) are used to treat diseases in which
 CC CD30+ cells are implicated, particularly tumors and specifically Hodgkin
 CC or Reed-Sternberg diseases. (I) have a stronger lytic action than known
 CC bispecific antibodies, can be produced on a large scale with high purity,
 CC and contain no components that can induce unwanted immune responses.
 XX
 SQ Sequence 273 AA;

Query Match 78.7%; Score 42.5; DB 22; Length 273;
 Best Local Similarity 72.7%; Pred. No. 9.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
 QY 1 YGNY---WFAV 8
 DB 104 ygnyeYtwfay 114

RESULT 10
 AAW01585
 ID AAW01585 standard; Protein; 119 AA.
 XX
 AC AAW01585;
 XX
 DT 22-AUG-1997 (first entry)
 XX
 DE Lead binding MAB 11D11 heavy chain variable region.
 XX
 KW Monoclonal antibody; Fd fragment; lead cation; perfume; cosmetic;
 KW pharmaceutical; health care; skin treatment; pesticide; herbicide;
 XX heavy metal.
 OS Mus musculus.
 XX
 PN WO9639518-A1.
 XX
 PD 12-DEC-1996.
 XX
 PF 05-JUN-1996; 96WO-US09258.
 XX
 PR 10-OCT-1995; 95US-0541373.
 PR 05-JUN-1995; 95US-0462798.
 XX
 PA (BION-) BIONEERASKA INC.
 XX
 PI Lopez O, Murray PJ, Wylie DE;
 XX

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DR WPI; 1997-043140/04.
DR N-PSDB; AAT58259.
XX
XX DNA encoding heavy metal binding polypeptide sequences - used for
XX detecting, removing, adding or neutralising heavy metals, such as
XX lead cations
XX
XX Claim 12; Page 73; 125pp; English.
XX
XX The present sequence represents the heavy chain variable region for
XX monoclonal antibody (MAB) 10f4, which immunoreacts with a lead cation.
XX The sequence was derived from RNA isolated from mouse hybridoma cells.
XX The protein can be used for binding heavy metals, such as lead cations.
XX It can be used for detecting, removing, adding or neutralising the
XX heavy metals in biological and inanimate systems. It can be used in
XX e.g. aqueous liquid systems, in biological or environmental systems or
XX in such compositions as perfumes, cosmetics, pharmaceuticals, health
XX care products, skin treatment products, pesticides, herbicides,
XX solvents used in the production of semi-conductor and integrated
XX circuit components and production materials for electronic components.
XX The products can provide for applications involving minute amounts of
XX specific heavy metals.
XX
XX Sequence 119 AA;
SQ
Query Match 75.9%; Score 41; DB 18; Length 119;
Best Local Similarity 75.0%; Pred. No. 7.3;
Matches 6; Conservative 1; Mismatches 0; Indels 1; Gaps 0;
QY 1 YGNYWFAY 8
DB 101 yghlwfay 108
||:||||
AAW04592
ID AAW04592 standard; Protein; 116 AA.
AC AAW04592;
XX
XX 11-AUG-1997 (first entry)
XX
XX Anti-DNA antibody 10f4 heavy chain variable region.
XX
XX Heavy chain; variable region; anti-DNA; monoclonal; antibody;
XX MAB 10f4; hairpin; diagnosis; inflammatory glomerulonephritis;
XX systemic lupus erythematosus; screening; treatment; prevention;
XX SLE; disease.
XX
XX Mus spp.
XX
XX Key Location/Qualifiers
FH Region 1..22 /label= framework_I
FT Region 23..27 /label= CDR_I
FT Region 28..41 /label= framework_II
FT Region 42..58 /label= CDR_II
FT Region 59..90 /label= framework_III
FT Region 91..105 /label= CDR_III
FT Region 106..116 /label= J_region
FT
FT WO9636361-AL.
XX
XX 21-NOV-1996.
XX
XX 16-MAY-1996; 96WO-US07113.
XX
18-MAY-1995; 95US-0443540.
XX
XX (UNMI ) UNIV MICHIGAN.
XX
XX Glick GD, Swanson PC;
XX
XX WPI; 1997-011854/01.
XX N-PSDB; AAT43736.
XX
XX Anti-DNA antibody which specifically binds DNA hairpin - useful to
XX develop prods. for diagnosis and treatment of disorders, e.g.
XX glomerulonephritis or systemic lupus erythematosus
XX
XX Example; Fig 7; 102pp; English.
XX
XX The present sequence is the heavy chain variable region of the
XX anti-DNA monoclonal antibody (MAB) 10f4, which has a high affinity
XX for single stranded DNA, low or no affinity for double stranded DNA
XX and specifically binds a DNA hairpin. The MAB can be used to diagnose
XX disorders associated with the pathological complexation of DNA,
XX e.g. inflammatory glomerulonephritis and systemic lupus
XX erythematosus. It can also be used to generate reagents to screen
XX for pharmaceutical agents, and treat and/or prevent an above
XX disorder.
XX
XX Calf thymus DNA was used to immunise a MRL-lpr mouse, spleen cells
XX from which were then fused with Sp2/0 myeloma cells to give
XX hybridomas producing the anti-DNA MAB. 10f4 was found to react
XX strongly with single stranded DNA and poly(dT), moderately with
XX poly(dG) and weakly with poly(dI).
XX
XX Sequence 116 AA;
Query Match 69.4%; Score 37.5; DB 18; Length 116;
Best Local Similarity 77.8%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1 YGNY-WFAY 8
DB 97 ysnypwfay 105
||:||||
RESULT 12
AAW05038
ID AAW05038 standard; peptide; 17 AA.
XX
XX AAW05038;
XX
XX 29-MAY-1997 (first entry)
XX
XX Synthetic peptide for treating systemic lupus erythematosus.
XX
XX SLE; systemic lupus erythematosus; autoimmune disease; monoclonal;
XX anti-DNA antibody; CDR; complementarity determining region; 16/6 Id;
XX idioype; nuclear antigen.
XX
XX Synthetic.
XX
XX WO9630057-AL.
XX
XX 03-OCT-1996.
XX
XX 27-MAR-1996; 96WO-US04206.
XX
XX 28-MAR-1995; 95IL-0113159.
XX
XX (RYCU/) RYCUS A.
XX
XX (YEDA ) YEDA RES & DEV CO LTD.
XX
XX Mozes E, Waisman A;
XX
XX WPI; 1996-455014/45.
XX

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XX New synthetic peptide(s) for treating systemic lupus erythematosus -
 PT based on complementarity determining region of pathogenic anti-DNA
 PT monoclonal antibody that induces SLE-like disease in mice
 XX
 PS Claim 8; Page 37; 51pp; English.
 XX
 CC AAM05029-W05038 are synthetic peptides based on the complementarity-
 CC determining region (CDR) of the heavy or light chain of a pathogenic
 CC 16/6 Id anti-DNA monoclonal antibody (MAB), that induces a systemic
 CC lupus erythematosus (SLE)-like disease in mice. The peptides and their
 CC derivatives are used for treating SLE. The peptides inhibit or suppress
 CC specific antigen responses of SLE patients without affecting all other
 CC immune responses.
 XX
 SQ Sequence 17 AA;

Query Match 68.5%; Score 37; DB 17; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4.8;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGNW 5
 Db 9 YGNW 13

RESULT 13

AAB18127
 ID AAB18127 standard; Protein; 158 AA.

AC AAB18127;

XX 08-NOV-2000 (first entry)

XX Pinus radiata methyl sterol oxidase protein SEQ ID NO:288.

XX Eucalyptus grandis; Pinus radiata; modification; isoprenoid; plant;
 KW metabolism; isoprenoid biosynthetic pathway; terpenoid; steroid;
 KW genome mapping; physical mapping; positional cloning; forestry;
 KW agriculture; medicine; fermentation; plant development; pest resistance;
 KW pinene; myrcene; Monterey pine.

XX Pinus radiata.

XX WO200036081-A2.

XX 22-JUN-2000.

PF 16-DEC-1999; 99WO-NZ00219.

XX 17-DEC-1998; 98US-0215504.

PR 29-JUL-1999; 99US-0146441.

XX (GENE-) GENESIS RES & DEV CORP LTD.

PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.

XX Havukkala IJ;

XX WPI: 2000-431575/37.

DR N-PSDB; AAA69563.

XX New plant polynucleotides encoding polypeptides involved in the
 PT production and modification of isoprenoids, useful in forestry and
 PT agriculture for manipulation of isoprenoid metabolism -

PS Claim 26; Page 158; 164pp; English.

XX The present invention describes plant polynucleotides encoding
 CC polypeptides involved in the production and modification of isoprenoids,
 CC such as terpenoid and steroid compounds. The polynucleotides are used
 CC in genome mapping, in physical mapping and in positional cloning of
 CC genes. The polynucleotides and polypeptides are useful in forestry and

CC agriculture for manipulation of isoprenoid metabolism, in medicine for
 CC therapeutic effects, including direct application in diseased organisms
 CC or indirect application by transgenic organisms and in fermentation and
 CC chemical processing industries involving isoprenoids. In plant
 CC applications, manipulating isoprenoid pathways or isoprenoid composition
 CC may, for example, affect plant development, pest resistance, and the
 CC value of extractives (e.g. pinene and myrcene). The ubiquitous and
 CC varied roles of isoprenoids make the polynucleotides attractive targets
 CC for biotechnical applications in a variety of fields. AAA69527 to
 CC AAG69690 and AAB18004 to AAB18143 represent Eucalyptus grandis and Pinus
 CC radiata polynucleotides and proteins used in the exemplification of the
 CC present invention.

XX Sequence 158 AA;

Query Match 68.5%; Score 37; DB 21; Length 158;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGNW 5
 Db 45 YGNW 49

RESULT 14

AAB18064

XX AAB18064 standard; Protein; 210 AA.

AC AAB18064;

XX 08-NOV-2000 (first entry)

XX Pinus radiata methyl sterol oxidase protein SEQ ID NO:225.

XX Eucalyptus grandis; Pinus radiata; modification; isoprenoid; plant;
 KW metabolism; isoprenoid biosynthetic pathway; terpenoid; steroid;
 KW genome mapping; physical mapping; positional cloning; forestry;
 KW agriculture; medicine; fermentation; plant development; pest resistance;
 KW pinene; myrcene; Monterey pine.

XX Pinus radiata.

XX WO200036081-A2.

XX 22-JUN-2000.

PF 16-DEC-1999; 99WO-NZ00219.

XX 17-DEC-1998; 98US-0215504.

PR 29-JUL-1999; 99US-0146441.

XX (GENE-) GENESIS RES & DEV CORP LTD.

PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.

XX Havukkala IJ;

XX WPI: 2000-431575/37.

DR N-PSDB; AAA69664.

XX New plant polynucleotides encoding polypeptides involved in the
 PT production and modification of isoprenoids, useful in forestry and
 PT agriculture for manipulation of isoprenoid metabolism -

PS Claim 26; Page 129; 164pp; English.

XX The present invention describes plant polynucleotides encoding
 CC polypeptides involved in the production and modification of isoprenoids,
 CC such as terpenoid and steroid compounds. The polynucleotides are used
 CC in genome mapping, in physical mapping and in positional cloning of
 CC genes. The polynucleotides and polypeptides are useful in forestry and
 CC agriculture for manipulation of isoprenoid metabolism, in medicine for
 CC therapeutic effects, including direct application in diseased organisms

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Db 50 nywfty 55

Search completed: June 28, 2001, 16:14:34
Job time: 1322 sec

CC or indirect application by transgenic organisms and in fermentation and
 CC chemical processing industries involving isoprenoids. In plant
 CC applications, manipulating isoprenoid pathways or isoprenoid composition
 CC may, for example, affect plant development, pest resistance, and the
 CC value of extractives (e.g. pinene and myrcene). The ubiquitous and
 CC varied roles of isoprenoids make the polynucleotides attractive targets
 CC for biotechnical applications in a variety of fields. AA69527 to
 CC AA69690 and AAB18004 to AAB18143 represent Eucalyptus grandis and Pinus
 CC radiata polynucleotides and proteins used in the exemplification of the
 CC present invention.

XX SQ Sequence 210 AA;

Query Match 68.5%; Score 37; DB 21; Length 210;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGNW 5
 Db 45 ygnw 49
 |||||

RESULT 15

AA22171
 ID . AA22171 standard; Protein; 234 AA.

XX AC AA22171;

XX DT 09-SEP-1999 (first entry)

XX DE Drosophila Acp29AB protein.

XX KW Accessory gland protein; Acp; toxin; insecticide; Drosophila; mating;
 XX KX caterpillar; development inhibitor; insect pest; plant protection.

XX OS Drosophila melanogaster.

XX PN WO9932149-A1.

XX PD 01-JUL-1999.

XX PF 23-DEC-1998; 98WO-US27603.

XX PR 23-DEC-1997; 97US-0071315.

XX PA (CORR) CORNELL RES FOUND INC.

XX PI Lung O, Tram K, Wolfner MF;

XX WPI: 1999-418871/35.

XX DR N-PSDB; AAX84364.

XX PT Nucleic acid encoding accessory gland proteins of Drosophila

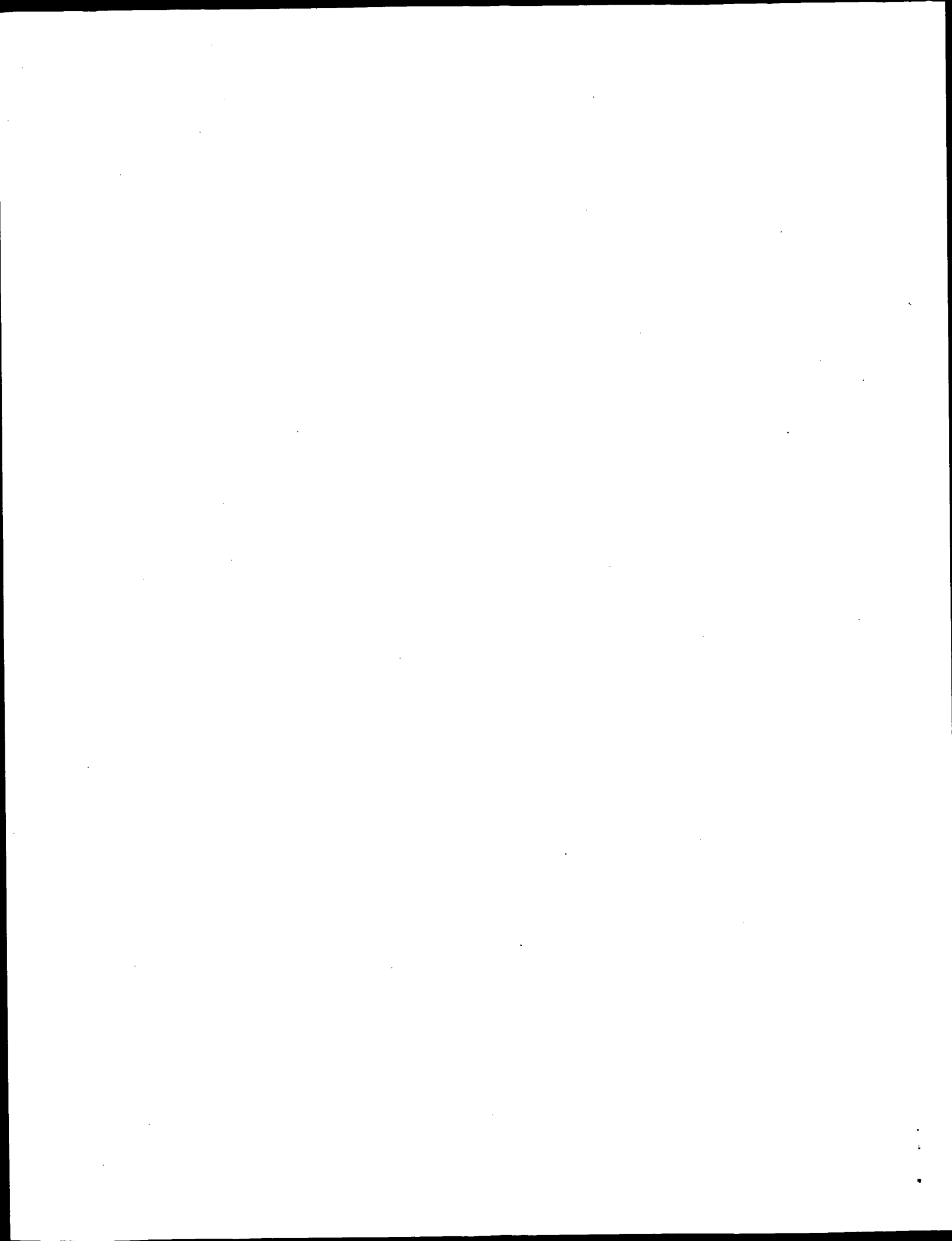
XX PS Claim 38; Page 20; 89pp; English.

XX CC This sequence is a Drosophila melanogaster accessory gland protein
 CC (Acp) of the invention. A particular Acp, designated Acp62F, is toxic to
 CC insects, particularly to Drosophila and caterpillars, and it (or vectors
 CC that express it) can be used to kill or inhibit development of insect
 CC pests, for plant protection. More generally detection of Acp's in a
 CC female fruit fly is indicative of recent mating.

XX SQ Sequence 234 AA;

Query Match 68.5%; Score 37; DB 20; Length 234;
 Best Local Similarity 83.3%; Pred. No. 64;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 NYWFAY 8
 |||||



GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 28, 2001, 16:01:13 ; Search time 138.34 Seconds
(without alignments)
1.165 Million cell updates/sec

Title: US-09-724-406-8
Perfect score: 54
Sequence: 1 YGNYWYAY 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43.5	80.6	116	2	US-08-888-366-10
2	43.5	80.6	116	2	US-08-888-366-12
3	43	79.6	122	4	US-08-767-128-4
4	41	75.9	119	4	US-08-767-128-20
5	37.5	69.4	116	3	US-08-881-037-19
6	37	68.5	221	4	US-08-448-489-19
7	37	68.5	731	2	US-08-696-944-20
8	36.5	67.6	119	1	US-08-458-516-10
9	36.5	67.6	119	1	US-08-458-516-11
10	36.5	67.6	138	1	US-08-458-516-7
11	36.5	67.6	222	1	US-08-458-516-22
12	36.5	67.6	235	1	US-08-458-516-23
13	36.5	67.6	449	1	US-08-991-531-1
14	36	66.7	573	2	US-08-032-315-10
15	36	66.7	573	2	US-09-028-887-1
16	36	66.7	573	2	US-08-993-318A-10
17	36	66.7	573	3	US-09-028-887-1
18	36	66.7	573	4	US-09-399-886-10
19	36	66.7	573	4	US-09-396-260-10
20	36	66.7	573	4	US-09-518-901-1
21	36	66.7	616	1	US-08-149-100-2
22	36	66.7	616	1	US-08-749-882A-2
23	36	66.7	616	2	US-08-539-134-2
24	36	66.7	616	2	US-08-991-531-2
25	36	66.7	616	2	US-09-032-315-9
26	36	66.7	616	2	US-08-993-318A-9
27	36	66.7	616	3	US-09-028-887-2

ALIGNMENTS

RESULT 1
US-08-888-366-10
; Sequence 10, Application US/08888366
; Patent No. 5972656
; GENERAL INFORMATION:
; APPLICANT: Lopez, Osvaldo
; APPLICANT: Wylie, Dwane E.
; APPLICANT: Wagner, Fred W.
; TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefo
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/888,366
; FILING DATE: 03-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/187,407
; FILING DATE: 27-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,542
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/493,299
; FILING DATE: 14-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/324,392
; FILING DATE: 14-MAR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.39USC1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

28 36 66.7 616 4 US-09-399-886-9 Sequence 9, Appli
29 36 66.7 616 4 US-09-396-260-9 Sequence 9, Appli
30 36 66.7 616 4 US-09-518-901-2 Sequence 2, Appli
31 36 66.7 616 5 PCT-US95-06816-2 Sequence 2, Appli
32 36 66.7 620 1 US-08-706-037-27 Sequence 27, Appli
33 36 66.7 620 1 US-08-940-661A-2 Sequence 2, Appli
34 36 66.7 620 2 US-09-083-485-2 Sequence 2, Appli
35 36 66.7 620 2 US-09-005-397-27 Sequence 2, Appli
36 36 66.7 620 2 US-08-939-218A-2 Sequence 27, Appli
37 36 66.7 620 5 PCT-US95-06815-2 Sequence 2, Appli
38 36 66.7 989 2 US-08-070-301-14 Sequence 14, Appli
39 35 64.8 437 4 US-08-961-083-70 Sequence 70, Appli
40 34 63.0 401 2 US-08-846-762-9 Sequence 9, Appli
41 34 63.0 401 2 US-08-820-521-2 Sequence 2, Appli
42 34 63.0 401 4 US-09-248-715-2 Sequence 2, Appli
43 34 63.0 430 1 US-08-601-435-2 Sequence 2, Appli
44 34 63.0 430 2 US-08-931-047-2 Sequence 2, Appli
45 34 63.0 430 2 US-08-783-202-2 Sequence 2, Appli

MOLECULE TYPE: protein
US-08-888-366-10

Query Match 80.6%; Score 43.5; DB 2; Length 116;
Best Local Similarity 88.9%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 YGNY-WFAY 8
|||||
Db 97 YGNYWFAY 105

RESULT 2

US-08-888-366-12
; Sequence 12, Application US/08888366
; Patent No. 5972656
; GENERAL INFORMATION:
; APPLICANT: Lopez, Osvaldo
; APPLICANT: Wylie, Dwane E.
; APPLICANT: Wagner, Fred W.
; TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefore
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/888,366
; APPLICATION NUMBER: US/08/888,366
; FILING DATE: 03-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/187,407
; FILING DATE: 27-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,542
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/493,299
; FILING DATE: 14-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/324,392
; FILING DATE: 14-MAR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.39USC1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-888-366-12

Query Match 80.6%; Score 43.5; DB 2; Length 116;
Best Local Similarity 88.9%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 YGNY-WFAY 8
|||||

Db 97 YGNYWFAY 105

RESULT 3

US-08-767-128-4
; Sequence 4, Application US/08767128
; Patent No. 6111079
; GENERAL INFORMATION:
; APPLICANT: WYLIE, DWANE E.
; APPLICANT: LOPEZ, OSVALDO
; APPLICANT: MURRAY, PETER JOSEPH
; APPLICANT: GOEBEL, PETER
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6111079west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,128
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09258
; FILING DATE: 05-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/541,373
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,798
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.49USF1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/371-5278
; TELEFAX: 612/332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-767-128-4

Query Match 79.6%; Score 43; DB 4; Length 122;
Best Local Similarity 80.0%; Pred. No. 2.1;
Matches 8; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

Qy 1 YGNY--WFAY 8
|||||
Db 102 YGNYVAFAY 111

RESULT 4
US-08-767-128-20
; Sequence 20, Application US/08767128
; Patent No. 6111079
; GENERAL INFORMATION:
; APPLICANT: WYLIE, DWANE E.
; APPLICANT: LOPEZ, OSVALDO
; APPLICANT: MURRAY, PETER JOSEPH
; APPLICANT: GOEBEL, PETER
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; NUCLEOTIDES CODING THEREFORE
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6111079west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,128
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09258
; FILING DATE: 05-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/541,373
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,798
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.49USF1
; TELEPHONE: 612/371-5278
; TELEFAX: 612/332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-767-128-20

Query Match 75.9%; Score 41; DB 4; Length 119;
Best Local Similarity 75.0%; Pred. No. 4.3;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YGNYWFAY 8
||: |||||
Db 101 YGHLWFAY 108

RESULT 5
US-08-881-037-19
; Sequence 19, Application US/08881037
; Patent No. 6080588
; GENERAL INFORMATION:
; APPLICANT: Glick, Gary D.
; APPLICANT: Swanson, Patrick C.
; TITLE OF INVENTION: DNA BINDING ANTIBODIES
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/881,037
; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,540
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Konski, Antoinette F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: 203442110710
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-881-037-19

Query Match 69.4%; Score 37.5; DB 3; Length 116;
Best Local Similarity 77.8%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 YGNY-WFAY 8
||: |||||
Db 97 YSNYPWFAY 105

RESULT 6
US-08-448-489-19
; Sequence 19, Application US/08448489
; Patent No. 6184022
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/08/448,489
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 231
; TYPE: PRT

; ORGANISM: Unknown
 ; FEATURE:
 ; OTHER INFORMATION: Description of Unknown Organism: Known Member of
 ; OTHER INFORMATION: Matrix Metalloproteinase Family
 US-08-448-489-19

Query Match 68.5%; Score 37; DB 4; Length 231;
 Best Local Similarity 62.5%; Pred. No. 36;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGNWFWAY 8
 :|||||
 Db 190 FGNYWGGY 197

RESULT 7
 US-08-696-944-20
 ; Sequence 20, Application US/08696944
 ; Patent No. 5981831
 ; GENERAL INFORMATION:
 ; APPLICANT: Sumant CHENGAPPA
 ; APPLICANT: Susan A. HELLYER
 ; APPLICANT: John S. REID
 ; APPLICANT: Jacqueline DE SILVA
 ; TITLE OF INVENTION: No. 5981831el Exo-(1-4)-Beta-D Galactanase
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
 ; STREET: 1100 New York Avenue, N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: MS Word
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/696,944
 ; FILING DATE: 23-AUG-1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/GB95/00372
 ; FILING DATE: 23-FEB-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 9403423.8
 ; FILING DATE: 23-FEB-1994
 ; INFORMATION FOR SEQ ID NO: 20:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 731 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-696-944-20

Query Match 68.5%; Score 37; DB 2; Length 731;
 Best Local Similarity 62.5%; Pred. No. 1.le-02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGNWFWAY 8
 :||| |:
 Db 28 YGNVWYDY 35

RESULT 8
 US-08-458-516-10
 ; Sequence 10, Application US/08458516
 ; Patent No. 5777085
 ; GENERAL INFORMATION:
 ; APPLICANT: Co, Man Sung
 ; APPLICANT: Tso, J. Yun

; TITLE OF INVENTION: Humanized Antibodies Reactive with
 ; TITLE OF INVENTION: GPIIB/IIIA
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: William M. Smith
 ; STREET: One Market Plaza, Steuart Tower, Suite 2000
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94105
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/458,516
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/059,159
 ; FILING DATE: 03-MAY-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith, William M.
 ; REGISTRATION NUMBER: 30,223
 ; REFERENCE/DOCKET NUMBER: 11823-37-3
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-326-2400
 ; TELEFAX: 415-326-2422
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 119 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FRAGMENT TYPE: N-terminal fragment
 US-08-458-516-10

Query Match 67.6%; Score 36.5; DB 1; Length 119;
 Best Local Similarity 87.5%; Pred. No. 23;
 Matches 7; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 GNY-WFAY 8
 :||| ||||
 Db 101 GNYGWFWAY 108

RESULT 9
 US-08-458-516-11
 ; Sequence 11, Application US/08458516
 ; Patent No. 5777085
 ; GENERAL INFORMATION:
 ; APPLICANT: Co, Man Sung
 ; APPLICANT: Tso, J. Yun
 ; TITLE OF INVENTION: Humanized Antibodies Reactive with
 ; TITLE OF INVENTION: GPIIB/IIIA
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: William M. Smith
 ; STREET: One Market Plaza, Steuart Tower, Suite 2000
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94105
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/458,516
 ; FILING DATE:

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/059,159
FILING DATE: 03-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-37-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: N-terminal fragment
US-08-458-516-11

Query Match 67.6%; Score 36.5; DB 1; Length 119;
Best Local Similarity 87.5%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 GNY-WFAY 8
111 1111
Db 101 GNYGWFAF 108

RESULT 10
US-08-458-516-7
Sequence 7, Application US/08458516
Patent No. 5777085
GENERAL INFORMATION:
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: Humanized Antibodies Reactive with
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/059,159
FILING DATE: 03-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-37-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-458-516-7

Query Match 67.6%; Score 36.5; DB 1; Length 138;
Best Local Similarity 87.5%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 2 GNY-WFAY 8
111 1111
Db 120 GNYGWFAF 127

RESULT 11
US-08-458-516-22
Sequence 22, Application US/08458516
Patent No. 5777085
GENERAL INFORMATION:
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: Humanized Antibodies Reactive with
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/059,159
FILING DATE: 03-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-37-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-458-516-22

Query Match 67.6%; Score 36.5; DB 1; Length 222;
Best Local Similarity 87.5%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 2 GNY-WFAY 8
111 1111
Db 101 GNYGWFAF 108

RESULT 12
US-08-458-516-23
Sequence 23, Application US/08458516
Patent No. 5777085
GENERAL INFORMATION:
APPLICANT: Tso, J. Yun

;; TITLE OF INVENTION: Humanized Antibodies Reactive with
;; TITLE OF INVENTION: GPIIB/IIIA
;; NUMBER OF SEQUENCES: 23
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: William M. Smith
;; STREET: One Market Plaza, Steuart Tower, Suite 2000
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94105
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/458,516
;; FILING DATE:
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/059,159
;; FILING DATE: 03-MAY-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, William M.
;; REGISTRATION NUMBER: 30,223
;; REFERENCE/DOCKET NUMBER: 11823-37-3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-326-2400
;; TELEFAX: 415-326-2422
;; INFORMATION FOR SEQ ID NO: 23:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 235 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-458-516-23

Query Match 67.6%; Score 36.5; DB 1; Length 235;
Best Local Similarity 87.5%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 2 GNY-WFAY 8
||| ||||
Db 101 GNYGWFFAY 108

RESULT 13
US-08-458-516-13
; Sequence 13, Application US/08458516
; Patent No. 5777085
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIB/IIIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:

;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/059,159
;; FILING DATE: 03-MAY-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, William M.
;; REGISTRATION NUMBER: 30,223
;; REFERENCE/DOCKET NUMBER: 11823-37-3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-326-2400
;; TELEFAX: 415-326-2422
;; INFORMATION FOR SEQ ID NO: 13:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 449 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-458-516-13

Query Match 67.6%; Score 36.5; DB 1; Length 449;
Best Local Similarity 87.5%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 2 GNY-WFAY 8
||| ||||
Db 101 GNYGWFFAY 108

RESULT 14
US-08-991-531-1
; Sequence 1, Application US/08991531
; Patent No. 5925554
; GENERAL INFORMATION:
; APPLICANT: Pedersen, Anders Hjelholt
; APPLICANT: Svendsen, Allan
; APPLICANT: Schneider, Palle
; APPLICANT: Rasmussen, Grethe
; APPLICANT: Cherry, Joel
; TITLE OF INVENTION: Myceliophthora And Scytalidium Laccase
; TITLE OF INVENTION: Variants
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 59255540 No. 5925554disk of No. 5925554th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/991,531
; FILING DATE: 16-DEC-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rozek, Carol
; REGISTRATION NUMBER: 36,993
; REFERENCE/DOCKET NUMBER: 5125.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 573 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

Fri Jun 29 08:05:23 2001

us-09-724-406-8.ra

US-08-991-531-1

Query Match 66.7%; Score 36; DB 2; Length 573;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GNYWF 6
|||||
Db 284 GNYWF 288

RESULT 15

US-09-032-315-10
; Sequence 10, Application US/09032315
; Patent No. 5985818
; GENERAL INFORMATION:
; APPLICANT: Svendsen; Allan
; APPLICANT: Xu, Feng
; TITLE OF INVENTION: LACCASE MUTANTS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5985818o No. 5985818disk of No. 5985818th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,315
; FILING DATE: 27-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Rozek, Carol
; REGISTRATION NUMBER: 36,993
; REFERENCE/DOCKET NUMBER: 5200.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 573 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-032-315-10

Query Match 66.7%; Score 36; DB 2; Length 573;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GNYWF 6
|||||
Db 284 GNYWF 288

Search completed: June 28, 2001, 16:01:13
Job time: 521 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2001, 15:58:42 ; Search time 234.85 Seconds
(without alignments)
2.595 Million cell updates/sec

Title: US-09-724-406-8
Perfect score: 54
Sequence: 1 YGNWFWAY 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_68:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	88.9	142	2 C34903	Ig heavy chain pre
2	46	85.2	137	2 E29380	Ig heavy chain pre
3	43	79.6	528	2 S24344	glucose transport
4	40	74.1	112	2 S26327	Ig heavy chain v r
5	40	74.1	115	2 S13694	Ig heavy chain v r
6	40	74.1	116	2 S13691	Ig heavy chain v r
7	40	74.1	137	2 S03326	Ig heavy chain pre
8	39	72.2	115	2 B25387	hypothetical prote
9	39	72.2	117	2 S01822	Ig heavy chain v-D
10	39	72.2	520	2 T18124	probable capsid pr
11	38	70.4	109	2 PL0233	Ig heavy chain v r
12	38	70.4	112	2 PL0232	Ig heavy chain v r
13	38	70.4	151	2 I80310	sepo protein - Esc
14	38	70.4	246	2 B86047	hypothetical prote
15	38	70.4	251	2 T28166	hypothetical prote
16	38	70.4	398	2 B71193	hypothetical prote
17	38	70.4	491	1 ISECKR	ketol-acid reducto
18	38	70.4	491	2 E86063	ketol-acid reducto
19	38	70.4	552	2 T39121	amino-acid permeas
20	38	70.4	732	2 B49002	hypothetical prote
21	38	70.4	790	2 T47959	hypothetical prote
22	37	68.5	108	2 C65013	hypothetical prote
23	37	68.5	108	2 H85881	hypothetical prote
24	37	68.5	118	2 S18316	ribulose-bisphosph
25	37	68.5	137	2 S24267	Ig heavy chain v r
26	37	68.5	140	2 S09216	Ig heavy chain pre
27	37	68.5	247	2 S23474	rod-core linker po
28	37	68.5	247	2 JS0593	rod-core linker po
29	37	68.5	353	1 S56750	single stranded D

30 37 68.5 467 2 S38535 cytochrome P450 76
31 37 68.5 638 2 JC2139 phenylethylamine o
32 37 68.5 684 2 A56102 amine oxidase (cop
33 37 68.5 731 2 S16595 gene CARSR12 prote
34 36.5 67.6 382 2 T45851 hypothetical prote
35 36 66.7 128 2 PH0094 Ig heavy chain v r
36 36 66.7 128 2 PH0095 Ig kappa chain v r
37 36 66.7 225 2 T24226 hypothetical prote
38 36 66.7 279 2 H84361 proline dehydrogen
39 36 66.7 361 1 F69254 probable hexosyltr
40 36 66.7 400 1 F69142 probable hexosyltr
41 36 66.7 616 2 S50998 transporter protei
42 36 66.7 619 1 KSNCLT laccase (EC 1.10.3
43 36 66.7 619 1 KSNCLT laccase (EC 1.10.3
44 36 66.7 621 2 S72493 laccase (EC 1.10.3
45 36 66.7 972 1 URBOAP peptidylglycine mo

ALIGNMENTS

RESULT 1

C34903

Ig heavy chain precursor V region (5-27) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 16-Aug-1996

C:Accession: C34903

R:Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.

J. Biol. Chem. 265, 133-138, 1990

A:Title: Active site structure and antigen binding properties of idiotypically cross-

A:Reference number: A34903; MUID:90094387

A:Accession: C34903

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-142 <BED>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-119/Domain: immunoglobulin homology <IMM>

Query Match 88.9%; Score 48; DB 2; Length 142;
Best Local Similarity 87.5%; Pred. No. 0.35;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNWFWAY 8

DB 124 YGGYWFAY 131

RESULT 2

E29380

Ig heavy chain precursor V region (AC-1001) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 23-Jul-1999

C:Accession: E29380

R:Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.

J. Biol. Chem. 262, 13579-13583, 1987

A:Title: Nucleotide and translated amino acid sequences of cDNA coding for the variab

A:Reference number: A92612; MUID:88007582

A:Accession: E29380

A:Molecule type: mRNA

A:Residues: 1-137 <CEE>

A:Cross-references: GB:M17164; GB:J02815; NID:g195411; PIDN:AAA38295.1; PID:g195412

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 85.2%; Score 46; DB 2; Length 137;
Best Local Similarity 87.5%; Pred. No. 0.73;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNWFWAY 8

Db 119 YGNLWFPAY 126
|||||

RESULT 3

S24344
glucose transport protein Glut7 - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 04-Sep-1998
C:Accession: S24344
R:Waddell, I.D.; Zomerschoe, A.G.; Voice, M.W.; Burchell, A.
Biochem. J. 286, 173-177, 1992
A:Title: Cloning and expression of a hepatic microsomal glucose transport protein. Comp
A:Reference number: S24344; MUID:92392274
A:Accession: S24344
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-528 <WAD>
C:Cross-references: EMBL:X66031; NID:g56266; PID:g56267
C:Superfamily: glucose transport protein
C:Keywords: transmembrane protein

Query Match 79.6%; Score 43; DB 2; Length 528;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGNWYF 6
|||||

Db 475 YGNWYF 480

RESULT 4

S26327
Ig heavy chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000
C:Accession: S26327
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protein e
A:Reference number: S26309; MUID:91341421
A:Accession: S26327
A:Molecule type: mRNA
A:Residues: 1-112 <STA>
C:Cross-references: EMBL:X59192
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:9-91/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 40; DB 2; Length 112;
Best Local Similarity 83.3%; Pred. No. 5.9;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGNWYF 6
|||||

Db 93 YGNWYF 98

RESULT 5

S13694
Ig heavy chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S13694
R:Pennell, C.A.; Mercollino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H.
Eur. J. Immunol. 19, 1289-1295, 1989
A:Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to cl
A:Reference number: S13685; MUID:89338557
A:Accession: S13694
A:Molecule type: mRNA
A:Residues: 1-115 <PEN>

A:Cross-references: EMBL:X53347; NID:g55240; PIDN:CAA37433.1; PID:g930210
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 40; DB 2; Length 115;
Best Local Similarity 83.3%; Pred. No. 6.1;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGNWYF 6
|||||

Db 99 YGNWYF 104

RESULT 6

S13691
Ig heavy chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S13691
R:Pennell, C.A.; Mercollino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.
Eur. J. Immunol. 19, 1289-1295, 1989
A:Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to
A:Reference number: S13685; MUID:89338557
A:Accession: S13691
A:Molecule type: mRNA
A:Residues: 1-116 <PEN>
C:Cross-references: EMBL:X53344; NID:g55235; PIDN:CAA37430.1; PID:g930207
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 40; DB 2; Length 116;
Best Local Similarity 83.3%; Pred. No. 6.1;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGNWYF 6
|||||

Db 99 YGNWYF 104

RESULT 7

S03326
Ig heavy chain precursor V-D-J region (clone pcP12) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 23-Jul-1999
C:Accession: S03326
R:Reininger, L.; Kaushik, A.; Izui, S.; Jaton, J.C.
Eur. J. Immunol. 18, 1521-1526, 1988
A:Title: A member of a new V(H) gene family encodes antibromelinated mouse red blood
A:Reference number: S03326; MUID:89052754
A:Accession: S03326
A:Molecule type: mRNA
A:Residues: 1-137 <REI>

A:Cross-references: EMBL:Y00743; NID:g52483; PIDN:CAA68712.1; PID:g52484
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-117/Product: Ig heavy chain V region pcP12 #status predicted <WAT>
F:34-117/Domain: immunoglobulin homology <IMM>
F:118-120/Domain: D region #status predicted <DRE>
F:121-137/Domain: J region #status predicted <JRE>

Query Match 74.1%; Score 40; DB 2; Length 137;
Best Local Similarity 83.3%; Pred. No. 7.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGNWYF 6
|||||

Db 118 YGNWYF 123

RESULT 8

B25387

hypothetical protein 2 - phage T5

C:Species: phage T5

A:Note: host Escherichia coli

C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 24-Nov-1999

C:Accession: B25387

R:Shiyapnikov, M.G.; Ksenzenko, V.N.; Kryukov, V.M.; Bayev, A.A.

Eur. J. Biochem. 156, 285-289, 1986

A:Title: Nucleotide sequence of the bacteriophage T5 DNA fragment which contains the gene

A:Reference number: A91166; MUID:86192452

A:Accession: B25387

A:Molecule type: DNA

A:Residues: 1-115 <SHL>

A:Cross-references: GB:X03798; NID:g15472; PIDN:CAA27425.1; PID:g15474

C:Superfamily: phage T5 hypothetical protein 2

Query Match 72.2%; Score 39; DB 2; Length 115;
 Best Local Similarity 85.7%; Pred. No. 8.9;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNWFEA 7

||| |||

Db 67 YGNWFEA 73

RESULT 9

S01822

Ig heavy chain V-D-J region (hybridoma 10B10S) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000

C:Accession: S01822

R:Forster, I.; Gu, H.; Rajewsky, K.

EMBO J. 7, 3693-3703, 1988

A:Title: Germ-line antibody V regions as determinants of clonal persistence and malignant

A:Reference number: S01822; MUID:89091115

A:Accession: S01822

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-117 <FOE>

A:Cross-references: EMBL:X12388; NID:g51924; PIDN:CAA30945.1; PID:g930158

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:11-94/Domain: immunoglobulin homology <IMM>

Query Match 72.2%; Score 39; DB 2; Length 117;
 Best Local Similarity 75.0%; Pred. No. 9;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNWFEA 8

||| |||

Db 99 YGNWFEA 106

RESULT 10

T18124

probable capsid protein A622L - Chlorella virus PBCV-1

C:Species: Chlorella virus PBCV-1

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T18124

R:Graves, M.V.; Van Etten, J.L.

submitted to the EMBL Data Library, May 1999

A:Reference number: Z18806

A:Accession: T18124

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-520 <GRA>

A:Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAC96953.1

A:Experimental source: specific host Chlorella strain NC64A

C:Genetics:

A:Note: A622L

C:Keywords: coat protein

Query Match 72.2%; Score 39; DB 2; Length 520;
 Best Local Similarity 62.5%; Pred. No. 38;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGNWFEA 8

||| |||

Db 107 YNNYWWTY 114

RESULT 11

P10233

Ig heavy chain V region (anti-DNA, DP11VH) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996

C:Accession: P10233

R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein

J. Exp. Med. 171, 265-297, 1990

A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat

A:Reference number: P10231; MUID:90111618

A:Accession: P10233

A:Molecule type: mRNA

A:Residues: 1-109 <SHL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:1-30/Region: framework 1

F:15-98/Domain: immunoglobulin homology <IMM>

F:31-35/Region: complementarity-determining 1

F:36-49/Region: framework 2

F:50-66/Region: complementarity-determining 2

F:67-96/Region: framework 3

F:97-104/Region: complementarity-determining 3

F:105-109/Region: framework 4

Query Match 70.4%; Score 38; DB 2; Length 109;
 Best Local Similarity 85.7%; Pred. No. 12;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GNVWFAY 8

||| |||

Db 98 GNVWFAY 104

RESULT 12

P10232

Ig heavy chain V region (anti-DNA, DP7VH) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996

C:Accession: P10232

R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein

J. Exp. Med. 171, 265-297, 1990

A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat

A:Reference number: P10231; MUID:90111618

A:Accession: P10232

A:Molecule type: mRNA

A:Residues: 1-112 <SHL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:1-30/Region: framework 1

F:15-98/Domain: immunoglobulin homology <IMM>

F:31-35/Region: complementarity-determining 1

F:36-49/Region: framework 2

F:50-66/Region: complementarity-determining 2

F:67-96/Region: framework 3

F:97-104/Region: complementarity-determining 3

F:105-112/Region: framework 4

Query Match 70.4%; Score 38; DB 2; Length 112;
 Best Local Similarity 85.7%; Pred. No. 13;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GNYWFAY 8
 || ||||
 Db 98 GNRWFAY 104

RESULT 13
 I80310
 sepD protein - Escherichia coli
 C:Species: Escherichia coli
 C>Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 08-Oct-1999
 C:Accession: I80310; S57615
 R:Jarvis, K.G.; Giron, J.A.; Jerse, A.E.; McDaniel, T.K.; Donnenberg, M.S.; Kaper, J.B.
 Proc. Natl. Acad. Sci. U.S.A. 92, 7996-8000, 1995
 A:Title: Enteropathogenic Escherichia coli contains a putative type III secretion system
 A:Reference number: I59412; MUID:95372406
 A:Accession: I80310
 A>Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-151 <RES>
 A:Cross-references: EMBL:Z49972; NID:g886475; PIDN:CAA90273.1; PID:g886476
 C:Genetics:
 A:Gene: sepD
 C:Superfamily: Escherichia coli sepD protein

Query Match 70.4%; Score 38; DB 2; Length 151;
 Best Local Similarity 62.5%; Pred. No. 17;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGNYWFAY 8
 :||| |
 Db 45 FGNYWVLY 52

RESULT 14
 B86047
 hypothetical protein Z5125 [imported] - Escherichia coli (strain O157:H7)
 C:Species: Escherichia coli
 C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
 C:Accession: B86047
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: B86047
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-151 <STO>
 A:Cross-references: GB:AE005174; NID:g12518465; PIDN:AAG58938.1; GSPDB:GN00145; UWGP:Z51
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: Z5125
 C:Superfamily: Escherichia coli sepD protein

Query Match 70.4%; Score 38; DB 2; Length 151;
 Best Local Similarity 62.5%; Pred. No. 17;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGNYWFAY 8
 :||| |
 Db 45 FGNYWVLY 52

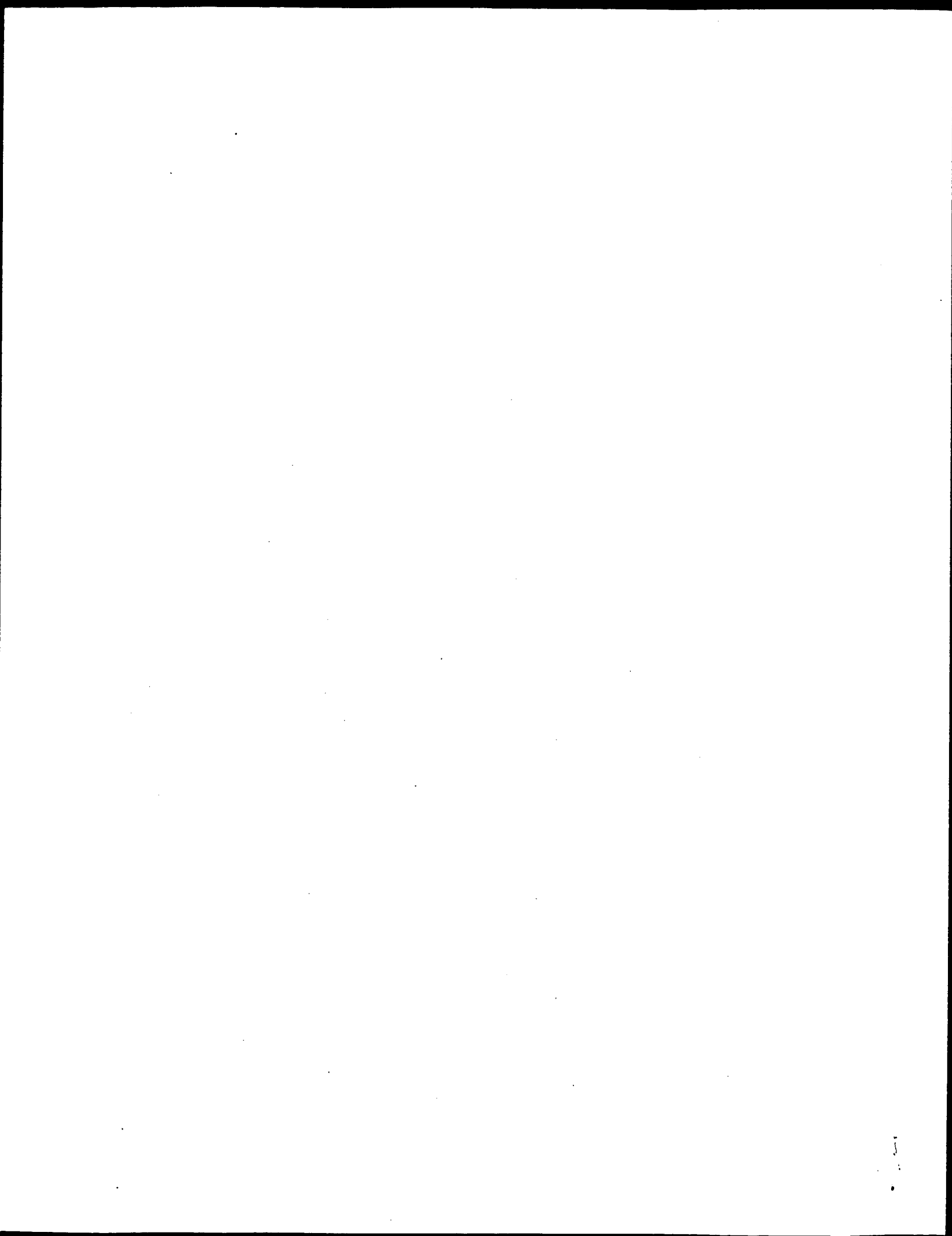
RESULT 15
 T28166
 hypothetical protein ORF5 - Melanoplus sanguinipes entomopoxvirus (isolate Tuscon)
 C:Species: Melanoplus sanguinipes entomopoxvirus

A:Variety: isolate Tuscon
 C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
 C:Accession: T28166
 R:Afonso, C.D.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.
 J. Virol. 73, 533-552, 1999
 A:Title: The genome of Melanoplus sanguinipes entomopoxvirus.
 A:Reference number: Z20484; MUID:99102612
 A:Accession: T28166
 A>Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-246 <AFO>
 A:Cross-references: EMBL:AF053866; NID:g4049647; PIDN:AAC97860.1; PID:g4049900
 A:Experimental source: isolate Tuscon
 C:Genetics:
 A:Note: MSV005

Query Match 70.4%; Score 38; DB 2; Length 246;
 Best Local Similarity 62.5%; Pred. No. 27;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGNYWFAY 8
 || || |
 Db 230 YGYWYIY 237

Search completed: June 28, 2001, 15:58:43
 Job time: 371 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2001, 15:54:34 ; Search time 105.36 Seconds
(without alignments)
2.601 Million cell updates/sec

Title: US-09-724-406-8
Perfect score: 54
Sequence: 1 YGNYWEAY 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	38	70.4	490	1 ILVC_ECOLI	P05793 escherichia
2	37	68.5	108	1 YPEC_ECOLI	P76527 escherichia
3	37	68.5	118	1 RBS2_THIFE	Q07088 thiobacilli
4	37	68.5	234	1 A29B_DROME	O46197 drosophila
5	37	68.5	234	1 A29B_DROSI	Q9u568 drosophila
6	37	68.5	246	1 PYG2_ANASP	P29987 anabaena sp
7	37	68.5	247	1 PYG2_NASLA	P29732 mastigoclad
8	37	68.5	457	1 C761_SOLME	P37121 solanum mel
9	37	68.5	638	1 PAOX_ARTGO	P46881 arthrobacte
10	37	68.5	683	1 AMOH_ARTGO	Q59118 arthrobacte
11	37	68.5	731	1 BGAL_DIACA	Q00662 dianthus ca
12	36	66.7	619	1 LACL_NEUCR	P06811 neurospora
13	36	66.7	619	1 LACL_NEUCR	P10574 neurospora
14	36	66.7	621	1 LAC2_PODAN	P78722 podospora a
15	36	66.7	972	1 AMD_BOVIN	P10731 bos taurus
16	35	64.8	123	1 HV24_MOUSE	P01793 mus musculu
17	35	64.8	214	1 YQGE_BACST	P28754 bacillus st
18	35	64.8	387	1 O94A_DROME	Q9vc59 drosophila
19	35	64.8	430	1 YQGE_BACSU	P54487 bacillus su
20	35	64.8	436	1 CYB_RHOCA	P08502 rhodobacter
21	35	64.8	440	1 CYB_PARDE	P05418 paracoccus
22	35	64.8	444	1 CYB_RHOSH	Q02761 rhodobacter
23	35	64.8	658	1 GUN3_FIBSU	P14250 fibrobacter
24	35	64.8	1500	1 SSP5_STRGN	P16552 streptococc
25	34	63.0	260	1 ERS1_YEAST	P17261 saccharomyc
26	34	63.0	346	1 GP41_HUMAN	O14843 homo sapien
27	34	63.0	346	1 GP42_HUMAN	O15529 homo sapien
28	34	63.0	459	1 MCRB_ECOLI	P15005 escherichia
29	34	63.0	599	1 VG9_BPPH2	P04331 bacterioph
30	34	63.0	599	1 VG9_BPPZA	P07534 bacterioph
31	34	63.0	837	1 YP84_CAEEL	Q09225 caenorhabd
32	34	63.0	903	1 DPOL_BPR69	Q38087 bacterioph
33	33	61.1	108	1 VMEM_PVSP	P16651 potato viru

RESULT 1

ID	ILVC_ECOLI	STANDARD;	PRT;	490 AA.
AC	P05793;			
DT	01-NOV-1988 (Rel. 09, Created)			
DT	01-FEB-1995 (Rel. 31, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	KETOL-ACID REDUCTOISOMERASE (EC 1.1.1.86) (ACETOHYDROXY-ACID ISOMEROREDUCTASE) (ALPHA-KETO-BETA-HYDROXYLACIL REDUCTOISOMERASE).			
DE	ILVC.			
GN	Escherichia coli.			
OS	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;			
OC	Escherichia.			
OX	NCBI_TaxID=562;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=K12 / MG.855;			
RX	MEDLINE=92358234; PubMed=1379743;			
RA	Daniels D.L., Plunkett G. III, Burland V.D., Blattner F.R.;			
RT	"Analysis of the Escherichia coli genome: DNA sequence of the region from 84.5 to 86.5 minutes.";			
RT	Science 257:771-778(1992).			
RL	[2]			
RN	SEQUENCE FROM N.A.			
RP	STRAIN=K12;			
RC	MEDLINE=86111952; PubMed=3003115;			
RX	Wek R.C., Hatfield G.W.;			
RA	"Nucleotide sequence and in vivo expression of the ilvX and ilvC genes in Escherichia coli K12. Transcription from divergent overlapping promoters.";			
RT	J. Biol. Chem. 261:2441-2450(1986).			
RL	[3]			
RN	SEQUENCE OF 1-12.			
RP	STRAIN=K12 / BMG2;			
RC	MEDLINE=97443975; PubMed=9298646;			
RX	Link A.J., Robison K., Church G.M.;			
RA	"Comparing the predicted and observed properties of proteins encoded in the genome of Escherichia coli K-12.";			
RT	Electrophoresis 18:1259-1313(1997).			
RL	[4]			
CC	-1- CATALYTIC ACTIVITY: (R)-2,3-DIHYDROXY-3-METHYLBUTANOATE + NADP(+) = (S)-2-HYDROXY-2-METHYL-3-OXOBUTANOATE + NADPH.			
CC	-1- PATHWAY: SECOND STEP IN VALINE AND ISOLEUCINE BIOSYNTHESIS.			
CC	-1- INDUCTION: IN THE PRESENCE OF ACETOHYDROXYBUTYRATE & ACETOLACTATE, THE SUBSTRATES OF KETOL-ACID REDUCTOISOMERASE.			
CC	-1- SIMILARITY: BELONGS TO THE KETOL-ACID REDUCTOISOMERASE FAMILY.			
CC	-----			
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CC	-----			
DR	EMBL; M87049; AAC67577.1; -.			
DR	EMBL; AE000454; AAC76779.1; -.			

P08732 escherichia
O50165 borrelia bu
P40218 saccharomyc
Q95008 caenorhabd
O34504 bacillus su
Q95000 brachioosto
O88895 mus musculu
P56520 gallus galli
O15379 homo sapien
Q9hy11 pseudomonas
P19843 pseudomonas
P20584 aspergillus

DR EMBL; M11689; AAA24029.1; -.
 DR PIR; A26287; ISECKR.
 DR PIR; S30672; S30672.
 DR SWISS-2DPAGE; P05793; COLI.
 DR EcoGene; EG10495; IIVC.
 DR InterPro; IPR000506; -.
 DR Pfam; PF01450; IIVC; 1.
 KW Oxidoreductase; Branched-chain amino acid biosynthesis; NADP.
 FT INIT_MET 0
 FT ACT_SITE 131 131 POTENTIAL.
 FT CONFLICT 250 250 E->K (IN REF. 2).
 SQ SEQUENCE 490 AA; 53938 MW; 4587C397031B13A5 CRC64;

Query Match 70.4%; Score 38; DB 1; Length 490;
 Best Local Similarity 75.0%; Pred. No. 31;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YGNWYFAY 8
 |||||
 Db 418 YGNVLFYS 425

RESULT 2
 YPEC_ECOLI
 ID YPEC_ECOLI STANDARD; PRT; 108 AA.
 AC P76527;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE HYPOTHETICAL 13.3 KDA PROTEIN IN GLK-NUPC INTERGENIC REGION PRECURSOR.
 GN YPEC.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]

SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RA MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glaesner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 CC -1- SIMILARITY: TO E.COLI YAAK.

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 DR EMBL; AE000327; AAC75449.1; -.
 DR EcoGene; EG14385; YPEC.
 KW Hypothetical protein; Signal.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 108 HYPOTHETICAL PROTEIN YPEC.
 SQ SEQUENCE 108 AA; 13263 MW; 77418AE4140139B4 CRC64;

Query Match 68.5%; Score 37; DB 1; Length 108;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGNWY 5
 |||||
 Db 40 YGNWY 44

RESULT 3
 RBS2_THIFE
 ID RES2_THIFE STANDARD; PRT; 118 AA.
 AC Q07088;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2 (EC 4.1.1.39) (RUBISCO
 DE SMALL SUBUNIT 2).
 DE GN CBB52 OR RECS2.
 OS Thiobacillus ferrooxidans.
 OC Bacteria; Proteobacteria; gamma subdivision; Acidithiobacillus.
 OX NCBI_TaxID=920;
 RN [1]

SEQUENCE FROM N.A.
 RP MEDLINE=92070528; PubMed=1959634;
 RX Pulgar V., Gaete L., Allende J., Orellana O., Jordana X.,
 RA Jedlicki E.;
 RT "Isolation and nucleotide sequence of the Thiobacillus ferrooxidans
 RT genes for the small and large subunits of ribulose 1,5-bisphosphate
 RT carboxylase/oxygenase.";
 RL FEBS Lett. 292:85-89(1991).

CC -1- FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF
 CC D-RIBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC
 CC CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION OF
 CC THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH
 CC REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME
 CC ACTIVE SITE.

CC -1- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2) =
 CC 2 3-PHOSPHO-D-GLYCERATE.
 CC -1- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + O(2) =
 CC 3-PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCOLATE.

CC -1- SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS.
 CC -1- SIMILARITY: BELONGS TO THE RUBISCO SMALL CHAIN FAMILY.

CC -1- CAUTION: IN T.FERROXIDANS TWO SIMILAR SET OF GENES CODE FOR
 CC RUBISCO LARGE AND SMALL CHAINS: THE RBCL1-RBCS1 AND THE RBCL2-
 CC RBCS2 SETS.

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 DR EMBL; X70355; CAA49815.1; -.
 DR HSP; P00870; IAU5.
 DR InterPro; IPR0000894; -.
 DR Pfam; PF00101; Rubisco_small; 1.
 KW Carbon dioxide fixation; Photorespiration; Lyase; Oxidoreductase;
 KW Monooxygenase; Calvin cycle; Multigene family.
 SQ SEQUENCE 118 AA; 13627 MW; 1B063498DECA6DD3 CRC64;

Query Match 68.5%; Score 37; DB 1; Length 118;
 Best Local Similarity 50.0%; Pred. No. 12;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YGNWYFAY 8
 :||||:
 Db 58 FGNYWYMW 65

RESULT 4
 A29B_DROME
 ID A29B_DROME STANDARD; PRT; 234 AA.
 AC A46197; Q9TVT3; Q9TW06; Q9TW07; Q9U976; Q9U977; Q9U978;
 AC Q9U979; Q9V3Q5;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE ACCESSORY GLAND PROTEIN ACP29AB PRECURSOR.


```

DR FlyBase; FBgn0015583; Acp29AB.
DR InterPro; IPR001304; -.
DR Pfam; PF00059; lectin_c.1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
KW Behavior; Signal; Polymorphism.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 234 ACCESSORY GLAND PROTEIN ACP29AB.
FT DOMAIN 137 228 C-TYPE LECTIN (LONG FORM).
FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 29 29 K -> R (IN STRAINS LA1, LA3, LA4, LA5,
FT VARIANT 59 59 K -> R (IN STRAINS LA1, LA3, LA4, LA5,
FT LA14, LA15, LA16, LA21, LA25, LA34, LA35,
FT M01B, M052B, M080B, MA5, MA8, MA13, MA18,
FT MA20, MA21, MA45, MA48, MA52, MA67,
FT ZIM26, ZIM29, ZIM30, ZIM56, WS6 AND
FT WS19).
FT VARIANT 105 105 A -> S (IN STRAINS LA16 AND LA35).
FT VARIANT 113 113 R -> L (IN STRAINS LA14, LA14, LA16,
FT LA35, M02B, M015B, M034A, M036A, M037A,
FT M047A, M052B, M058B, M080B, MA5, MA7,
FT MA13, MA18, MA20, MA21, MA45, MA48, MA50,
FT MA52, MA67, WS1, WS6, WS9, WS12, WS16,
FT WS26, WS47, WS56, ZIM2, ZIM26, ZIM29,
FT ZIM30, ZIM32, ZIM37, ZIM42 AND ZIM56).
FT K -> M (IN STRAINS BERKELEY, LA13, LA14,
FT LA15, LA16, M01B, M08B, M040B, M052B,
FT MA5, MA21, MA45, MA52, MA67, ZIM29,
FT ZIM30, ZIM42 AND ZIM56).
FT E -> D (IN STRAIN MA7).
SQ SEQUENCE 234 AA; 27173 MW; 8954CD3215480F3E CRC64;

Query Match 68.5%; Score 37; DB 1; Length 234;
Best Local Similarity 83.3%; Pred. No. 23;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 NYWEAY 8
| | | | |
DB 50 NYWFTY 55

RESULT 5
A29B_DROSI STANDARD; PRT; 234 AA.
AC Q9U968;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DE ACCESSORY GLAND PROTEIN ACP29AB PRECURSOR.
GN ACP29AB.
OS Drosophila simulans (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7240;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=59; PubMed=10353898;
RX MEDLINE=99282496; PubMed=10353898;
RA Aguade M.;
RT "Positive selection drives the evolution of the Acp29AB accessory
RL gland protein in Drosophila.";
RL Genetics 152:543-551(1999).
CC -!- FUNCTION: RESPONSIBLE FOR PHYSIOLOGICAL AND BEHAVIORAL CHANGES IN
CC MATED FEMALE FLIES.
CC -!- SUBCELLULAR LOCATION: SECRETED (PROBABLE).
CC -!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC
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DR EMBL; M80435; AAA22037.1; -.
DR PIR; JS0593; JS0593.

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CC EMBL; AJ240552; CAB53227.1; -.
CC FlyBase; FBgn007777; Dsim\Acp29AB.
CC InterPro; IPR001304; -.
CC Pfam; PF00059; lectin_c.1.
CC PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
CC PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
KW Behavior; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 234 ACCESSORY GLAND PROTEIN ACP29AB.
FT DOMAIN 137 228 C-TYPE LECTIN (LONG FORM).
FT CARBOHYD 29 29 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 234 AA; 26915 MW; EB9C556E02EFED98 CRC64;

Query Match 68.5%; Score 37; DB 1; Length 234;
Best Local Similarity 83.3%; Pred. No. 23;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 NYWEAY 8
| | | | |
DB 50 NYWFTY 55

RESULT 6
PYG2_ANASP STANDARD; PRT; 246 AA.
AC P29987;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DE PHCOBILISOME ROD-CORE LINKER POLYPEPTIDE CPCG2 (L-RC 28.5).
DE PHCOBILISOME ROD-CORE LINKER POLYPEPTIDE CPCG2 (L-RC 28.5).
GN CPCG2
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-26.
RX MEDLINE=92077441; PubMed=1743523;
RA Bryant D.A., Stirewalt V.L., Glauser M., Frank G., Sidler W.,
RA Zuber H.;
RT "A small multigene family encodes the rod-core linker polypeptides of
RL Anabaena sp. PCC7120 phycobilisomes.";
RL Gene 107:91-99(1991).
CC -!- FUNCTION: ROD-CORE LINKER PROTEIN REQUIRED FOR ATTACHMENT OF
CC PHYCOCYANIN TO ALLOPHYCOCYANIN IN CORES OF PHYCOBILISOMES.
CC -!- FUNCTION: LINKER POLYPEPTIDES DETERMINE THE STATE OF AGGREGATION
CC AND THE LOCATION OF THE DISC-SHAPED PHYCOBILIPROTEIN UNITS WITHIN
CC THE PHYCOBILISOME AND MODULATE THEIR SPECTROSCOPIC PROPERTIES IN
CC ORDER TO MEDIATE A DIRECTED AND OPTIMAL ENERGY TRANSFER.
CC -!- SURUNIT: THE PHYCOBILISOME IS A HEMIDISCOIDAL STRUCTURE THAT IS
CC COMPOSED OF TWO DISTINCT SUBSTRUCTURES: A CORE COMPLEX (THAT
CC CONTAINS PHYCOBILIPROTEINS) AND A NUMBER OF RODS RADIATING FROM
CC THE CORE.
CC -!- SIMILARITY: TO OTHER PHYCOBILISOME LINKER PROTEINS.
CC
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DR EMBL; M80435; AAA22037.1; -.
DR PIR; JS0593; JS0593.

```

DR InterPro: IPR001297; -
 DR Pfam: PF00427; PBS_linker_poly; 1.
 KW Phycobilisome; Photosynthesis; Multigene family.
 FT INIT_MET 0
 SQ SEQUENCE 246 AA; 28520 MW; 19461DAD372F2DCA CRC64;

Query Match 68.5%; Score 37; DB 1; Length 246;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGNW 5
 |||||
 Db 176 YGNW 180

RESULT 7
 PYG2_MASLA STANDARD; PRT; 247 AA.
 ID PYG2_MASLA
 AC P29732;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE PHYCIBILISOME ROD-CORE LINKER POLYPEPTIDE CPCG2 (L-RC 28.7).
 GN CPCG2.
 OS Mastigocladus laminosus (Fischerella sp.).
 OC Bacteria; Cyanobacteria; Stigonematales; Fischerella.
 OX NCBI_TaxID=1191;
 RN SEQUENCE FROM N.A.
 RP STRAIN=PCC 7603;
 RC MEDLINE=92249337; PubMed=1577010;
 RA Glauser M., Stirewalt V.L., Bryant D.A., Sidler W., Zuber H.;
 RT "Structure of the genes encoding the rod-core linker polypeptides of
 RT Mastigocladus laminosus phycobilisomes and functional aspects of the
 RT phycobilliprotein/linker-polypeptide interactions.";
 RL Eur. J. Biochem. 205:927-937(1992).
 CC -1- FUNCTION: ROD-CORE LINKER PROTEIN REQUIRED FOR ATTACHMENT OF
 CC PHYCOCYANIN TO ALLOPHYCOCYANIN IN CORES OF PHYCIBILISOMES
 CC -1- FUNCTION: LINKER POLYPEPTIDES DETERMINE THE STATE OF AGGREGATION
 CC AND THE LOCATION OF THE DISC-SHAPED PHYCIBILIPROTEIN UNITS WITHIN
 CC THE PHYCIBILISOME AND MODULATE THEIR SPECTROSCOPIC PROPERTIES IN
 CC ORDER TO MEDIATE A DIRECTED AND OPTIMAL ENERGY TRANSFER.
 CC -1- SUBUNIT: THE PHYCIBILISOME IS A HEMIDISCAL STRUCTURE THAT IS
 CC COMPOSED OF TWO DISTINCT SUBSTRUCTURES: A CORE COMPLEX (THAT
 CC CONTAINS PHYCIBILIPROTEINS) AND A NUMBER OF RODS RADIATING FROM
 CC THE CORE.
 CC -1- SIMILARITY: TO OTHER PHYCIBILISOME LINKER PROTEINS.

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EMBL: X59763; CAA2434.1; -
 DR PIR: S16059; S16059.
 DR PIR: S23474; S23474.
 DR InterPro: IPR001297; -
 KW Pfam: PF00427; PBS_linker_poly; 1.
 DR Phycobilisome; Photosynthesis; Multigene family.
 SQ SEQUENCE 247 AA; 28707 MW; 5E183B4F1C2C77B8 CRC64;

Query Match 68.5%; Score 37; DB 1; Length 247;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGNW 5
 |||||
 Db 177 YGNW 181

RESULT 8
 C761_SOLME STANDARD; PRT; 467 AA.
 ID C761_SOLME
 AC P37121;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE CYTOCHROME P450 70A1 (EC 1.14.-.-) (CYPLXXVIAL) (P-450EG8) (FRAGMENT).
 GN CYP70A1 OR CYPE38.
 OS Solanum melongena (Eggplant) (Aubergine).
 OC Eukaryota; Viridiplantae; Embryophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
 OC Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4111;
 RN SEQUENCE FROM N.A.
 RP STRAIN=CV. SINSADOHARANASU; TISSUE=Hypocotyl;
 RC MEDLINE=94032483; PubMed=8218411;
 RA Toquri T., Kobayashi O., Umamoto N.;
 RT "The cloning of eggplant seedling cDNAs encoding proteins from a
 RT novel cytochrome P-450 family (CYP76).";
 RL Biochim. Biophys. Acta 1216:165-169(1993).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
 CC -----
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EMBL: X71638; CAA50649.1; -
 DR PIR: S38535; S38535.
 DR InterPro: IPR001128; -
 DR Pfam: PF00067; P450; 1.
 DR PROSITE: PS00086; CYTOCHROME_P450; 1.
 KW Oxidoreductase; Monooxygenase; Heme; Multigene family.
 FT NON_TER 1
 FT BINDING 410 410 HEME (BY SIMILARITY).
 SQ SEQUENCE 467 AA; 53287 MW; D9A9B38DB5BF2108 CRC64;

Query Match 68.5%; Score 37; DB 1; Length 467;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGNW 5
 |||||
 Db 81 YGNW 85

RESULT 9
 PAOX_ARTGO STANDARD; PRT; 638 AA.
 ID PAOX_ARTGO
 AC P46881;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE PHENYLETHYLAMINE OXIDASE PRECURSOR (EC 1.4.3.6) (AMINE OXIDASE).
 OS Arthrobacter globiformis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Micrococcales; Micrococcaceae; Arthrobacter.
 OX NCBI_TaxID=1665;
 RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RP STRAIN=IFO 12137 / ATCC 8010;
 RC MEDLINE=94197650; PubMed=8147851;
 RA Tanizawa K., Matsuzaki R., Shimizu E., Yorifuji T., Fukui T.;
 RT "Cloning and sequencing of phenylethylamine oxidase from Arthrobacter
 RT globiformis and implication of Tyr-382 as the precursor to its

RT covalently bound quinone cofactor.";
 RL Biochem. Biophys. Res. Commun. 199;1096-1102(1994).
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 9-628.
 RX MEDLINE=98070236; PubMed=9405045;
 RA Wilce M.C., Dooley D.M., Freeman H.C., Guss J.M., Matsunami H.,
 RA McIntire W.S., Ruggiero C.E., Tanizawa K., Yamaguchi H.;
 RT "Crystal structures of the copper-containing amine oxidase from
 RT Arthrobacter globiformis in the holo and apo forms: implications for
 RT the biogenesis of topaquinoxine.";
 RL Biochemistry 36:16116-16133(1997).
 CC -1- CATALYTIC ACTIVITY: RCH(2)NH(2) + H(2)O + O(2) -> RCHO + NH(3) +
 CC H(2)O(2).
 CC -1- COFACTOR: COPPER AND TOPAQUINONE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- INDUCTION: BY PHENETHYLAMINE.
 CC -1- PTM: THE TOPA QUINONE IS GENERATED BY COPPER-DEPENDENT
 CC AUTOXIDATION OF A SPECIFIC TYROSYL RESIDUE.
 CC -1- SIMILARITY: BELONGS TO THE COPPER/TOPAQUINONE OXIDASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: U03517; AAA18114.1;
 DR PDB: 1AVK; 18-MAR-98.
 DR PDB: 1AVL; 18-MAR-98.
 DR PDB: 1AV4; 25-MAR-98.
 DR InterPro: IPR000269;
 DR Pfam: PF01179; Cu_amine_oxid; 1.
 DR PROSITE: PS01164; COPPER_AMINE_OXID_1; 1.
 DR PROSITE: PS01165; COPPER_AMINE_OXID_2; 1.
 KW Oxidoreductase; Copper; TPQ; 3D-structure.
 FT PROPEP 1 2
 FT CHAIN 3 638 PHENYLETHYLAMINE OXIDASE.
 FT BINDING 382 382 TOPAQUINONE.
 FT METAL 431 431 COPPER.
 FT METAL 433 433 COPPER.
 FT METAL 592 592 COPPER.
 FT DISULFID 317 343
 FT MUTAGEN 382 382 Y->F: LOSS OF ACTIVITY.
 SQ SEQUENCE 638 AA; 70646 MW; 1800396BA7A983F2 CRC64;
 Y->F: LOSS OF ACTIVITY.
 Query Match 68.5%; Score 37; DB 1; Length 638;
 Best Local Similarity 62.5%; Pred. No. 57;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 YGNYWEAY 8
 Db 384 YGFYWLY 391
 ||| |
 RESULT 10
 ID AMOH_ARTGO STANDARD; PRT; 583 AA.
 AC Q59118;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HISTAMINE OXIDASE (EC 1.4.3.6) (COPPER AMINE OXIDASE).
 OS Arthrobacter globiformis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Micrococcales; Micrococcaceae; Arthrobacter.
 OX NCBI_TaxID=1665;
 RN [1]
 RC SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RP STRAIN-IFO 12137 / ATCC 8010;
 RX MEDLINE=9518149; PubMed=7876243;

RA Choi Y.-H., Matsuzaki R., Fukui T., Shimizu E., Yorifuji T., Sato H.,
 RA Ozaki Y., Tanizawa K.;
 RT "Copper/topa quinone-containing histamine oxidase from Arthrobacter
 RT globiformis. Molecular cloning and sequencing, overproduction of
 RT precursor enzyme, and generation of topa quinone cofactor.";
 RL J. Biol. Chem. 270:4712-4720(1995).
 CC -1- FUNCTION: OXIDIZE HISTAMINE. OTHER AMINES INCLUDING
 CC PHENETHYLAMINE, TYRAMINE, TRYPTAMINE, PUTRESCINE, AND BENZYLAMINE
 CC ALSO SERVE AS SUBSTRATE.
 CC -1- CATALYTIC ACTIVITY: RCH(2)NH(2) + H(2)O + O(2) ->
 CC RCHO + NH(3) + H(2)O(2).
 CC -1- COFACTOR: COPPER AND TOPAQUINONE.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- INDUCTION: BY HISTAMINE.
 CC -1- PTM: THE TOPA QUINONE IS GENERATED BY COPPER-DEPENDENT
 CC AUTOXIDATION OF A SPECIFIC TYROSYL RESIDUE.
 CC -1- SIMILARITY: BELONGS TO THE COPPER/TOPAQUINONE OXIDASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: D38508; BAA07517.1;
 DR HSP: P46881; 1AVL.
 DR InterPro: IPR000269;
 DR Pfam: PF01179; Cu_amine_oxid; 1.
 DR PROSITE: PS01164; COPPER_AMINE_OXID_1; 1.
 DR PROSITE: PS01165; COPPER_AMINE_OXID_2; FALSE_NEG.
 KW Oxidoreductase; Copper; TPQ.
 FT INIT_MET 0 0
 FT BINDING 401 401 TOPAQUINONE.
 FT METAL 450 450 COPPER (POTENTIAL).
 FT METAL 452 452 COPPER (POTENTIAL).
 FT METAL 611 611 COPPER (POTENTIAL).
 SQ SEQUENCE 683 AA; 74979 MW; 233C46C017201AA0 CRC64;
 Query Match 68.5%; Score 37; DB 1; Length 683;
 Best Local Similarity 62.5%; Pred. No. 60;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 YGNYWEAY 8
 Db 403 YGFYWLY 410
 ||| |
 RESULT 11
 ID BGAL_DIACA STANDARD; PRT; 731 AA.
 AC Q00662;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE PUTATIVE BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE)
 DE (SR12 PROTEIN).
 GN CARS12.
 OS Dianthus caryophyllus (Carnation) (Clove pink).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales;
 OC Caryophyllaceae; Dianthus.
 OX NCBI_TaxID=3570;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. WHITE SIM; TISSUE=Petal;
 RX MEDLINE=91329738; PubMed=1868223;
 RA Raghothama K.G., Lawton K.A., Goldsbrough P.B., Woodson W.R.;
 RT "Characterization of an ethylene-regulated flower senescence-related
 RT gene from carnation.";
 RL Plant Mol. Biol. 17:61-71(1991).

CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL, NON-REDUCING BETA-D-
CC GALACTOSE RESIDUES IN BETA-D-GALACTOSIDES.
CC -1- TISSUE SPECIFICITY: SENESCING FLOWER PETALS.
CC -1- INDUCTION: REGULATED BY THE PHYTOHORMONE ETHYLENE.
CC -1- SIMILARITY: BELONGS TO FAMILY 35 OF GLYCOSYL HYDROLASES.
CC -----
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CC -----
CC EMBL: X57171; CAA40459.1; -
CC EMBL: S16595; S16595.
CC InterPro: IPR001944; -
CC Pfam: PF01301; Glyco_hydro_35; 1.
CC PRINTS: PR00742; GLYDRLASE35.
CC PROSITE: PS01182; GLYCOSYL_HYDROL_F35; 1.
CC Hydrolase; Glycosidase; Signal.
CC KW CHATN 30 731 PUTATIVE BETA-GALACTOSIDASE.
CC FT ACT_SITE 187 187 PROTON DONOR (POTENTIAL).
CC FT ACT_SITE 257 257 NUCLEOPHILE (POTENTIAL).
CC SQ SEQUENCE 731 AA; 82864 MW; 83FA8B5A3779C051 CRC64;

Query Match 68.5%; Score 37; DB 1; Length 731;
Best Local Similarity 62.5%; Pred. No. 64;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGNWYFAY 8
||| |:
Db 28 YGNWYDY 35

RESULT 12
LAC2_NEUCR STANDARD; PRT; 619 AA.
AC P06811;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE LACCASE PRECURSOR (EC 1.10.3.2) (BENZENEDIOL-OXYGEN OXIDOREDUCTASE)
DE (URISHIOL OXIDASE) (ALLELE OR).
GN LACC.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RX MEDLINE=88087214; PubMed=2961749;
RA Hermann U.A., Mueller G., Hunziker P.E., Lerch K.;
RT "Characterization of two allelic forms of Neurospora crassa laccase.
RL Amino- and carboxyl-terminal processing of a precursor.";
RL J. Biol. Chem. 263:885-896(1988).
RN [2]
RX SEQUENCE OF 379-619 FROM N.A.
RX MEDLINE=87067412; PubMed=2947240;
RA Hermann U.A., Lerch K.;
RT "Isolation and partial nucleotide sequence of the laccase gene from
RT Neurospora crassa: amino acid sequence homology of the protein to
RT human ceruloplasmin.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:8854-8858(1986).
CC -1- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED
CC PRODUCTS (PROBABLE).
CC -1- CATALYTIC ACTIVITY: 4 BENZENEDIOL + O(2) = 4 BENZOSEMIQUINONE +
CC 2 H(2)O.
CC -1- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU
CC CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE
CC 3 OR COUPLED BINUCLEAR (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: SECRETED (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
CC -1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
CC -----
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CC -----
CC EMBL: M14554; AAA33590.1; -
CC EMBL: M18333; AAA33591.1; -
CC PIR: A28523; KSNGLQ.
CC PIR: A29762; A29762.
CC InterPro: IPR001117; -
CC Pfam: PF00394; Cu-oxidase; 2.
CC PROSITE: PS00079; MULTICOPPER_OXIDASE1; 1.
CC PROSITE: PS00080; MULTICOPPER_OXIDASE2; 1.
CC Oxidoreductase; Signal; Copper; Metal-binding; Lignin degradation;
CC Glycoprotein; Repeat.
CC KW SIGNAL 1 21 POTENTIAL.
CC FT PROPEP 22 49 LACCASE.
CC FT CHAIN 50 606
CC FT PROPEP 607 619
CC FT DOMAIN 84 207
CC FT DOMAIN 216 373
CC FT DOMAIN 431 566
CC FT METAL 144 144 PLASTOCYANIN-LIKE 2.
CC FT METAL 146 146 PLASTOCYANIN-LIKE 3.
CC FT METAL 189 189 COPPER (TYPE 2) (PROBABLE).
CC FT METAL 191 191 COPPER (TYPE 3) (PROBABLE).
CC FT METAL 477 477 COPPER (TYPE 3) (PROBABLE).
CC FT METAL 480 480 COPPER (TYPE 1) (PROBABLE).
CC FT METAL 482 482 COPPER (TYPE 2) (PROBABLE).
CC FT METAL 548 548 COPPER (TYPE 3) (PROBABLE).
CC FT METAL 549 549 COPPER (TYPE 1) (PROBABLE).
CC FT METAL 550 550 COPPER (TYPE 3) (PROBABLE).
CC FT METAL 554 554 COPPER (TYPE 3) (PROBABLE).
CC FT METAL 559 559 COPPER (TYPE 1) (PROBABLE).
CC FT METAL 559 559 COPPER (TYPE 1) (PROBABLE).
CC FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 282 282 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 340 340 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 422 422 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 444 444 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SQ SEQUENCE 619 AA; 68198 MW; FDED6D78B65048E3 CRC64;

Query Match 66.7%; Score 36; DB 1; Length 619;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GNYWF 6
|||||
Db 335 GNYWF 339

RESULT 13
LAC2_NEUCR STANDARD; PRT; 619 AA.
AC P10574;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE LACCASE PRECURSOR (EC 1.10.3.2) (BENZENEDIOL-OXYGEN OXIDOREDUCTASE)
DE (URISHIOL OXIDASE) (ALLELE TS).
GN LACC.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.

```

OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88087214; PubMed=2961749;
RA Germann U.A., Mueller G., Hunziker P.E., Lerch K.;
RT "Characterization of two allelic forms of Neurospora crassa laccase.
RT Amino- and carboxyl-terminal processing of a precursor.";
RL J. Biol. Chem. 263:885-896(1988).
CC -!- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED
CC PRODUCTS (PROBABLE).
CC -!- CATALYTIC ACTIVITY: 4 BENZENEDIOL + O(2) = 4 BENZOSEMIQUINONE +
CC 2 H(2)O.
CC -!- COFACTOR: BINDS 4 CU-TONS PER MOLECULE. THREE DISTINCT CU
CC CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE
CC 3 OR COUPLED BINUCLEAR (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: SECRETED (POTENTIAL).
CC -!- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
CC -!- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
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CC -----
DR EMBL; M18334; AAA33592.1; -.
DR PIR; B28523; KGNCLT.
DR InterPro; IPR001117; -.
DR IntraPro; IPR002355; -.
DR Pfam; PF00394; Cu-oxidase; 2
DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.
DR PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.
DR OXidoreductase; Signal; Copper; Metal-binding; Lignin degradation;
KW Glycoprotein; Repeat.
KW SIGNAL 1 21
KW PROPEP 22 49
KW CHAIN 50 606
KW PROPEP 607 619
KW DOMAIN 84 207
KW DOMAIN 216 373
KW DOMAIN 431 566
KW METAL 144 144
KW METAL 146 146
KW METAL 189 189
KW METAL 191 191
KW METAL 477 477
KW METAL 480 480
KW METAL 548 548
KW METAL 549 549
KW METAL 550 550
KW METAL 554 554
KW METAL 559 559
KW CARBOHYD 139 139
KW CARBOHYD 282 282
KW CARBOHYD 295 295
KW CARBOHYD 340 340
KW CARBOHYD 422 422
KW CARBOHYD 444 444
KW SEQUENCE 619 AA; 68120 MW; 0B86CCDE18841145 CRC64;
SQ

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Query Match          66.7%; Score 36; DB 1; Length 619;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GNYWF 6
          | | | |
Db      335 GNYWF 339

```

RESULT 14

LAC2_PODAN	STANDARD;	PRT;	621 AA.
ID	LAC2_PODAN		
AC	P78722;		
DT	01-NOV-1997 (Rel. 35, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	01-NOV-1997 (Rel. 35, Last annotation update)		
DE	LACCASE II PRECURSOR (RC 1.10.3.2) (BENZENEDIOL:OXYGEN OXIDOREDUCTASE)		
DE	(IRISHTOL OXIDASE) (DIPHENOL OXIDASE) (LACCASE-C).		
GN	LAC2.		
OS	Podospora anserina.		
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;		
OC	Sordariales; Sordariaceae; Podospora.		
OX	NCBI_TaxID=5145;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=ATCC 26003;		
RX	MEDLINE=97071669; PubMed=8914515;		
RA	Fernandez-Larrea J., Stahl U.		
RT	"Isolation and characterization of a laccase gene from Podospora		
RT	anserina.";		
RL	Mol. Gen. Genet. 252:539-551(1996).		
CC	-I- DETECTION: PROBABLY INVOLVED IN LIGNIN DEGRADATION AND IN THE		
CC	DEFUNCTIONATION OF LIGNIN-DERIVED PRODUCTS IN ITS NATURAL HABITAT		
CC	(HERBIVOROUS DUNG), WHICH IS RICH IN LIGNIN OF GRASSES AND STRAW.		
CC	PROBABLY INVOLVED IN MELANIN SYNTHESIS AND IN PERITHECIA		
CC	DEVELOPMENT.		
CC	-I- CATALYTIC ACTIVITY: 4 BENZENEDIOL + O(2) = 4 BENZOSEMIQUINONE +		
CC	2 H(2)O.		
CC	-I- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU		
CC	CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE		
CC	3 OR COUPLED BINUCLEAR (BY SIMILARITY).		
CC	-I- SUBUNIT: MONOMER.		
CC	-I- SUBCELLULAR LOCATION: SECRETED.		
CC	-I- DEVELOPMENTAL STAGE: LOW BASIC LEVELS THROUGHOUT THE GROWTH PHASE;		
CC	INCREASES AT LEAST 20-FOLD AT THE BEGINNING OF THE AUTOLYTIC PHASE		
CC	AND DECREASES AGAIN THEREAFTER.		
CC	-I- INDUCTION: UNDER OXIDATIVE STRESS ON THE MYCELIUM BY AROMATIC		
CC	XENOBIOLOGICS (GUAIACOL, HYDROQUINONE, BENZOQUINONE), AND BY COPPER		
CC	SALT AT A CONCENTRATION OF 1MM (GROWING MYCELIUM).		
CC	-I- PTM: LACCASE II IS PROCESSED AT BOTH ITS N-TERMINUS AND ITS C-		
CC	TERMINUS.		
CC	-I- MISCELLANEOUS: PODOSPORA ANSERINA CONTAINS AT LEAST 3 LACCASE		
CC	ISOMYSES NAMED I, II, AND III. THEY DIFFER IN THEIR SUBSTRATE		
CC	SPECIFICITY, NUMBER OF SUBUNITS, ISOELECTRONIC POINT AND HEAT		
CC	STABILITY.		
CC	-I- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.		
CC	-I- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.		
CC	-I- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
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CC	use by non-profit institutions as long as its content is in no way		
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announcement/		
CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL; Y08827; CAAT70061.1; -		
DR	InterPro; IPR001117; -		
DR	InterPro; IPR002355; -		
DR	RefSeq; PF00394; Cu-oxidase; 2.		
DR	PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.		
DR	PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.		
KW	Oxidoreductase; Signal; Copper; Metal-binding; Glycoprotein; Repeat;		
KW	Lignin degradation; Melanin biosynthesis; Multigene family.		
FT	SIGNAL 1 23 POTENTIAL.		
FT	PROPEP 24 48 POTENTIAL.		
FT	CHAIN 49 605 LACCASE II.		
FT	PROPEP 606 621 POTENTIAL.		
FT	DOMAIN 78 201 POTENTIAL.		
FT	DOMAIN 210 367 PLASTOCYANIN-LIKE 1.		
FT	DOMAIN 430 566 PLASTOCYANIN-LIKE 2.		
FT	DOMAIN 138 138 PLASTOCYANIN-LIKE 3.		
FT	METAL 138 138 COPPER (TYPE 2) (BY SIMILARITY).		

FT METAL 140 140 COPPER (TYPE 3) (BY SIMILARITY).
 FT METAL 183 183 COPPER (TYPE 3) (BY SIMILARITY).
 FT METAL 185 185 COPPER (TYPE 3) (BY SIMILARITY).
 FT METAL 476 476 COPPER (TYPE 2) (BY SIMILARITY).
 FT METAL 479 479 COPPER (TYPE 3) (BY SIMILARITY).
 FT METAL 481 481 COPPER (TYPE 3) (BY SIMILARITY).
 FT METAL 548 548 COPPER (TYPE 1) (BY SIMILARITY).
 FT METAL 549 549 COPPER (TYPE 3) (BY SIMILARITY).
 FT METAL 550 550 COPPER (TYPE 1) (BY SIMILARITY).
 FT METAL 554 554 COPPER (TYPE 1) (BY SIMILARITY).
 FT METAL ? ? N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 325 325 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 334 334 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 421 421 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 441 441 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 621 AA; 68129 MW; 79F85E2ED25C1CA7 CRC64;

 Query Match 66.7%; Score 36; DB 1; Length 621;
 Best Local Similarity 100.0%; Pred. No. 80;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 2 GNYWF 6
 DB 329 GNYWF 333

 RESULT 15
 AMD_BOVIN
 ID AND_BOVIN STANDARD; PRT; 972 AA.
 AC F10731;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR
 DE (EC 1.14.17.3) (PAM).
 GN PAM.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Plutitary;
 RX MEDLINE=91042563; PubMed=3153462;
 RA Eipper B.A., Park L.P., Dickerson I.M., Keutmann H.T., Thiele E.A.,
 RA Rodriguez H., Schofield P.R., Mains R.E.;
 RT "Structure of the precursor to an enzyme mediating COOH-terminal
 amidation in peptide biosynthesis."
 RL Mol. Endocrinol. 1:777-790(1987).
 CC -1- FUNCTION: C-TERMINAL ALPHA-AMIDATION OF PEPTIDES.
 CC -1- CATALYTIC ACTIVITY: PEPTIDYLGLYCINE + ASCORBATE + O(2) =
 CC PEPTIDYL(2-HYDROXYGLYCINE) + DEHYDROASCORBATE + H(2)O.
 CC (THE PRODUCT IS UNSTABLE AND DISMUTATES TO GLYOXYLATE AND THE
 CC CORRESPONDING DESGLYCINE PEPTIDE AMIDE).
 CC -1- COFACTOR: COPPER, AND ASCORBATE.
 CC -1- SUBCELLULAR LOCATION: SECRETORY GRANULES.
 CC -1- SIMILARITY: BELONGS TO THE COPPER TYPE II, ASCORBATE-DEPENDENT
 CC MONOOXYGENASE FAMILY.

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CC EMBL; M18683; AAA30683.1; -
 DR PIR; A40063; URBOAP.
 DR InterPro; IPR000323; -
 DR InterPro; IPR000720; -
 DR InterPro; IPR001258; -
 DR Pfam; PF01082; CU2_monooxygen; 1.
 DR Pfam; PF01436; NHL; 4.
 DR PRINTS; PR00790; PAMONOXGNASE.
 DR PROSITE; PS00084; CU2_MONOOXYGENASE_1; 1.
 DR PROSITE; PS00085; CU2_MONOOXYGENASE_2; 1.
 KW Oxidoreductase; Monooxygenase; Copper; Vitamin C; Transmembrane;
 KW Glycoprotein; Phosphorylation; Signal.
 FT SIGNAL 1 20 POTENTIAL.
 FT PROPEP 21 30 POTENTIAL.
 FT CHAIN 31 972 POTENTIAL.
 FT DOMAIN 31 873 PEPTIDYL-GLYCINE ALPHA-AMIDATING
 FT TRANSMEM 874 897 MONOOXYGENASE.
 FT DOMAIN 898 972 INTRAGANULAR (POTENTIAL).
 FT METAL 237 237 POTENTIAL.
 FT METAL 239 239 CYTOPLASMIC (POTENTIAL).
 FT METAL 240 240 COPPER (POTENTIAL).
 FT METAL 359 359 COPPER (POTENTIAL).
 FT METAL 361 361 COPPER (POTENTIAL).
 FT METAL 362 362 COPPER (POTENTIAL).
 FT CARBOHYD 762 762 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 972 AA; 108176 MW; EBD41F83E341BAF1 CRC64;

Query Match 66.7%; Score 36; DB 1; Length 972;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GNYWF 6
 DB 116 GNYWF 120

Search completed: June 28, 2001, 15:54:35
 Job time: 123 sec

Fri Jun 29 08:05:24 2001

us-09-724-406-8.rsp

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2001, 16:08:19 ; Search time 411.58 Seconds
(without alignments)
2.572 Million cell updates/sec

Title: US-09-724-406-8
Perfect score: 54
Sequence: 1 YGNWFA 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL16:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_unclassified:*
- 13: sp_vertebrate:*
- 14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	72.2	115	9 Q38444	Q38444 bacteriophage
2	39	72.2	519	2 Q9RG14	Q9RG14 bacterioides
3	39	72.2	520	14 Q41104	Q41104 parametrium
4	38	70.4	151	2 Q47630	Q47630 escherichia
5	38	70.4	151	2 Q85635	Q85635 escherichia
6	38	70.4	246	14 Q9YW87	Q9YW87 melanopius
7	38	70.4	398	1 Q59482	Q59482 pyrococcus
8	38	70.4	491	2 Q9L6S4	Q9L6S4 salmonella
9	38	70.4	552	3 Q9URZ3	Q9URZ3 schizosacch
10	38	70.4	732	10 Q9SKE1	Q9SKE1 arabidopsis
11	38	70.4	790	10 Q9M371	Q9M371 arabidopsis
12	37	68.5	115	8 Q9TE75	Q9TE75 echinococcus
13	37	68.5	229	5 Q9GPE5	Q9GPE5 drosophila
14	37	68.5	229	5 Q9GPE4	Q9GPE4 drosophila
15	37	68.5	229	5 Q9GNI1	Q9GNI1 drosophila
16	37	68.5	229	5 Q9GN93	Q9GN93 drosophila
17	37	68.5	229	5 Q9GN92	Q9GN92 drosophila
18	37	68.5	331	4 Q99729	Q99729 homo sapien
19	37	68.5	331	11 Q88311	Q88311 rattus norv

20	37	68.5	332	11 Q9QX81	Q9QX81 rattus norv
21	37	68.5	495	10 Q98183	Q98183 catharanthu
22	37	68.5	499	10 Q9SWE3	Q9SWE3 nicotiana t
23	36.5	67.6	382	10 Q9SN20	Q9SN20 arabidopsis
24	36	66.7	225	5 Q90950	Q90950 caenorhabdi
25	36	66.7	267	10 Q9FYA1	Q9FYA1 arabidopsis
26	36	66.7	279	1 Q9HNGO	Q9HNGO halobacteri
27	36	66.7	361	1 Q30197	Q30197 archaeoglob
28	36	66.7	400	1 Q26432	Q26432 methanobact
29	36	66.7	592	4 Q9NP91	Q9NP91 homo sapien
30	36	66.7	616	11 Q64093	Q64093 rattus norv
31	36	66.7	635	11 Q88575	Q88575 mus musculu
32	35	64.8	101	2 P95154	P95154 mycobacteri
33	35	64.8	119	9 Q80057	Q80057 bacterioph
34	35	64.8	238	10 Q81922	Q81922 capsicum an
35	35	64.8	289	2 Q9JIV2	Q9JIV2 neisseria m
36	35	64.8	289	2 Q9JUT4	Q9JUT4 neisseria m
37	35	64.8	302	2 Q32179	Q32179 bacillus su
38	35	64.8	310	2 Q9RW55	Q9RW55 deinococcus
39	35	64.8	310	2 Q9EXF1	Q9EXF1 listeria mo
40	35	64.8	319	2 Q9KBI8	Q9KBI8 bacillus ha
41	35	64.8	376	10 Q9FVH5	Q9FVH5 prunus arme
42	35	64.8	407	2 Q9KIV1	Q9KIV1 streptomyce
43	35	64.8	437	3 Q99036	Q99036 trichoderma
44	35	64.8	453	2 Q9ZDV3	Q9ZDV3 rickettsia
45	35	64.8	496	9 Q9MBP0	Q9MBP0 staphylococ

ALIGNMENTS

RESULT 1

Q38444 PRELIMINARY; PRT; 115 AA.

AC Q38444; (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)

DE ORF2

OS Bacteriophage T5.

OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae.

OX NCBI_TaxID=10726;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=86192453; PubMed=3516691;

RA Shlyapnikov M.G., Ksenzenko V.N., Kryukov V.M., Bayev A.A.;

RT "Nucleotide sequence of the bacteriophage T5 DNA fragment which contains the gene for trNA^{asp}."

RL Eur. J. Biochem. 156:285-289(1986).

DR EMBL; X03798; CAA27425.1; -.

SQ SEQUENCE 115 AA; 13375 MW; AF2864283F53BC11 CRC64;

Query Match 72.2%; Score 39; DB 9; Length 115;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNWFA 7
Db 67 YGNWFA 73

RESULT 2

Q9RG14 PRELIMINARY; PRT; 519 AA.

ID Q9RG14; (TrEMBLrel. 13, Created)

AC Q9RG14; 2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)

DE HYPOTHETICAL 61.2 KDA PROTEIN.

OS Bacteroides fragilis.

OC Bacteria; CFB group; Bacteroidaceae; Bacteroides.

OX NCBI_TaxID=817;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-638R;
 RA MEDLINE-99429872; PubMed=10498737;
 RX Comstock L.E., Coyne M.J., Tzianabos A.O., Kasper D.L.;
 RT "Interstrain variation of the polysaccharide B biosynthesis locus of
 RT Bacteroides fragilis: Characterization of the region from strain
 RT 638R.";
 RL J. Bacteriol. 181:6192-6196(1999).
 DR EMBL; AF125164; AAD56750.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 519 AA; 61151 MW; CFF7FC629006A741 CRC64;

Query Match 72.2%; Score 39; DB 2; Length 519;
 Best Local Similarity 83.3%; Pred. No. 79;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGNYWF 6
 Db 289 FGNYWF 294
 :|||||

RESULT 3
 O41104 PRELIMINARY; PRT; 520 AA.
 ID O41104
 AC O41104
 DT 01-JAN-1998 (TRENBLrel. 05, Created)
 DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
 DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)
 DE A622L PROTEIN.
 GN A622L.
 OS Parametium bursaria chlorella virus 1 (PBCV-1).
 OC Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Phycodnavirus.
 OX NCBI_TaxID=10506;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-98022962; PubMed=9356347;
 RA Li Y., Lu Z., Sun L., Ropp S., Kutish G.F., Rock D.L., Van Etten J.L.;
 RT "Analysis of 74 kb of DNA located at the right end of the 330-kb
 RT chlorella virus PBCV-1 genome.";
 RL Virology 237:360-377(1997).
 DR EMBL; U42580; AAC96953.1; -
 SQ SEQUENCE 520 AA; 58097 MW; OCC143D64C1640D7 CRC64;

Query Match 72.2%; Score 39; DB 14; Length 520;
 Best Local Similarity 62.5%; Pred. No. 79;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGNYWFAY 8
 Db 107 YNNYWTY 114
 :|||||

RESULT 4
 Q47630 PRELIMINARY; PRT; 151 AA.
 ID Q47630
 AC Q47630
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)
 DE SEPD.
 GN SEPD.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-E2348/69; (ENTEROPATHOGENIC E. COLI, LEE);
 RX MEDLINE-95372406; PubMed=7644527;
 RA Jarvis K.G., Giron J.A., Jerse A.E., McDaniel T.K., Donnenberg M.S.,

RA Kaper J.B.;
 RT "Enteropathogenic Escherichia coli contains a putative type III
 RT secretion system necessary for the export of proteins involved in
 RT attaching and effacing lesion formation.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:7996-8000(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Elliott S.J., Wainwright L.A., McDaniel T.K., Jarvis K.G., Deng Y.K.,
 RA Lai L.C., McNamara B.P., Donnenberg M.S., Kaper J.B.;
 RL Mol. Microbiol. 0:0-0(1998).
 DR EMBL; Z49972; CAA90273.1; -
 DR EMBL; AF022236; AAC38378.1; -
 SQ SEQUENCE 151 AA; 17563 MW; A100D54677FDF89B CRC64;

Query Match 70.4%; Score 38; DB 2; Length 151;
 Best Local Similarity 62.5%; Pred. No. 31;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGNYWFAY 8
 Db 45 FGNYWVLY 52
 :|||||

RESULT 5
 O85635 PRELIMINARY; PRT; 151 AA.
 ID O85635
 AC O85635
 DT 01-NOV-1998 (TRENBLrel. 08, Created)
 DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
 DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)
 DE L0040.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-EDL933.
 RX MEDLINE-98339885; PubMed=9673266;
 RA Perna N.T., Mayhew G.F., Posfai G., Elliott S., Donnenberg M.S.,
 RA Kaper J.B., Blattner F.R.;
 RT "Molecular evolution of a pathogenicity island from enterohemorrhagic
 RT Escherichia coli O157:H7.";
 RL Infect. Immun. 66:3810-3817(1998).
 DR EMBL; AF071034; AAC31519.1; -
 SQ SEQUENCE 151 AA; 17561 MW; A11A6F09942B6774 CRC64;

Query Match 70.4%; Score 38; DB 2; Length 151;
 Best Local Similarity 62.5%; Pred. No. 31;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGNYWFAY 8
 Db 45 FGNYWVLY 52
 :|||||

RESULT 6
 Q9YW87 PRELIMINARY; PRT; 246 AA.
 ID Q9YW87
 AC Q9YW87
 DT 01-MAY-1999 (TRENBLrel. 10, Created)
 DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
 DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
 DE ORF MSV005 HYPOTHETICAL PROTEIN.
 GN MSV005.
 OS Melanoplus sanguinipes entomopoxvirus (MsePV).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
 OC Entomopoxvirus B.
 OX NCBI_TaxID=83191;
 RN [1]
 RP SEQUENCE FROM N.A.

Fri Jun 29 08:05:25 2001

us-09-724-406-8.rspt

RC STRAIN-TUCSON;
RA MEDLINE-99102612; PubMed-9847359;
RA Afonso C.L., Tulman E.R., Lu Z., Oma E., Kutish G.F., Rock D.L.;
RT "The genome of Melanoplus sanguinipes entomopoxvirus";
RL J. Virol. 73:533-552(1999).
RN [2]
RN SEQUENCE FROM N.A.
RP
RC STRAIN-TUCSON;
RA Afonso C.L., Tulman E.R., Lu Z., Oma E., Kutish G.F., Rock D.L.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF063866; AAC97860.1; -. 098823A3E5D28ACB CRC64;
SQ SEQUENCE 246 AA; 30090 MW; 098823A3E5D28ACB CRC64;

Query Match 70.4%; Score 38; DB 14; Length 246;
Best Local Similarity 62.5%; Pred. No. 52;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGNYWFAY 8
II IIII
Db 230 YGYWYIY 237

RESULT 7
ID O59482 PRELIMINARY; PRT; 398 AA.
AC O59482;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE HYPOTHETICAL 44.8 KDA PROTEIN PH1818.
GN PH1818.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
OX NCBI_TaxID=53953;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN-OT3;
RC MEDLINE-98344137; PubMed-9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudo H., Yamazaki J., Kishida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
DR EMBL; AF000007; BAA30937.1; -.
KW Hypothetical protein.
SQ SEQUENCE 398 AA; 44808 MW; 7A33583CCF449AA2 CRC64;

Query Match 70.4%; Score 38; DB 1; Length 398;
Best Local Similarity 83.3%; Pred. No. 87;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGNYWF 6
II IIII
Db 365 YGNYW 370

RESULT 8
ID Q9L6S4 PRELIMINARY; PRT; 491 AA.
AC Q9L6S4;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE S. TYPHIMURIUM KETOL-ACID REDUCTOISOMERASE (ILVC) (SP:P05989),
CONTAINS SIMILARITY TO PFAM FAMILY PF01450 (ACETOHYDROXY ACID
ISOMERASE), SCORE=628.8, E=3.1E-185, N=1.
GN ILVC.

OS Salmonella typhimurium LT2.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=99287;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN-SGSC1412;
RC STRAIN-SGSC1412;
RA Washu;
RT "The Salmonella typhimurium Genome Sequencing Project";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RP STRAIN-SGSC1412;
RC STRAIN-SGSC1412;
RA Waterston R.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF233324; AAF33476.1; -.
DR InterPro; IPR000506; -.
DR Pfam; PF01450; ILVC; 1.
KW Isomerase.
SQ SEQUENCE 491 AA; 53941 MW; 4080B60E1B9658F0 CRC64;

Query Match 70.4%; Score 38; DB 2; Length 491;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNYWFAY 8
II IIII
Db 419 YGNLYFSY 426

RESULT 9
ID Q9URZ3 PRELIMINARY; PRT; 552 AA.
AC Q9URZ3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE AMINO-ACID PERMEASE.
GN SPAC869.10C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN-972H-;
RC Hunt C., Aves S., McDougall R.C., Rajandream M.A., Barrell B.G.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL132779; CAB60020.1; -.
DR InterPro; IPR003027; -.
DR InterPro; IPR003293; -.
DR Pfam; PF003324; aa_permeases; 1.
DR PROSITE; PS00213; AMINO-ACID_PERMEASE; 1.
SQ SEQUENCE 552 AA; 61119 MW; BF067D5A8172E1A5 CRC64;

Query Match 70.4%; Score 38; DB 3; Length 552;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 NYWFAY 8
II IIII
Db 127 NYWYAY 132

RESULT 10
ID Q9SKE1 PRELIMINARY; PRT; 732 AA.
AC Q9SKE1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
 DE AT2G46380 PROTEIN.
 GN AT2G46380.
 OS Arabidopsis thaliana (Mouse-ear cross).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RX MEDLINE=20083487; PubMed=10617197;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
 RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
 RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
 RA Adams M.D., Carrera A.J., Cressy T.H., Goodman H.M., Somerville C.R.,
 RA Copenhaver G.P., Preuss D., Niernan W.C., White O., Eisen J.A.,
 RA Salzberg S.L., Fraser C.M., Venter J.C.;
 RT "Sequence and analysis of chromosome II of Arabidopsis thaliana";
 RL Nature 402:761-768(1999).
 DR EMBL; AC006526; AAD23041.1; -.
 SQ SEQUENCE 732 AA; 81362 MW; B8DECFE759A00C9 CRC64;

Query Match 70.4%; Score 38; DB 10; Length 732;
 Best Local Similarity 71.4%; Pred. No. 1.7e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GNYWFAY 8
 ||||: |
 Db 634 GNYWDY 640

RESULT 11
 Q9M371 PRELIMINARY; PRT; 790 AA.
 ID Q9M371;
 AC Q9M371;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
 DE HYPOTHETICAL 87.4 KDA PROTEIN.
 GN F15G16.60.
 OS Arabidopsis thaliana (Mouse-ear cross).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA De Haan M., Maarse A.C., Grivell L.A., Mewes H.W., Lemcke K.,
 RA Mayer K.F.X., Quetier F., Salanoubat M.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; ALI32959; CAB71097.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 790 AA; 87375 MW; B222724B75690F30 CRC64;

Query Match 70.4%; Score 38; DB 10; Length 790;
 Best Local Similarity 71.4%; Pred. No. 1.8e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GNYWFAY 8
 ||||: |
 Db 675 GNYWDY 681

RESULT 12
 Q9TE75

ID Q9TE75 PRELIMINARY; PRT; 115 AA.
 AC Q9TE75;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
 DE NADH DEHYDROGENASE SUBUNIT 3.
 GN ND3.
 OS Echinococcus multilocularis.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Platyhelminthes; Rhaditophora; Neodermata;
 OC Cestoda; Eucestoda; Cyclophyllidae; Taeniidae; Echinococcus.
 OX NCBI_TaxID=6211;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Fukunaga M.;
 RT "Echinococcus multilocularis mitochondrial DNA sequence";
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB018440; BAA84934.2; -.
 DR InterPro: IPR000440; -.
 DR Pfam: PF00507; oxidored_q4; 1.
 KW Mitochondrion.
 SQ SEQUENCE 115 AA; 13770 MW; 6FFDE02CB8BE9C02 CRC64;

Query Match 68.5%; Score 37; DB 8; Length 115;
 Best Local Similarity 50.0%; Pred. No. 33;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNYWFAY 8
 ||||: |
 Db 85 FGNYWYY 92

RESULT 13
 Q9GPE5 PRELIMINARY; PRT; 229 AA.
 ID Q9GPE5;
 AC Q9GPE5;
 DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
 DE ACP29 (FRAGMENT).
 GN ACP29.
 OS Drosophila simulans (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7240;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SIM7;
 RA Begun D., Whitely P., Todd B., Waldrup H., Clark A.;
 RT "Molecular population genetics of male accessory gland proteins in
 RT Drosophila";
 RL Genetics 0:0-0(2001).
 DR EMBL; AY010653; AAG37405.1; -.
 FT NON_TER 1 1
 FT NON_TER 229 229
 SQ SEQUENCE 229 AA; 26335 MW; 199E33332ADC21997 CRC64;

Query Match 68.5%; Score 37; DB 5; Length 229;
 Best Local Similarity 83.3%; Pred. No. 70;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 NYWFAY 8
 ||||: |
 Db 45 NYWFTY 50

RESULT 14
 Q9GPE4 PRELIMINARY; PRT; 229 AA.
 ID Q9GPE4
 AC Q9GPE4;

us-09-724-406-8.rspt

Fri Jun 29 08:05:25 2001

01-MAR-2001 (TREMBlrel. 16, Created)
 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 ACP29 (FRAGMENT).
 ACP29.
 Drosophila simulans (Fruit fly).
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7240;
 RN [1]
 SEQUENCE FROM N.A.
 RP STRAIN-SIM8.
 RA Begun D., Whitley P., Todd B., Waldrip H., Clark A.;
 RT "Molecular population genetics of male accessory gland proteins in
 Drosophila."
 RL Genetics 0:0-0(2001).
 DR EMBL: AY010654; AAG37406.1; -.
 FT NON_TER 1
 FT NON_TER 229 229
 SQ SEQUENCE 229 AA; 26320 MW; 2E824E1B4A5C6858 CRC64;

Query Match 68.5%; Score 37; DB 5; Length 229;
 Best Local Similarity 83.3%; Pred. No. 70;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 NYWFAY 8
 Db 45 NYWFTY 50

RESULT 15
 Q9GN11 PRELIMINARY; PRT; 229 AA.
 AC Q9GN11; 2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE ACP29 (FRAGMENT).
 GN ACP29.
 OS Drosophila simulans (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7240;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SIM8, AND SIM4;
 RA Begun D., Whitley P., Todd B., Waldrip H., Clark A.;
 RT "Molecular population genetics of male accessory gland proteins in
 Drosophila."
 RL Genetics 0:0-0(2001).
 DR EMBL: AY010652; AAG37404.1; -.
 DR EMBL: AY010650; AAG37402.1; -.
 FT NON_TER 1
 FT NON_TER 229 229
 SQ SEQUENCE 229 AA; 26333 MW; 199E333C33BFF097 CRC64;

Query Match 68.5%; Score 37; DB 5; Length 229;
 Best Local Similarity 83.3%; Pred. No. 70;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 NYWFAY 8
 Db 45 NYWFTY 50

Search completed: June 28, 2001, 16:08:20
 Job time: 948 sec

Result No.	Query		Length	DB	ID	Description
	Score	Match				
1	75	96.2	15	16	AAR70195	Mab 3B9 light chain
2	75	96.2	15	19	AAR83027	Anti-Fas Mab HEF7A
3	75	96.2	15	20	AAV23772	CDR of the light chain
4	75	96.2	15	20	AAV18114	Light chain CDR for
5	75	96.2	15	21	AAV14744	Mouse anti-Fas antibody
6	75	96.2	15	21	AAR90894	Murine anti-Fas antibody
7	75	96.2	15	21	AAV59259	Antibody 4H5 L chain
8	75	96.2	15	21	AAV51136	Murine CD4/CD34 reagent
9	75	96.2	19	15	AAR66143	CD-4 antibody variable region
10	75	96.2	103	21	AAV59263	Antibody 4H5 L chain
11	75	96.2	103	21	AAV51140	Murine derived protein

RESULT	1
AA70195	
ID	AA70195 standard; Protein; 15 AA.
XX	
XX	
AC	AA70195;
XX	
XX	
DT	20-SEP-1995 (first entry)
XX	
XX	
DE	MAB 3B9 light chain CDR.
XX	
XX	
KK	Chimeric antibody; humanized antibody; antibody engineering;
KK	monoclonal antibody; MAB; interleukin-4; IL-4; allergy; CDR;
KK	complementarity determining region.
KW	

Mus sp.
 WO9507301-A.
 16-MAR-1995.
 07-SEP-1994; 94WO-US10308.
 07-SEP-1993; 93US-0117366.
 14-OCT-1993; 93US-0136783.
 (SMIK) SMITHKLINE BEECHAM CORP.
 (SMIK) SMITHKLINE BEECHAM PLC.
 Gross MS, Holmes SD, Sylvester DR;
 WPI; 1995-123387/16.
 Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of IL-4-mediated

PT and IgE-mediated allergic conditions
 PS Disclosure; Page 54; 97pp; English.
 XX
 XX Spleen cells from mice immunized with human IL-4 were used to prepare
 CC hybridomas, which were screened for anti-IL-4 MAb secretion. Only
 CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy
 CC chains were cloned into pCEM7f+ and transformed into E. coli
 CC DH5-alpha. A light chain cDNA clone was sequenced (AA083490) that
 CC encoded the protein given in AAR70189. 3 CDRs (AAR70195-97) were
 CC identified.
 XX
 XX Sequence 15 AA:
 SQ
 Query Match 96.2%; Score 75; DB 16; Length 15;
 Best Local Similarity 93.3%; Pred. No. 1.8e-06;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KASQSVDFDGSYMN 15
 |||||||:|||||||
 Db 1 kasqsvdydgsymn 15
 RESULT 2
 AAW83027
 ID AAW83027 standard; Peptide; 15 AA.
 XX
 AC AAW83027;
 XX
 DT 15-MAR-1999 (first entry)
 XX
 DE Anti-Fas MAb HFE7A light chain CDR-LL.
 XX
 XX HFE7A: monoclonal antibody; mouse; Fas; humanised antibody;
 KW apoptosis; autoimmune disease; Hashimoto's disease;
 KW systemic lupus erythematosus; graft versus host disease;
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 KW transplant rejection; therapy; complementarity determining region;
 CDR.
 XX
 XX Mus musculus.
 XX AU9859701-A.
 XX
 XX 08-OCT-1998.
 XX
 XX 30-MAR-1998; 98AU-0059701.
 XX
 XX 08-OCT-1997; 97JP-0276064.
 XX 01-APR-1997; 97JP-0082953.
 XX 25-JUN-1997; 97JP-0169088.
 XX
 XX (SANY) SANKYO CO LTD.
 XX
 XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
 PI Masahiko O, Nobufusa S, Shin Y, Tohru T;
 XX
 XX WPI: 1998-543440/47.
 XX
 XX New antibodies and proteins bind conserved epitope of Fas antigen -
 PT used to evaluate drugs in animal models and to treat Fas-associated
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 PT myocarditis, hepatitis and AIDS
 XX
 XX Claim 9; Page 184; 292pp; English.
 PS
 XX

CC This is the amino acid of complementarity determining region 1
 CC (CDR-LL) of the light chain (see AAW83042) of murine anti-human Fas
 CC monoclonal antibody HFE7A. The invention relates to antibodies,
 CC especially humanised antibodies (see AAW83031-37), recognising the
 CC Fas antigen. Such antibodies preferably comprise a heavy chain and
 CC a light chain including CDRs (see AAW83024-29) from the heavy and
 CC light chains of HFE7A. Humanised antibodies are produced by CDR
 CC grafting. The antibodies are capable of inducing apoptosis in
 CC abnormal cells expressing Fas, and of inhibiting Fas-induced
 CC apoptosis in normal cells. They are used to evaluate, in animal
 CC models, treatments of diseases that involve Fas/Fas ligand
 CC interactions, and also to treat such diseases, including autoimmune
 CC disease (e.g. systemic lupus erythematosus, Hashimoto's disease,
 CC graft versus host disease, Sjogren syndrome, pernicious anaemia,
 CC Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, rheumatoid arthritis, autoimmune haemolytic anaemia,
 CC sterility, myasthenia gravis, multiple sclerosis, Basedow's
 CC disease, thrombopenia purpura and insulin-dependent diabetes),
 CC allergies, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
 CC glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and
 CC transplant rejection (all claimed).
 XX
 XX Sequence 15 AA;
 SQ
 Query Match 96.2%; Score 75; DB 19; Length 15;
 Best Local Similarity 93.3%; Pred. No. 1.8e-06;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KASQSVDFDGSYMN 15
 |||||||:|||||||
 Db 1 kasqsvdydgsymn 15
 RESULT 3
 AAY23772
 ID AAY23772 standard; Peptide; 15 AA.
 XX
 AC AAY23772;
 XX
 DT 13-SEP-1999 (first entry)
 XX
 DE CDR of the light chain variable region of antibody 3B9.
 XX
 XX Light chain variable region; interleukin-4; IL-4; antibody 3B9;
 KW chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;
 KW immunoglobulin E-mediated allergic reaction; allergic rhinitis;
 KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
 KW rheumatoid arthritis; host-versus-graft disease; renal disease;
 KW allergy; complementarity determining region.
 XX
 XX Mus sp.
 XX US5928904-A.
 XX
 XX 27-JUL-1999.
 XX
 XX 07-JUN-1995; 95US-0483632.
 XX
 XX 07-JUN-1995; 95US-0483632.
 XX 07-SEP-1993; 93US-0117366.
 XX 14-OCT-1993; 93US-0136783.
 XX 07-SEP-1994; 94WO-US10308.
 XX
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 XX (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 XX Gross MS, Holmes SD, Sylvester DR;
 XX WPI: 1999-429500/36.
 XX N-PSDB; AAX85889.
 XX
 XX New DNA molecules encoding recombinant antibodies useful for
 PT

PT treating IL4-mediated conditions
 XX Example 3; Column 43-44; 50pp; English.
 XX The present sequence represents a complementarity determining region
 CC (CDR) of the light chain variable region of murine interleukin-4
 CC (IL-4) antibody 3B9. The specification describes chimeric and
 CC humanised IL-4 monoclonal antibodies. The antibodies of the
 CC invention are used in therapeutic and pharmaceutical compositions
 CC for treating IL-4 mediated and immunoglobulin E-mediated allergic
 CC reactions e.g. allergic rhinitis, conjunctivitis, atopic dermatitis,
 CC atopic asthma, anaphylactic shock, rheumatoid arthritis,
 CC host-versus-graft disease and renal disease. They are also useful
 CC in the diagnosis of an allergy or condition associated with excess
 CC IL-4 production through the measurement e.g. by ELISA of circulating
 CC endogenous IL-4 levels in humans.
 XX Sequence 15 AA;

Query Match 96.2%; Score 75; DB 20; Length 15;
 Best Local Similarity 93.3%; Pred. No. 1.8e-06;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQSVDFDGDSSYNN 15
 | | | | | : | | | | |
 Db 1 kasqsvdydgdsynn 15

RESULT 4
 AAY18114
 ID AAY18114 standard; peptide; 15 AA.

AC AAY18114;

DT 11-AUG-1999 (first entry)

DE Light chain CDR for hIL-4 specific antibody.

KW Antibody: interleukin-4; IL4; immunoglobulin E; IgE mediated disease;
 KW allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;
 KW atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;
 KW autoimmune disease; graft versus host disease;
 KW complementarity determining region; CDR.

OS Synthetic.

PN US5914110-A.

PD 22-JUN-1999.

PF 07-JUN-1995; 95US-0483636.

PR 07-JUN-1995; 95US-0483636.

PR 07-SEP-1993; 93US-0117366.

PR 14-OCT-1993; 93US-0136783.

PR 07-SEP-1994; 94WO-US10308.

PA (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

PI Gross MS, Holmes SD, Sylvester DR;

DR WPI: 1999-370482/31.

DR N-PSDB; AAX79513.

XX Recombinant IL4 antibodies

PT Claim 7; Column 43; 50pp; English.

XX This sequence represents a light chain complementarity determining region
 CC (CDR) from an antibody of the invention. The antibody is a chimeric or
 CC humanised interleukin-4 (IL4) monoclonal antibody for the treatment of

CC immunoglobulin E (IgE) mediated diseases. The antibodies are useful for
 CC the treatment of allergic disorders such as allergic rhinitis,
 CC conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock.
 CC The antibodies are also useful for regulating B and T cell proliferation
 CC and as such are useful in the treatment of autoimmune diseases and graft
 CC versus host disease.
 XX Sequence 15 AA;

Query Match 96.2%; Score 75; DB 20; Length 15;
 Best Local Similarity 93.3%; Pred. No. 1.8e-06;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQSVDFDGDSSYNN 15
 | | | | | : | | | | |
 Db 1 kasqsvdydgdsynn 15

RESULT 5
 AAB14744

ID AAB14744 standard; peptide; 15 AA.

XX AAB14744;

DT 24-NOV-2000 (first entry)

DE Mouse anti-Fas antibody HFE7A light chain CDR1.

KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
 KW murine; complementarity determining region; CDR; human Fas;
 KW Fas ligand; complementarity determining region; programmed cell death;
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;
 KW hepatitis; AIDS; graft rejection; light chain.

OS Mus musculus.

PN JP2000169393-A.

PD 20-JUN-2000.

PF 30-SEP-1999; 99JP-0278301.

PR 30-SEP-1998; 98JP-0276883.

PA (SANY) SANKYO CO LTD.

PA WPI: 2000-485645/43.

DR Preventive or treating agent for the diseases caused by an abnormality
 in the Fas/Fas ligand system e.g. autoimmune diseases, contains
 anti-Fas antibody -

Claim 10; Page 65; 139pp; Japanese.

XX The invention relates to compositions for the prevention or treatment
 of diseases caused by an abnormality in the Fas/Fas ligand system
 containing an anti-Fas antibody as the active component. The anti-Fas
 antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
 or a humanised version of HFE7A containing identical CDRs
 (complementarity determining regions) to antibody HFE7A. Via its
 interaction with Fas, the antibody of the invention acts as a modulator
 of apoptosis. The compositions of the invention may therefore be used in
 the treatment or prevention of conditions such as autoimmune diseases,
 allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
 CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
 CC and organ graft rejection. Sequences AAB14744-B14746 represent CDRs 1-3
 CC of the light chain of the murine anti-human Fas monoclonal antibody
 CC HFE7A, which is produced by hybridoma HFE7A (FERM-BP-5828).

XX Sequence 15 AA;

Query Match 96.2%; Score 75; DB 21; Length 15;
 Best Local Similarity 93.3%; Pred. No. 1.8e-06;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFGDSYMN 15
 |||||:|||||
 Db 1 kasqsvdygdsymn 15

RESULT 6
 AAW90894
 ID AAW90894 standard; peptide; 15 AA.
 AC AAW90894;
 XX
 XX 08-AUG-2000 (first entry)
 XX
 DE Murine anti-Fas antibody peptide fragment #4.
 XX
 XX Fas; antibody; murine; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antinfertility; neuroprotective; antiarteriosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 XX
 OS Mus musculus.
 XX
 XX EP990663-A2.
 XX
 PD 05-APR-2000.
 XX
 XX 29-SEP-1999; 99EP-0307711.
 XX
 XX 30-SEP-1998; 98JP-0276881.
 PR 30-SEP-1998; 98JP-0276882.
 XX
 XX (SANY) SANKYO CO LTD.
 PA
 XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 PI
 XX WPI; 2000-258930/23.
 DR
 XX
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems
 XX
 PS Disclosure; Page 98; 263pp; English.
 XX
 CC This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiac and hepatropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,

CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a murine anti-Fas antibody peptide fragment described in the method
 CC of the invention.
 XX
 XX Sequence 15 AA;
 SQ

Query Match 96.2%; Score 75; DB 21; Length 15;
 Best Local Similarity 93.3%; Pred. No. 1.8e-06;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFGDSYMN 15
 |||||:|||||
 Db 1 kasqsvdygdsymn 15

RESULT 7
 AAY59259
 ID AAY59259 standard; peptide; 15 AA.
 XX
 XX AAY59259;
 XX
 XX 17-APR-2000 (first entry)
 DT
 XX Antibody 4H5 L chain variable region CDR1 fragment.
 DE
 XX CD4 antigen; anti-human; antibody; 4H5; drug; CDR;
 KW complementarity determining region.
 XX
 XX Mus sp.
 OS
 XX JP11332563-A.
 PN
 XX 07-DEC-1999.
 PD
 XX 26-MAY-1998; 98JP-0163034.
 XX
 XX 26-MAY-1998; 98JP-0163034.
 PR
 XX (ASAH) ASAH KASEI KOGYO KK.
 PA
 XX WPI; 2000-091351/08.
 DR
 XX
 XX An antibody and the nucleic acid coding the antibody -
 PT
 PS Claim 2; Page 14; 25pp; Japanese.
 XX
 CC The invention provides an antibody having affinity to CD4 antigen. The
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and
 CC application for drugs. It is highly safe in human dose. Sequences
 CC AAY59259-61 represent the complementarity determining region (CDR)-1,
 CC CDR-2 and CDR-3 fragments in the L chain variable region of the
 CC antibody 4H5 respectively.
 XX
 XX Sequence 15 AA;
 SQ

Query Match 96.2%; Score 75; DB 21; Length 15;
 Best Local Similarity 93.3%; Pred. No. 1.8e-06;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFGDSYMN 15
 |||||:|||||
 Db 1 kasqsvdygdsymn 15

RESULT 8

AA51136
ID AAY51136 standard; Protein; 15 AA.
XX
AC AAY51136;
XX
DT 31-MAR-2000 (first entry)
XX
DE Murine CD4/CD34 recognizing antibody light chain CDR-1 region #1.
XX
KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
KW HIV infection; autoimmune disease; complementarity determining region;
KW CDR-1; light chain; murine.
XX
OS Mus sp.
XX
PN WO9961629-A1.
XX
PD 02-DEC-1999.
XX
PF 24-MAY-1999; 99WO-JP02711.
XX
PR 25-MAY-1998; 98JP-0159957.
PR 26-MAY-1998; 98JP-0163023.
XX
PA (ASAH) ASahi KASEI KOGYO KK.
PA (ASAH) ASahi MEDICAL CO LTD.
PI Ono M, Soka T, Morimoto I, Miyamura K;
XX
DR WPI; 2000-086720/07.
XX
DT Devices containing antibodies recognising CD4 or CD34 and their use for
PT the separation of CD4 or CD34 positive cells -
XX
PS Claim 3; Page 76; 11pp; Japanese.
XX
CC This invention describes a novel device (I) for separating cluster
CC differentiation (CD)-positive cells using a recombinant (chimeric or
CC single-chain) antibody recognising CD4 or CD34. The devices are useful
CC for the separation of CD4 or CD34 positive cells, which is useful for
CC the collection of hematopoietic undifferentiated cells, elimination of
CC lymphocytes from cells to be used in bone marrow transplantation, the
CC detection of leukemic cells and the production of medicinal
CC compositions for the treatment of HIV infection and autoimmune diseases.
CC This sequence represents a murine derived complementarity determining
CC region CDR-1 protein fragment which is used to illustrate the method of
CC the invention.
XX
SQ Sequence 15 AA;

Query Match 96.2%; Score 75; DB 21; Length 15;
Best Local Similarity 93.3%; Pred. NO. 1.8e-06;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQSVDFDGSYNN 15
Db 1 kasqsvdydgsynn 15

RESULT 9
AAR66143
ID AAR66143 standard; peptide; 19 AA.
XX
AC AAR66143;
XX
DT 12-JUL-1995 (first entry)
XX
DE CD-4 antibody variable region complementary peptide.
XX
KW CD-4 antibody variable region; complementary peptide;
KW extra-corporeal blood circulation; cell filter material.

XX Synthetic.
OS
PN JP06269663-A.
XX
PD 27-SEP-1994.
XX
PF 17-MAR-1993; 93JP-0057206.
XX
PR 17-MAR-1993; 93JP-0057206.
XX
PA (TOYM) TOYOSO KK.
XX
WPI; 1994-346316/43.
XX
PT Material for collecting cells positive for CD-4 antibody -
PT comprises nonwoven fabric having keto-alkyl halide functional gp
XX
PS Example 1; Page 6; 9pp; Japanese.
XX
CC AAR66140-B66146 are peptides complementary to the variable region
CC of the CD-4 antibody, these peptides are fixed onto a claimed
CC nonwoven fabric (average fibre dia. of 1-30 microns) coated with
CC keto-alkyl halide functional groups. This material can be used
CC as a filter for CD-4 positive cells in a medical treatment
CC involving the extra-corporeal circulation of blood.
XX
SQ Sequence 19 AA;

Query Match 96.2%; Score 75; DB 15; Length 19;
Best Local Similarity 93.3%; Pred. NO. 2.3e-06;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQSVDFDGSYNN 15
Db 5 kasqsvdydgsynn 19

RESULT 10
AAY59263
ID AAY59263 standard; protein; 103 AA.
XX
AC AAY59263;
XX
DT 17-APR-2000 (first entry)
XX
DE Antibody 4H5 L chain variable region.
XX
KW CD4 antigen; anti-human; antibody; 4H5; drug.
XX
OS Mus sp.
XX
PN JP11332563-A.
XX
PD 07-DEC-1999.
XX
PF 26-MAY-1998; 98JP-0163034.
XX
PR 26-MAY-1998; 98JP-0163034.
XX
PA (ASAH) ASahi KASEI KOGYO KK.
XX
DR WPI; 2000-091351/08.
XX
N-PSDB; AAZ58662.
XX
PT An antibody and the nucleic acid coding the antibody -
XX
PS Claim 5; Page 15-16; 25pp; Japanese.
XX
CC The invention provides an antibody having affinity to CD4 antigen. The
CC anti-human CD4 antibody 4H5 is used for the detection of antigen and
CC application for drugs. It is highly safe in human dose. The present

CC sequence represents the L chain variable region of the antibody 4H5.

SQ Sequence 103 AA;

Query Match 96.2%; Score 75; DB 21; Length 103;
Best Local Similarity 93.3%; Pred. No. 1.5e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQSVDFDGSYMN 15
| | | | | : | | | | |
Db 16 kasqsvdydgdsym 30

RESULT 11

AA51140
ID AAY51140 standard; Protein; 103 AA.

XX AC AAY51140;

XX 31-MAR-2000 (first entry)

XX Murine derived protein fragment #2.

XX Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
KW HIV infection; autoimmune disease; murine.

OS Mus sp.

XX W09961629-A1.

XX 02-DEC-1999.

XX 24-MAY-1999; 99WO-JP02711.

XX 25-MAY-1998; 98JP-0159957.

XX 26-MAY-1998; 98JP-0163023.

XX (ASAH) ASAH KASEI KOGYO KK.
XX (ASAH) ASAH MEDICAL CO LTD.

XX Ono M, Soka T, Morimoto I, Miyamura K;

XX WPI; 2000-086720/07.

XX N-PSDB; AA44204.

XX Devices containing antibodies recognising CD4 or CD34 and their use for
the separation of CD4 or CD34 positive cells

XX Claim 22; Page 79; 111pp; Japanese.

CC This invention describes a novel device (1) for separating cluster
differentiation (CD)-positive cells using a recombinant (chimeric or
single-chain) antibody recognising CD4 or CD34. The devices are useful
for the separation of CD4 or CD34 positive cells, which is useful for
the collection of hematopoietic undifferentiated cells, elimination of
lymphocytes from cells to be used in bone marrow transplantation, the
detection of leukemic cells and the production of medicinal
compositions for the treatment of HIV infection and autoimmune diseases.
CC This sequence represents a murine derived protein fragment which is used
to illustrate the method of the invention.

XX Sequence 103 AA;

Query Match 96.2%; Score 75; DB 21; Length 103;
Best Local Similarity 93.3%; Pred. No. 1.5e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQSVDFDGSYMN 15
| | | | | : | | | | |
Db 16 kasqsvdydgdsym 30

RESULT 12

AAR33309

ID AAR33309 standard; Protein; 106 AA.

XX AC AAR33309;

XX 05-JUL-1993 (first entry)

XX MAE15 light chain.

XX Antibody; high affinity; FCEH; low affinity; FCEL;
KW IgE receptor; histamine; mast cell; basophil; Kabat;
KW CDR; murine; MAE11; MAE13; MAE15; MAE17.

XX Synthetic.

XX W09304173-A.

XX 04-MAR-1993.

XX 14-AUG-1992; 92WO-US06860.

XX 14-AUG-1991; 91US-0744768.

XX 07-MAY-1992; 92US-0879495.

XX (GETH) GENENTECH INC.

XX Jardieu PM, Presta LG;

XX WPI; 1993-094004/11.

XX Polypeptide(s) binding to specific Fc epsilon receptors - act as
PT IgE antagonists; useful for treating and preventing IgE-mediated
PT disorders e.g. allergies

XX Disclosure; Fig 2; 113pp; English.

XX Antibodies capable of binding FCEL-bound IgE but which are
CC substantially incapable of binding FCEH-bound IgE or inducing
CC histamine release from mast cells or basophils, comprise a human
CC Kabat CDR domain into which has been substituted a positionally
CC analogous residue from a Kabat CDR domain of the murine anti-huIgE
CC antibodies MAE11, MAE13, MAE15 or MAE17.

XX Sequence 106 AA;

Query Match 96.2%; Score 75; DB 14; Length 106;
Best Local Similarity 93.3%; Pred. No. 1.5e-05;

Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQSVDFDGSYMN 15

Db 24 kasqsvdydgdsym 38

RESULT 13

AA5197

ID AAY85197 standard; protein; 106 AA.

XX AC AAY85197;

XX 29-JUN-2000 (first entry)

XX Light chain amino acid sequence of mouse antibody MAE15.

XX Immunoglobulin E; IgE; anti-human IgE; bispecific antibody; FCEL; FCEH;
KW low affinity binding receptor; high affinity binding receptor; allergy;
KW diagnosis; treatment; histamine release; prevent; light chain.

OS Mus sp.

US6037453-A.
14-MAR-2000.
06-JUN-1995; 95US-0466151.
15-MAR-1995; 95US-0405617.
14-AUG-1992; 92WO-US06860.
26-JAN-1994; 94US-0185899.
(GETH) GENENTECH INC.
Presta LG, Jardieu PM;
WPI; 2000-269913/23.
New bispecific antibodies, useful for treating immunoglobulin
E-mediated disease, binds to IgE, but only when on the low affinity
receptor, and to an antigen other than IgE -
Claim 1; Fig 2; 48pp; English.
This sequence represents the light chain amino acid sequence of a mouse
anti-human immunoglobulin E (IgE) antibody. The invention relates to a
bispecific antibody that binds specifically to IgE when IgE is bound to
its low affinity receptor (FcεR), but does not bind to IgE, when IgE is
bound to its high affinity receptor (FcεR). The bispecific antibody
comprises an IgE-binding arm with human framework residues of a recipient
human antibody and donor murine CDR (complementarity determining region)
residues, but with at least one human CDR residue replacing the analogous
murine residue. The antibody also comprises an Fv that is specific for a
predetermined antigen other than IgE. The antibodies work by displacing
bound IgE from its receptor, or via competitive inhibition of its
binding. The bispecific antibodies are used for diagnosis, treatment and
prevention of allergy and other IgE-mediated diseases, also, when
immunolysed, for the isolation of FcεR from cells (for research or
therapy). The bispecific antibodies of the invention do not cause
granulation or release of histamine from mast cells.

Query Match 96.2%; Score 75; DB 21; Length 106;
Best Local Similarity 93.3%; Pred. No. 1.5e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 KASQSVDFDGD SYMN 15
DB 24 kasqsvdydgdsynn 38
RESULT 14
AAP90541
ID AAP90541 standard; protein; 111 AA.
AC AAP90541;
XX
XX 20-OCT-1989 (first entry)
DE Immunoglobulin L chain variable region.
XX Immunoglobulin; L chain variable region; HIV.
KW Mus musculus.
XX EP327000-A.
XX 09-AUG-1989.
XX 30-JAN-1989; 89EP-0101583.
XX 30-JAN-1988; 88JP-0020255.

08-JUL-1988; 88JP-0171385.
(KAGA) THE CHEMO-SERO-THERAPEUTIC RESEARCH INSTITUTE.
Maeda H, Eda Y, Kimachi K, Tokiyoshi S, Matsushita S, Hattori T;
Takatsuki K;
WPI; 1989-229050/32.
N-PSDB; AAN90491, AAN90492, AAN90493.
Chimeric anti-human immune virus antibodies - contg. mouse variable
regions and human constant regions for diagnosis, treatment and
prevention of AIDS
XX Claim 5; page 15; 33pp; English.
XX The sequence is an L chain variable region from an immunoglobulin with
anti-HIV neutralising activity. See AAN90491-3, and AAN90495.
XX Sequence 111 AA;
SQ

Query Match 96.2%; Score 75; DB 10; Length 111;
Best Local Similarity 93.3%; Pred. No. 1.6e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 KASQSVDFDGD SYMN 15
DB 24 kasqsvdydgdsynn 38
RESULT 15
AAR33305
ID AAR33305 standard; protein; 111 AA.
XX
AC AAR33305;
XX
XX 05-JUL-1993 (first entry)
DE MaE11 light chain.
XX Antibody; high affinity; FcεH; low affinity; FcεL;
KW IgE receptor; histamine; mast cell; basophil; Kabat;
KW CDR; murine; MAE11; MAE15; MAE17.
XX Synthetic.
XX WO9304173-A.
XX 04-MAR-1993.
XX 14-AUG-1992; 92WO-US06860.
XX 14-AUG-1991; 91US-0744768.
XX 07-MAY-1992; 92US-0879495.
XX (GETH) GENENTECH INC.
XX Jardieu PM, Presta LG;
XX WPI; 1993-094004/11.
XX Polypeptide(s) binding to specific Fc epsilon receptors - act as
PT IgE antagonists; useful for treating and preventing IgE-mediated
PT disorders e.g. allergies
XX Disclosure; Fig 2; 113pp; English.
XX Antibodies capable of binding FcεL-bound IgE but which are
CC substantially incapable of binding FcεH-bound IgE or inducing
CC histamine release from mast cells or basophils, comprise a human
CC Kabat CDR domain into which has been substituted a positionally
CC analogous residue from a Kabat CDR domain of the murine anti-huIgE

CC antibodies MAE11, MAE13, MAE15 or MAE17.

XX
SQ Sequence 111 AA;

Query Match 96.2%; Score 75; DB 14; Length 111;
Best Local Similarity 93.3%; Pred. No. 1.6e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFDGD SYMN 15
| | | | | : | | | | |
Db 24 kasqsvdydgsymn 38

Search completed: June 28, 2001, 16:14:35
Job time: 1323 sec

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OM protein - protein search, using sw model

Run on: June 28, 2001, 16:01:13 ; Search time 138.34 Seconds
(without alignments)
2.184 Million cell updates/sec

Title: US-09-724-406-12

Perfect score: 78

Sequence: 1 KASQSVDFDGDYSYM 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued_Patents_AA:*
- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
 - 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
 - 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
 - 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
 - 5: /cgn2_6/ptodata/2/iaa/8B_COMB.pep:*
 - 6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75	96.2	15	2	US-08-483-636-16
2	75	96.2	15	2	US-08-483-632-16
3	75	96.2	106	3	US-08-466-151-6
4	75	96.2	111	1	US-08-491-845-8
5	75	96.2	111	1	US-08-491-845-16
6	75	96.2	111	2	US-08-483-636-73
7	75	96.2	111	2	US-08-483-632-73
8	75	96.2	111	2	US-08-887-352B-5
9	75	96.2	111	3	US-08-466-151-2
10	75	96.2	111	4	US-09-109-207C-5
11	75	96.2	115	4	US-08-513-968-51
12	75	96.2	120	1	US-08-111-080-24
13	75	96.2	120	1	US-08-211-980-24
14	75	96.2	120	5	PCT-US93-07967-24
15	75	96.2	131	2	US-08-483-636-14
16	75	96.2	131	2	US-08-483-636-58
17	75	96.2	131	2	US-08-483-632-14
18	75	96.2	131	2	US-08-483-632-58
19	75	96.2	131	4	US-08-579-378A-14
20	75	96.2	131	4	US-08-579-378A-18
21	75	96.2	132	2	US-08-483-636-2
22	75	96.2	132	2	US-08-483-632-2
23	75	96.2	218	5	PCT-US96-13152-2
24	72	92.3	111	2	US-08-887-352B-6
25	72	92.3	111	4	US-09-109-207C-10
26	72	92.3	114	2	US-08-887-352B-10
27	72	92.3	114	4	US-09-109-207C-10

28	72	92.3	218	2	US-08-887-352B-13	Sequence 13, Appl
29	72	92.3	218	3	US-08-466-151-9	Sequence 9, Appl
30	72	92.3	218	4	US-09-109-207C-13	Sequence 13, Appl
31	69	88.5	41	3	US-08-984-277-5	Sequence 5, Appl
32	69	88.5	239	2	US-08-553-497A-18	Sequence 18, Appl
33	68	87.2	114	2	US-08-887-352B-9	Sequence 9, Appl
34	65	83.3	114	2	US-09-109-207C-9	Sequence 9, Appl
35	53	67.9	114	2	US-08-887-352B-8	Sequence 8, Appl
36	53	67.9	218	4	US-08-282-505-1	Sequence 1, Appl
37	53	67.9	218	4	US-05-054-255-1	Sequence 1, Appl
38	50	64.1	114	4	US-09-109-207C-8	Sequence 8, Appl
39	50	64.1	218	2	US-08-887-352B-15	Sequence 15, Appl
40	50	64.1	218	2	US-08-887-352B-17	Sequence 17, Appl
41	50	64.1	218	2	US-08-887-352B-19	Sequence 19, Appl
42	50	64.1	218	2	US-08-887-352B-24	Sequence 24, Appl
43	50	64.1	218	4	US-09-109-207C-15	Sequence 15, Appl
44	50	64.1	218	4	US-09-109-207C-17	Sequence 17, Appl
45	50	64.1	218	4	US-09-109-207C-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-08-483-636-16
; Sequence 16, Application US/08483636
; Patent No. 5914110
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithkline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0539
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,636
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-483-636-16

Query Match 96.2%; Score 75; DB 2; Length 15;
Best Local Similarity 93.3%; Pred. No. 3e-07;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFDGSYMN 15
|||||:|||||
Db 1 KASQSVYDGDYSYN 15

RESULT 2

US-08-483-632-16
; Sequence 16, Application US/08483632
; Patent No. 5928904
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESS: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,632
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-483-632-16

Query Match 96.2%; Score 75; DB 2; Length 15;
Best Local Similarity 93.3%; Pred. No. 3e-07;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFDGSYMN 15
|||||:|||||
Db 1 KASQSVYDGDYSYN 15

RESULT 3

US-08-466-151-6
; Sequence 6, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-466-151-6

Query Match 96.2%; Score 75; DB 3; Length 106;
Best Local Similarity 93.3%; Pred. No. 2.8e-06;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFDGSYMN 15
|||||:|||||
Db 24 KASQSVYDGDYSYN 38

RESULT 4

US-08-491-845-8
; Sequence 8, Application US/08491845
; Patent No. 5773247
; GENERAL INFORMATION:
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: EDA, Yasuyuki
; APPLICANT: SHIOSAKI, Kouichi

```

; APPLICANT: OSATOMI, Kiyoshi
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: RECOMBINANT ANTI-HIV ANTIBODY AND
; TITLE OF INVENTION: PROCESS FOR PREPARING THE SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/491,845
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00039
; FILING DATE: 14-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: MAEDA-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-491-845-8

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```

Query Match 96.2%; Score 75; DB 1; Length 111;
Best Local Similarity 93.3%; Pred. No. 3e-06;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQSVDFDGDGYNN 15
   |||||:|||||
Db 24 KASQSVDFDGDGYNN 38

RESULT 5
US-08-491-845-16
; Sequence 16, Application US/08491845
; Patent No. 5773247
; GENERAL INFORMATION:
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: EDA, Yasuyuki
; APPLICANT: SHIOSAKI, Kouichi
; APPLICANT: OSATOMI, Kiyoshi
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: RECOMBINANT ANTI-HIV ANTIBODY AND
; TITLE OF INVENTION: PROCESS FOR PREPARING THE SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/491,845
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00039
; FILING DATE: 14-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: MAEDA-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-491-845-16

Query Match 96.2%; Score 75; DB 1; Length 111;
Best Local Similarity 93.3%; Pred. No. 3e-06;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQSVDFDGDGYNN 15
   |||||:|||||
Db 24 KASQSVDFDGDGYNN 38

RESULT 6
US-08-483-636-73
; Sequence 73, Application US/08483636
; Patent No. 5914110
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,636
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.

```

REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-483-632-73

Query Match 96.2%; Score 75; DB 2; Length 111;
Best Local Similarity 93.3%; Pred. No. 3e-06;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KASQSVDFDGD SYMN 15
Db 24 KASQSVDFDGD SYMN 38

RESULT 7

US-08-483-632-73
Sequence 73, Application US/08483632
Patent No. 5928904
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESS: Intellectual Property
STREET: P.O. Box 1539 / UW220
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,632
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-483-632-73

Query Match 96.2%; Score 75; DB 2; Length 111;
Best Local Similarity 93.3%; Pred. No. 3e-06;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KASQSVDFDGD SYMN 15
Db 24 KASQSVDFDGD SYMN 38

RESULT 8

US-08-887-352B-5
Sequence 5, Application US/08887352B
Patent No. 5994511
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-887-352B-5

Query Match 96.2%; Score 75; DB 2; Length 111;
Best Local Similarity 93.3%; Pred. No. 3e-06;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KASQSVDFDGD SYMN 15
Db 24 KASQSVDFDGD SYMN 38

RESULT 9
US-08-466-151-2
Sequence 2, Application US/08466151
Patent No. 6037453
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Winpatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/466,151
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/466163
 FILING DATE: 06-JUN-1995
 APPLICATION NUMBER: 08/405617
 FILING DATE: 15-MAR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/185899
 FILING DATE: 26-JAN-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/879495
 FILING DATE: 07-MAY-1992
 APPLICATION NUMBER: 07/744768
 FILING DATE: 14-AUG-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Svoboda, Craig G.
 REGISTRATION NUMBER: 39,044
 REFERENCE/DOCKET INFORMATION: P0718P2C1D1
 TELEPHONE: 650/225-1489
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 111 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-08-466-151-2

Query Match 96.2%; Score 75; DB 3; Length 111;
 Best Local Similarity 93.3%; Pred. No. 3e-06;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFDGD SYNM 15
 DB 24 KASQSVDFDGD SYNM 38

RESULT 10
 US-09-109-207C-5
 ; Sequence 5, Application US/09109207C
 ; Patent No. 6172213
 ; GENERAL INFORMATION:
 ; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
 ; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
 ; FILE REFERENCE: P1123R1
 ; CURRENT APPLICATION NUMBER: US/09/109,207C
 ; PRIOR FILING DATE: 1998-06-30
 ; PRIOR APPLICATION NUMBER: US 60/051,554
 ; PRIOR FILING DATE: 1997-07-03
 ; NUMBER OF SEQ ID NOS: 44
 ; SEQ ID NO 5
 ; LENGTH: 111
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-109-207C-5

Query Match 96.2%; Score 75; DB 4; Length 111;
 Best Local Similarity 93.3%; Pred. No. 3e-06;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFDGD SYNM 15
 DB 24 KASQSVDFDGD SYNM 38

RESULT 11
 US-08-513-968-51
 ; Sequence 51, Application US/08513968
 ; Patent No. 6114143
 ; GENERAL INFORMATION:
 ; APPLICANT: EDA, Yasuyuki.
 ; APPLICANT: MAEDA, Hiroaki
 ; APPLICANT: MAKIZUMI, Keiichi
 ; APPLICANT: SHIOSAKI, Kouichi
 ; APPLICANT: OSATOMI, Kiyoshi
 ; APPLICANT: KIMACHI, Kazuhiko
 ; APPLICANT: HIGUCHI, Hiroyumi
 ; APPLICANT: TOKIYOSHI, Sachio
 ; TITLE OF INVENTION: ANTI-HIV MONOCLONAL ANTIBODY
 ; NUMBER OF SEQUENCES: 86
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BROWDY AND NEIMARK
 ; STREET: 419 Seventh Street, N.W., Suite 300
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/513,968
 ; FILING DATE: 11-SEP-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 78913/1993
 ; FILING DATE: 11-MAR-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BROWDY, Roger L.
 ; REGISTRATION NUMBER: 25,618
 ; REFERENCE/DOCKET NUMBER: EDA=1
 ; TELEPHONE: 202-628-5197
 ; TELEFAX: 202-737-3528
 ; TELEX: 248633
 ; INFORMATION FOR SEQ ID NO: 51:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 115 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-513-968-51

Query Match 96.2%; Score 75; DB 4; Length 115;
 Best Local Similarity 93.3%; Pred. No. 3.1e-06;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFDGD SYNM 15
 DB 28 KASQSVDFDGD SYNM 42

RESULT 12
 US-08-111-080-24
 ; Sequence 24, Application 08/111080
 ; Patent No. 5538865

Fri Jun 29 08:04:22 2001

us-09-724-406-12.ra1

GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
TITLE OF INVENTION: HIV Immunotherapeutics
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/111.080
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/748,562
FILING DATE: 22-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07111
FILING DATE: 24-AUG-1992
APPLICATION DATA:
APPLICATION NUMBER: US 08/039,457
FILING DATE: 22-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 31629
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-111-080-24

Query Match 96.2%; Score 75; DB 1; Length 120;
Best Local Similarity 93.3%; Pred. No. 3.3e-06;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFDGSYMN 15
|||||:|||||
Db 24 KASQSVDFDGSYMN 38

RESULT 13
US-08-211-980-24
Sequence 24, Application US/08211980
Patent No. 5665569
GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
TITLE OF INVENTION: HIV Immunotherapeutics
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,980
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07111
FILING DATE: 24-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,457
FILING DATE: 22-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 31629
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-211-980-24

Query Match 96.2%; Score 75; DB 1; Length 120;
Best Local Similarity 93.3%; Pred. No. 3.3e-06;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFDGSYMN 15
|||||:|||||
Db 24 KASQSVDFDGSYMN 38

RESULT 14
PCT-US93-07967-24
Sequence 24, Application PC/TUS9307967
GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
TITLE OF INVENTION: HIV Immunotherapeutics
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07967
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07111
FILING DATE: 24-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,457
FILING DATE: 22-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447

REFERENCE/DOCKET NUMBER: 31629
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-07967-24

Query Match 96.2%; Score 75; DB 5; Length 120;
Best Local Similarity 93.3%; Pred. No. 3.3e-06;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFDGD SYMN 15
|||||:|||||
DB 24 KASQSVDYDGD SYMN 38

RESULT 15
US-08-483-636-14
Sequence 14, Application US/08483636
Patent No. 5914110
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESSEE: Intellectual Property
STREET: P.O. Box 1539 / UW2220
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,636
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-483-636-14

Query Match 96.2%; Score 75; DB 2; Length 131;
Best Local Similarity 93.3%; Pred. No. 3.6e-06;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KASQSVDFDGD SYMN 15
|||||:|||||
DB 43 KASQSVDYDGD SYMN 57

Search completed: June 28, 2001, 16:01:14
Job time: 522 sec

Matches 14; Conservative 1; Mismatches 0

QY 1 KASQSVDFDGD SYNM 15
 DB 5 KASQSVDFDGD SYNM 19

RESULT 3

KVMS43
 Ig kappa chain V region (PC7043) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 21-Jan-2000
 C:Accession: A01937; S42187; S42194; S42190; S42189; S42188; S42191; S42192
 R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
 Nature 276, 785-790, 1978
 A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
 A:Reference number: A93204; MUID:79073152
 A:Accession: A01937
 A:Molecule type: protein
 A:Residues: 1-111 <WEI>
 R:Mo, J.A.; Bona, C.A.; Holmdahl, R.
 Eur. J. Immunol. 23, 2503-2510, 1993
 A:Title: Variable region gene selection of immunoglobulin G-expressing B cells with spec
 A:Reference number: S42187; MUID:94009207
 A:Accession: S42187
 A:Molecule type: DNA
 A:Residues: 10-99 <MO>
 A:Cross-references: EMBL:225444; NID:9407832; PIDN:CAA80931.1; PID:9407833
 A:Note: V-kappa-21E; anti-collagen
 A:Accession: S42194
 A:Molecule type: DNA
 A:Residues: 12-99 <MO>
 A:Cross-references: EMBL:225458; NID:9407844; PIDN:CAA80945.1; PID:9407845
 A:Note: V-kappa-21E; anti-collagen
 A:Accession: S42190
 A:Molecule type: DNA
 A:Residues: 13-99 <MO>
 A:Cross-references: EMBL:225450; NID:9407838; PIDN:CAA80937.1; PID:9407839
 A:Note: V-kappa-21E; anti-collagen
 A:Accession: S42189
 A:Molecule type: DNA
 A:Residues: 15-99 <MO>
 A:Cross-references: EMBL:225448; NID:9407836; PIDN:CAA80935.1; PID:9407837
 A:Note: V-kappa-21E; anti-collagen
 A:Accession: S42188
 A:Molecule type: DNA
 A:Residues: 12-99 <MO>
 A:Cross-references: EMBL:225446; NID:9407834; PIDN:CAA80933.1; PID:9407835
 A:Note: V-kappa-21E; anti-collagen
 A:Accession: S42191
 A:Molecule type: DNA
 A:Residues: 10-99 <MO>
 A:Cross-references: EMBL:225452; NID:9407840; PIDN:CAA80939.1; PID:9407841
 A:Note: V-kappa-21E; anti-collagen
 A:Accession: S42192
 A:Molecule type: DNA
 A:Residues: 10-99 <MO>
 A:Cross-references: EMBL:225454; NID:9407842; PIDN:CAA80941.1; PID:9407843
 A:Note: V-kappa-21E; anti-collagen
 A:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
 hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-94/Domain: immunoglobulin homology <IMM>
 F:23-92/Disulfide bonds: #status predicted

Query Match 96.2%; Score 75; DB 1; Length 111;
 Best Local Similarity 93.3%; Pred. No. 1.1e-05;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFDGD SYNM 15
 DB 24 KASQSVDFDGD SYNM 38

RESULT 4

KVMS83
 Ig kappa chain V region (PC7183) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
 C:Accession: B01937; A01937
 R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
 Nature 276, 785-790, 1978
 A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
 A:Reference number: A93204; MUID:79073152
 A:Accession: B01937
 A:Molecule type: protein
 A:Residues: 1-111 <WEI>
 A:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (I
 hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-94/Domain: immunoglobulin homology <IMM>
 F:23-92/Disulfide bonds: #status predicted

Query Match 96.2%; Score 75; DB 1; Length 111;
 Best Local Similarity 93.3%; Pred. No. 1.1e-05;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFDGD SYNM 15
 DB 24 KASQSVDFDGD SYNM 38

RESULT 5

KVMS08
 Ig kappa chain V region (PC6308) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
 C:Accession: C01937; A01937
 R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
 Nature 276, 785-790, 1978
 A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
 A:Reference number: A93204; MUID:79073152
 A:Accession: C01937
 A:Molecule type: protein
 A:Residues: 1-111 <WEI>
 A:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (I
 hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-94/Domain: immunoglobulin homology <IMM>
 F:23-92/Disulfide bonds: #status predicted

Query Match 96.2%; Score 75; DB 1; Length 111;
 Best Local Similarity 93.3%; Pred. No. 1.1e-05;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFDGD SYNM 15
 DB 24 KASQSVDFDGD SYNM 38

RESULT 6

KVMS69
 Ig kappa chain V region (PC7769) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
 C:Accession: E01937; A01937
 R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
 Nature 276, 785-790, 1978
 A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
 A:Reference number: A93204; MUID:79073152
 A:Accession: E01937
 A:Molecule type: protein

A:Residues: 1-111 <WEI>

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes. C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match 96.2%; Score 75; DB 1; Length 111;
Best Local Similarity 93.3%; Pred. No. 1.1e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFDGD SYNN 15
|||||:|||||
DB 24 KASQSVDFDGD SYNN 38

RESULT 7

KVMS10

Ig kappa chain V region (PC7210) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
C:Accession: D01937; A01937
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152
A:Accession: D01937

A:Molecule type: protein
A:Residues: 1-110 <WEI>
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes. C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match 92.3%; Score 72; DB 1; Length 110;
Best Local Similarity 86.7%; Pred. No. 3.6e-05;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFDGD SYNN 15
|||||:|||||
DB 24 KASQSLDYDGD SYNN 38

RESULT 8

SI9971

Ig kappa chain V region (CD4 mAb clone M-T310 and others) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: SI9971; SI9973
R:Weissenhorn, W.; Rietmueller, G.; Weiss, E.M.; Rieber, E.P.
Submitted to the EMBL Data Library, March 1992
A:Description: Structural characterization of CD4 mAb.
A:Reference number: SI9963
A:Accession: SI9971

A:Molecule type: mRNA
A:Residues: 1-112 <WEI>
A:Cross-references: EMBL:X65091; NID:g52288; PIDN:CAA46219.1; PID:g52289
A:Experimental source: clone M-T310
A:Accession: SI9973

A:Molecule type: mRNA

A:Residues: 1-112 <WEW>
A:Cross-references: EMBL:X65092; NID:g52292; PIDN:CAA46220.1; PID:g52293
A:Experimental source: M-T404
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 92.3%; Score 72; DB 2; Length 112;
Best Local Similarity 86.7%; Pred. No. 3.7e-05;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFDGD SYNN 15
|||||:|||||
DB 24 KASQSLDYDGD SYNN 38

RESULT 9

PHI226

Ig kappa chain precursor V region (M-T310) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jan-2000
C:Accession: PHI226
R:Weissenhorn, W.; Scheuer, W.; Kaluza, B.; Schwirzke, M.; Reiter, C.; Flieger, D.; L. Gene 121, 271-278, 1992
A:Title: Combinatorial functions of two chimeric antibodies directed to human CD4 and A:Reference number: PHI224; MUID:93077041
A:Accession: PHI226

A:Molecule type: mRNA
A:Residues: 1-131 <WEI>
A:Cross-references: GB:S50265; NID:g260765; PIDN:AAB24320.1; PID:g260766
A:Note: this mouse sequence was hybridized and fused with a human constant region gene C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-131/Product: Ig light chain V region #status predicted <MAT>
F:36-114/Domain: immunoglobulin homology <IMM>

Query Match 92.3%; Score 72; DB 2; Length 131;
Best Local Similarity 86.7%; Pred. No. 4.3e-05;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFDGD SYNN 15
|||||:|||||
DB 44 KASQSLDYDGD SYNN 58

RESULT 10

S09966

Ig kappa chain V-J region (1E10) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 21-Jan-2000
C:Accession: S09966
R:Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jatou, J.C.; Izui, S. Eur. J. Immunol. 20, 771-777, 1990
A:Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibody A:Reference number: S09955; MUID:90269328

A:Accession: S09966
A:Molecule type: mRNA
A:Residues: 1-111 <REI>
A:Cross-references: EMBL:X51854; NID:g55397; PIDN:CAA36147.1; PID:g930231
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 88.5%; Score 69; DB 2; Length 111;
Best Local Similarity 86.7%; Pred. No. 0.00012;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSVDFDGD SYNN 15
|||||:|||||
DB 24 KASQSLDYDGD SYNN 38

RESULT 11

KVMSCI

Ig kappa chain V region (CBPC 101) - mouse (tentative sequence)
C:Species: Mus musculus (house mouse)
C:Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 31-Mar-2000

C:Accession: A01936
R:McKean, D.J.; Bell, M.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978
A:Title: Mechanisms of antibody diversity: multiple genes encode structurally related molecules
A:Reference number: A93822; MUID:79012520
A:Accession: A01936
A:Molecule type: protein
A:Residues: 1-111 <MCK>
C:Comment: This chain was isolated from a myeloma protein.
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match 82.18; Score 64; DB 1; Length 111;
Best Local Similarity 80.0%; Pred. No. 0.00082;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSVDFDGSYMN 15
DB 24 KASQSVDFDGSYMN 38
|||||:|:|||||

RESULT 12
SI9976
Ig kappa chain V region (M-T413) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: SI9976
R:Weissenhorn, W.; Riettmueller, G.; Weiss, E.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A:Description: Structural characterization of CD4 mAb.
A:Reference number: SI9963
A:Accession: SI9976
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-112 <WEI>
A:Cross-references: EMBL:X65093; NID:g52298; PIDN:CAAA6221.1; PID:g52299
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 78.28; Score 61; DB 2; Length 112;
Best Local Similarity 73.3%; Pred. No. 0.0026;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSVDFDGSYMN 15
DB 24 KASQSLDYDADSYMH 38
|||||:|:|||||

RESULT 13
SI9972
Ig kappa chain V region (M-T321) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: SI9972
R:Weissenhorn, W.; Riettmueller, G.; Weiss, E.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A:Description: Structural characterization of CD4 mAb.
A:Reference number: SI9963
A:Accession: SI9972
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-112 <WEI>
A:Cross-references: EMBL:X65094; NID:g52290; PIDN:CAAA6222.1; PID:g52291
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>

C:Accession: A01936
R:McKean, D.J.; Bell, M.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978
A:Title: Mechanisms of antibody diversity: multiple genes encode structurally related molecules
A:Reference number: A93822; MUID:79012520
A:Accession: A01936
A:Molecule type: protein
A:Residues: 1-111 <MCK>
C:Comment: This chain was isolated from a myeloma protein.
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match 82.18; Score 64; DB 1; Length 111;
Best Local Similarity 80.0%; Pred. No. 0.00082;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSVDFDGSYMN 15
DB 24 KASQSVDFDGSYMN 38
|||||:|:|||||

RESULT 12
SI9976
Ig kappa chain V region (M-T413) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: SI9976
R:Weissenhorn, W.; Riettmueller, G.; Weiss, E.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A:Description: Structural characterization of CD4 mAb.
A:Reference number: SI9963
A:Accession: SI9976
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-112 <WEI>
A:Cross-references: EMBL:X65093; NID:g52298; PIDN:CAAA6221.1; PID:g52299
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 78.28; Score 61; DB 2; Length 112;
Best Local Similarity 73.3%; Pred. No. 0.0026;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSVDFDGSYMN 15
DB 24 KASQSLDYDADSYMH 38
|||||:|:|||||

RESULT 13
SI9972
Ig kappa chain V region (M-T321) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: SI9972
R:Weissenhorn, W.; Riettmueller, G.; Weiss, E.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A:Description: Structural characterization of CD4 mAb.
A:Reference number: SI9963
A:Accession: SI9972
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-112 <WEI>
A:Cross-references: EMBL:X65094; NID:g52290; PIDN:CAAA6222.1; PID:g52291
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 60.3%; Score 47; DB 2; Length 112;
Best Local Similarity 60.0%; Pred. No. 0.62;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 KASQSVDFDGSYMN 15
DB 24 RASQSVDYNAISYMH 38
:|||||:|:|

RESULT 14
B49442
Ig light chain V region (50.1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C:Accession: B49442
R:Stura, E.A.; Stanfield, R.L.; Fieser, G.G.; Silver, S.; Roguska, M.; Hincapié, L.M.
Proteins 14, 499-508, 1992
A:Title: Crystallization, sequence, and preliminary crystallographic data for an anti
A:Reference number: A49442; MUID:93066166
A:Accession: B49442
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-96 <STU>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:8-86/Domain: immunoglobulin homology <IMM>

Query Match 59.0%; Score 46; DB 2; Length 96;
Best Local Similarity 53.3%; Pred. No. 0.77;
Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSVDFDGSYMN 15
DB 16 RASESVDDGNSFLH 30
:|||||:|:|

RESULT 15
PH0093
Ig kappa chain V region (anti-cyclosporin E) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 21-Jan-2000
C:Accession: PH0093
R:Schmitter, D.; Poch, O.; Zeder, G.; Heinrich, G.F.; Koehler, H.P.; Quesniaux, V.F.J.
Mol. Immunol. 27, 1029-1038, 1990
A:Title: Analysis of the structural diversity of monoclonal antibodies to cyclosporin
A:Reference number: PH0087; MUID:91042649
A:Accession: PH0093
A:Molecule type: mRNA
A:Residues: 1-109 <SCH>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>
F:24-38/Region: complementarity-determining 1
F:54-60/Region: complementarity-determining 2
F:93-101/Region: complementarity-determining 3

Query Match 56.4%; Score 44; DB 2; Length 109;
Best Local Similarity 60.0%; Pred. No. 1.9;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 KASQSVDFDGSYMN 15
DB 24 RASESVDNSGFSFMN 38
:|||||:|:|

Search completed: June 28, 2001, 15:58:43
Job time: 371 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2001, 15:54:35 ; Search time 105.36 Seconds
(without alignments)
4.877 Million cell updates/sec

Title: US-09-724-406-12
Perfect score: 78
Sequence: 1 KASQSVDFDGSYMN 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	75	96.2	111	1	KV3M_MOUSE
2	75	96.2	111	1	KV3N_MOUSE
3	75	96.2	111	1	KV3O_MOUSE
4	75	96.2	111	1	KV3Q_MOUSE
5	72	92.3	110	1	KV3P_MOUSE
6	64	82.1	111	1	KV3L_MOUSE
7	44	56.4	111	1	KV3C_MOUSE
8	41	52.6	108	1	KV3V_MOUSE
9	41	52.6	111	1	KV3A_MOUSE
10	41	52.6	111	1	KV3H_MOUSE
11	41	52.6	111	1	KV3J_MOUSE
12	41	52.6	111	1	KV3K_MOUSE
13	41	52.6	112	1	KV3B_MOUSE
14	41	52.6	131	1	KV3I_MOUSE
15	40.5	51.9	350	1	Y4RM_RHLSN
16	40	51.3	1286	1	RPO1_VACC
17	40	51.3	1286	1	RPO1_VARY
18	40	51.3	1287	1	RPO1_VACCV
19	39	50.0	112	1	KV3G_MOUSE
20	39	50.0	559	1	KIF2_XENLA
21	39	50.0	749	1	PCRA_LEUCI
22	39	50.0	823	1	SCH9_YEAST
23	39	50.0	1173	1	TSP1_XENLA
24	38	48.7	348	1	CAPG_HUMAN
25	38	48.7	361	1	MLTB_ECOLI
26	38	48.7	405	1	PRSB_YEAST
27	38	48.7	409	1	THIL_PANTH
28	38	48.7	955	1	VP2_BT117
29	38	48.7	956	1	VP2_BT111
30	37	47.4	111	1	KV3R_MOUSE
31	37	47.4	111	1	KV3S_MOUSE
32	37	47.4	111	1	KV3U_MOUSE
33	37	47.4	123	1	Y131_CABEL

34 37 47.4 148 1 CALL_DROME
35 37 47.4 243 1 LPSB_LYTP1
36 37 47.4 321 1 LPSA_LYTP1
37 37 47.4 340 1 PURA_METTH
38 37 47.4 377 1 AMSH_ERWAM
39 37 47.4 459 1 CCMH_HAETN
40 37 47.4 465 1 TRAZ2_STRPN
41 37 47.4 692 1 Y650_METJA
42 37 47.4 1170 1 TSP2_BOVIN
43 37 47.4 1172 1 TSP2_HUMAN
44 37 47.4 1172 1 TSP2_MOUSE
45 37 47.4 1178 1 TSP2_CHICK

ALIGNMENTS

RESULT 1
KV3M_MOUSE
ID KV3M_MOUSE STANDARD; PRT; 111 AA.
AC P01665;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 7043.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RA MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gattaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR PIR: A01937; KVM543.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin v region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12002 MW; 7A5FCB586C306D29 CRC64;

Query Match 96.2%; Score 75; DB 1; Length 111;
Best Local Similarity 93.3%; Pred. No. 2.9e-06;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFDGSYMN 15
Db 24 KASQSVDFDGSYMN 38

RESULT 2
KV3N_MOUSE
ID KV3N_MOUSE STANDARD; PRT; 111 AA.
AC P01666;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 7183.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

1 KASQSVDFGDSYMN 15

FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 61 92 FRAMEWORK 3.
 FT DOMAIN 93 100 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 101 110 FRAMEWORK 4.
 FT DISULFID 23 92 BY SIMILARITY.
 FT NON_TER 110 110
 SQ SEQUENCE 110 AA; 11950 MW; 69FJA5CB86B1249 CRC64;

Query Match 92.3%; Score 72; DB 1; Length 110;
 Best Local Similarity 86.7%; Pred. No. 9.5e-06;
 Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDFDGDSDYNN 15
 |||||:|||||
 DB 24 KASQSLDYDGDSDYNN 38

RESULT 6

KV3L_MOUSE STANDARD; PRT; 111 AA.
 AC P01664;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION CBPC 101.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79012520; PubMed=99744;
 RA McKean D.J., Bell M., Potter M.;
 RT "Mechanisms of antibody diversity: multiple genes encode structurally
 related mouse kappa variable regions.";
 RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
 DR PIR: A01936; KVMSC1.
 DR InterPro: IPR003006; -.
 DR Pfam: PF00047; Ig; 1.
 DR Immunoglobulin V region.
 KW DOMAIN 1 23
 FT DOMAIN 24 38 FRAMEWORK 1.
 FT DOMAIN 39 53 FRAMEWORK 2.
 FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 61 92 FRAMEWORK 3.
 FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 102 111 FRAMEWORK 4.
 FT DISULFID 23 92 BY SIMILARITY.
 FT NON_TER 111 111
 SQ SEQUENCE 111 AA; 11964 MW; E2BIAD98AD965962 CRC64;

Query Match 82.1%; Score 64; DB 1; Length 111;
 Best Local Similarity 80.0%; Pred. No. 0.00023;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSVDFDGDSDYNN 15
 |||||:|||||
 DB 24 KASQSLDYDGDSDYNN 38

RESULT 7

KV3C_MOUSE STANDARD; PRT; 111 AA.
 AC P01656;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION MOPC 70.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=67056897; PubMed=4162931;
 RA Gray W.R., Dreyer W.J., Hood L.E.;
 RT "Mechanism of antibody synthesis: size differences between mouse
 kappa chains.";
 RL Science 155:465-467(1967).
 CC -1- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.
 DR PIR: A01930; KVM880.
 DR InterPro: IPR003006; -.
 DR Pfam: PF00047; Ig; 1.
 DR Immunoglobulin V region; Bence-Jones protein.
 KW DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 39 53 FRAMEWORK 2.
 FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 61 92 FRAMEWORK 3.
 FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 102 111 FRAMEWORK 4.
 FT DISULFID 23 92 BY SIMILARITY.
 FT NON_TER 111 111
 SQ SEQUENCE 111 AA; 11904 MW; 4FE7ABC9DF0FC125 CRC64;

Query Match 56.4%; Score 44; DB 1; Length 111;
 Best Local Similarity 60.0%; Pred. No. 0.65;
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 KASQSVDFDGDSDYNN 15
 |||||:|||||
 DB 24 RASEVDNDSGISPMN 38

RESULT 8

KV3V_MOUSE STANDARD; PRT; 108 AA.
 ID KV3V_MOUSE
 AC P01674;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION PC 2154.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gatmaitan L., Ioh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 diversity.";
 RL Nature 276:785-790(1978).
 DR PIR: A01940; KVM854.
 DR InterPro: IPR003006; -.
 DR Pfam: PF00047; Ig; 1.
 DR Immunoglobulin V region.
 KW DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 39 53 FRAMEWORK 2.
 FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 61 92 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 102 108 FRAMEWORK 4.
 FT DISULFID 23 92 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11699 MW; D4092D1D8DAC4B9E CRC64;

Query Match 52.6%; Score 41; DB 1; Length 108;
 Best Local Similarity 60.0%; Pred. No. 2.1;
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 KASQSVDFDGSYMN 15
:||||| I |||:

Db 24 RASQSVSTSGYSYMH 38

RESULT 9

KV3A_MOUSE STANDARD; PRT; 111 AA.
ID KV3A_MOUSE
AC P01654;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 2880/PC 1229.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.

RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
CC -I- MISCELLANEOUS: THE PC 2880 AND PC 1229 SEQUENCES ARE IDENTICAL.
DR PIR: A01930; KVM80.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11980 MW; AFEAC6A9D26FC12D CRC64;

Query Match 52.6%; Score 41; DB 1; Length 111;
Best Local Similarity 60.0%; Pred. No. 2.1;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 KASQSVDFDGSYMN 15
:||||| I |||:

Db 24 RASESVDNYSYFMN 38

RESULT 10

KV3H_MOUSE STANDARD; PRT; 111 AA.
ID KV3H_MOUSE
AC P01660;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 3741/TEPC 111.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (PC 3741).
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
RN [2]
RP SEQUENCE (TEPC 111).
RX MEDLINE=79012520; PubMed=99744;

tc

RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
CC -I- MISCELLANEOUS: THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL.
DR PIR: A01934; KVM837.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12099 MW; EC46C9D259213BE4 CRC64;

Query Match 52.6%; Score 41; DB 1; Length 111;
Best Local Similarity 53.3%; Pred. No. 2.1;
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 KASQSVDFDGSYMN 15
:||||| I |||:

Db 24 RASESVDSYGNSEFMH 38

RESULT 11

KV3J_MOUSE STANDARD; PRT; 111 AA.
ID KV3J_MOUSE
AC P01662;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION ABPC 22/PC 9245.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (ABPC 22).
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
RN [2]
RP SEQUENCE (PC 9245).

RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).

CC -I- MISCELLANEOUS: THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.
DR PIR: A01935; KVM86.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12041 MW; D7DF0609303453CE CRC64;

Query Match 52.6%; Score 41; DB 1; Length 111;
 Best Local Similarity 53.3%; Pred. No. 2.1;
 Matches 8; Conservative 5; Mismatches 0; Gaps 0;

QY 1 KASQSVDFDGSYMN 15
 :||:|||| |:||:
 Db 24 RASESVDSYGNFSMH 38

RESULT 12

KV3K_MOUSE STANDARD; PRT; 111 AA.
 AC P01663;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION PC 4050.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.

RA MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 RT diversity.";
 RL Nature 276:785-790(1978).

DR PIR: A01935; KVM5M6.
 DR InterPro: IPR003006; -.
 DR Pfam: PF00047; Ig 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT DOMAIN 102 111
 FT DISULFID 23 92
 FT NON_TER 111 111
 SQ SEQUENCE 111 AA; 12005 MW; 39D87619313453CB CRC64;

Query Match 52.6%; Score 41; DB 1; Length 111;
 Best Local Similarity 53.3%; Pred. No. 2.1;
 Matches 8; Conservative 5; Mismatches 0; Gaps 0;

QY 1 KASQSVDFDGSYMN 15
 :||:|||| |:||:
 Db 24 RASESVDSYGNFSMH 38

RESULT 13

KV3B_MOUSE STANDARD; PRT; 112 AA.
 AC P01655;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION PC 7132.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.

RA MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 RT diversity.";
 RL Nature 276:785-790(1978).
 DR PIR: A01930; KVM580.

DR InterPro: IPR003006; -.
 DR Pfam: PF00047; Ig 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 102
 FT DOMAIN 103 112
 FT DISULFID 23 92
 FT NON_TER 112 112
 SQ SEQUENCE 112 AA; 12054 MW; 5F0DD25EE20BE611 CRC64;

FRAMEWORK 1.
 COMPLEMENTARITY-DETERMINING 1.
 FRAMEWORK 2.
 COMPLEMENTARITY-DETERMINING 2.
 FRAMEWORK 3.
 COMPLEMENTARITY-DETERMINING 3.
 FRAMEWORK 4.
 BY SIMILARITY.

Query Match 52.6%; Score 41; DB 1; Length 112;
 Best Local Similarity 60.0%; Pred. No. 2.2;
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 KASQSVDFDGSYMN 15
 :||:|||| |:||:
 Db 24 RASESVDSYGNFSMH 38

RESULT 14

KV3L_MOUSE STANDARD; PRT; 131 AA.
 AC P01661;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION MOPC 63 PRECURSOR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE OF 1-35.
 RA MEDLINE=78235887; PubMed=98179;
 RA Burstein Y., Schechter I.;
 RT "Primary structures of N-terminal extra peptide segments linked to
 RT the variable and constant regions of immunoglobulin light chain
 RT precursors: implications on the organization and controlled
 RT expression of immunoglobulin genes.";
 RL Biochemistry 17:2392-2400(1978).
 RN [2]
 RP SEQUENCE OF 21-131.
 RX MEDLINE=73140225; PubMed=4691517;
 RA McKean D.J., Potter M., Hood L.E.;
 RT "Mouse immunoglobulin chains. Pattern of sequence variation among
 RT kappa chains with limited sequence differences.";
 RL Biochemistry 12:760-771(1973).
 RN [3]
 RP REVISIONS.

RX MEDLINE=79012520; PubMed=99744;
 RA McKean D.J., Bell M., Potter M.;
 RT "Mechanisms of antibody diversity: multiple genes encode structurally
 RT related mouse kappa variable regions.";
 RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
 DR PIR: A01935; KVM5M6.
 DR InterPro: IPR003006; -.
 DR Pfam: PF00047; Ig 1.
 KW Immunoglobulin V region; Signal.

FT CHAIN 1 20
 FT CHAIN 21 131
 FT DOMAIN 21 43
 FT DOMAIN 44 58
 FT DOMAIN 59 73
 FT DOMAIN 74 80
 FT DOMAIN 81 112
 FT DOMAIN 113 121
 FT DOMAIN 122 131
 FT DISULFID 43 112
 IG KAPPA CHAIN V-III REGION MOPC 63.
 FRAMEWORK 1.
 COMPLEMENTARITY-DETERMINING 1.
 FRAMEWORK 2.
 COMPLEMENTARITY-DETERMINING 2.
 FRAMEWORK 3.
 COMPLEMENTARITY-DETERMINING 3.
 FRAMEWORK 4.
 BY SIMILARITY.

Search completed: June 28, 2001, 15:54:35
Job time: 123 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2001, 16:08:20 ; Search time 411.58 Seconds
(without alignments)
4.822 Million cell updates/sec

Title: us-09-724-406-12

Perfect score: 78

Sequence: 1 KASQSVDFDGDSDYMN 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_16:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_unclassified:*
- 13: sp_vertebrate:*
- 14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	56.4	336	2 Q9X6V5	Q9X6V5 pseudomonas
2	44	56.4	340	2 Q9HX24	Q9HX24 pseudomonas
3	44	56.4	542	5 Q9NJD9	Q9NJD9 onchocerca
4	44	56.4	1868	10 Q9LVX3	Q9LVX3 arabisopsis
5	43	55.1	303	2 Q9KA25	Q9KA25 bacillus ha
6	43	55.1	2439	5 Q9VMS2	Q9VMS2 drosophila
7	41	52.6	264	2 Q9HXK0	Q9HXK0 pseudomonas
8	41	52.6	294	2 Q9X155	Q9X155 streptomyces
9	41	52.6	400	2 Q9Z4A1	Q9Z4A1 escherichia
10	41	52.6	400	2 Q9R2H5	Q9R2H5 salmonella
11	41	52.6	972	10 Q9ZW06	Q9ZW06 arabisopsis
12	40	51.3	131	10 Q9SRP5	Q9SRP5 arabisopsis
13	40	51.3	137	10 Q9SP4	Q9SP4 arabisopsis
14	40	51.3	171	10 Q9M7R0	Q9M7R0 olea europaea
15	40	51.3	171	10 Q9M7Q9	Q9M7Q9 olea europaea
16	40	51.3	311	2 Q86071	Q86071 pseudomonas
17	40	51.3	356	5 Q9NF90	Q9NF90 leishmania
18	40	51.3	985	14 Q9JFB4	Q9JFB4 vaccinia vi
19	40	51.3	1285	14 Q9QBB0	Q9QBB0 yaba monkey

20	40	51.3	1285	14	Q9DHP2
21	40	51.3	1286	14	O57204
22	40	51.3	1286	14	Q9QNI9
23	40	51.3	1286	14	Q9Q903
24	40	51.3	1286	14	Q9Q8N2
25	40	51.3	1287	14	Q9J593
26	40	51.3	1289	14	Q85289
27	40	51.3	1289	14	Q98246
28	39	50.0	137	11	P97596
29	39	50.0	186	5	Q9W210
30	39	50.0	262	5	Q05432
31	39	50.0	313	13	Q9YHF0
32	39	50.0	336	2	O69589
33	39	50.0	336	2	P96253
34	39	50.0	367	2	O9HVX3
35	39	50.0	379	10	Q9M7R4
36	39	50.0	458	5	P91079
37	39	50.0	551	10	P93370
38	39	50.0	609	4	Q9H2V9
39	39	50.0	1024	5	Q9VM97
40	38	48.7	522	3	O59740
41	38	48.7	761	2	Q9F7S9
42	38	48.7	896	10	Q9FV30
43	38	48.7	896	10	Q9FV29
44	38	48.7	900	5	O44838
45	38	48.7	907	10	Q9SS78

ALIGNMENTS

RESULT 1

Q9X6V5
ID Q9X6V5 PRELIMINARY; PRT; 336 AA.
AC Q9X6V5
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE MEMBRANE-BOUND LYCIC TRANSGLYCOSYLASE PRECURSOR.
GN MTB.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PA01;
RA Gagnon L.A., Castro-Urbina I.M., Liao X., Hancock R.E.W., Clarke A.J.,
RA Huletsky A.;
RT "Cloning and characterization of PBP5 of Pseudomonas aeruginosa."
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF147448; AAD32232.1;
DR HSSP; P41052; 1LTM.
KW Signal.
FT SIGNAL 1 29 POTENTIAL.
FT SIGNAL 336 336 POTENTIAL.
SQ SEQUENCE 336 AA; 37423 MW; 1DAFBE8991787BBE CRC64;

Query Match 56.4%; Score 44; DB 2; Length 336;
Best Local Similarity 63.6%; Pred No. 12;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 SVDFDGDSDYMN 15

Db 204 AVDFDGDGHIN 214

RESULT 2

Q9HX24
ID Q9HX24 PRELIMINARY; PRT; 340 AA.
AC Q9HX24
DT 01-MAR-2001 (TReMBLrel. 16, Created)

DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
 DE MEMBRANE-BOUND LYTC TRANSGLYCOSYLASE.
 GN MLT2 OR PA4001.
 OS Pseudomonas aeruginosa.
 OS Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=287;
 [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=PA01;
 RC MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-O.T., Erwin A.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Coltray L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Salier M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 RT opportunistic pathogen";
 RL Nature 406:959-964(2000).
 DR EMBL; AE004817; AAG07388.1; -- 7A00BD23A0695BD8 CRC64;
 SQ SEQUENCE 340 AA; 37867 MW; 7A00BD23A0695BD8 CRC64;

Query Match 56.4%; Score 44; DB 2; Length 340;
 Best Local Similarity 63.6%; Pred. No. 13;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 SVDFDGDGYM 15
 :|||||:
 Db 208 AVDFDGDGHIN 218

RESULT 3
 ID Q9NJD9 PRELIMINARY; PRT; 542 AA.
 AC Q9NJD9;
 DT 01-OCT-2000 (TRENBLrel. 15, Created)
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
 DE CALCIUM-BINDING PROTEIN CBP-1.
 GN CBP-1.
 OS Onchocerca volvulus.
 OS Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
 OC Onchocercidae; Onchocerca.
 OX NCBI_TaxID=6282;
 [1]
 RN SEQUENCE FROM N.A.
 RC MEDLINE=2078137; PubMed=10816503;
 RA Lizotte-Waniewski M., Tawe W., Guiliano D.B., Lu W., Liu J.,
 RA Williams S.A., Lustigman S.;
 RT "Identification of potential vaccine and drug target candidates by
 RT expressed sequence tag analysis and immunoscreening of Onchocerca
 RT volvulus larval cDNA libraries";
 RL Infect. Immun. 68:3491-3501(2000).
 CC -1- SIMILARITY: TO EF-HAND FAMILY.
 DR EMBL; AF153720; AAF64251.1; --
 DR InterPro: IPR002048; --
 DR Pfam: PF00036; ehand; 10.
 DR PROSITE; PS00018; EF-HAND; UNKNOWN_7.
 DR SMART; SM00054; EFH; 1.
 KW Calcium-binding.
 SQ SEQUENCE 542 AA; 61269 MW; 94E3D57FB7D805B CRC64;

Query Match 56.4%; Score 44; DB 5; Length 542;
 Best Local Similarity 58.3%; Pred. No. 21;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 QSVDFDGDGYM 15
 :|||||:
 Db 380 QSDSDGDGYIN 391

RESULT 4
 Q9LVX3 PRELIMINARY; PRT; 1868 AA.
 ID Q9LVX3
 AC Q9LVX3;
 DT 01-OCT-2000 (TRENBLrel. 15, Created)
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
 DE GENOMIC DNA, CHROMOSOME 3, PI CLONE: MGF10.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=COLUMBIA;
 RC Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
 RA Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=COLUMBIA;
 RC MEDLINE=20277480; PubMed=10819329;
 RX Nakamura Y.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
 RT features of the regions of 4,504,864 bp covered by sixty PI and TAC
 RT clones";
 RL DNA Res. 7:131-135(2000).
 DR EMBL; AB018114; BAB02691.1; --
 DR InterPro: IPR000276; --
 DR InterPro: IPR000345; --
 DR InterPro: IPR001395; --
 DR PROSITE; PS00063; ALDORETO_REDUCTASE_3; UNKNOWN_1.
 DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
 SQ SEQUENCE 1868 AA; 206711 MW; 0799ADC38CC05F0 CRC64;

Query Match 56.4%; Score 44; DB 10; Length 1868;
 Best Local Similarity 60.0%; Pred. No. 84;
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 KASQSVDFDGDGYM 15
 :|||||:
 Db 1074 EASASDDSDSYRN 1088

RESULT 5
 Q9KA25 PRELIMINARY; PRT; 303 AA.
 ID Q9KA25
 AC Q9KA25;
 DT 01-OCT-2000 (TRENBLrel. 15, Created)
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
 DE INTEGRASE/RECOMBINASE.
 GN CODV.
 OS Bacillus halodurans.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 OX NCBI_TaxID=86665;
 [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=C-125 / JCM 9153;
 RA Takami H., Nakasone K., Takaki Y.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF001515; BAB06184.1; --
 DR InterPro: IPR002104; --
 DR Pfam: PF00589; Phage_integrase; 1.
 SQ SEQUENCE 303 AA; 35035 MW; D10EA8AAFE1D6705 CRC64;

Query Match 55.1%; Score 43; DB 2; Length 303;

Best Local Similarity 53.3%; Pred. No. 16;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 KASQVDFDGSYMN 15
| : ||| | : ||
Db 204 KKSQVDFDGSYMN 15

RESULT 6
Q9VMS2 PRELIMINARY; PRT; 2439 AA.
AC Q9VMS2
DT 01-MAR-2000 (Tremblrel. 13, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DE CG14023 PROTEIN.
GN CG14023.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Hertz R.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abrial J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Bottier P.,
RA Burtis K.C., Susam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlike C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodde A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Maitel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merklov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nalson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Rhine B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster";
RL Science 287:2185-2195(2000).
DR EMBL; AF003609; AAF5239.2;
DR FlyBase; FBgn0031698; CG14023.
SQ SEQUENCE 2439 AA; 262189 MW; D335D5E891EDA05E CRC64;

Query Match 55.1%; Score 43; DB 5; Length 2439;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 OSVDFDGSYMN 15
| : ||| | : ||
Db 44 OSVDFDGSYMN 55

RESULT 7
Q9HXK0 PRELIMINARY; PRT; 264 AA.
AC Q9HXK0
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE HYPOTHETICAL PROTEIN PA3797.
GN PA3797.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltz L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Relzer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen";
RL Nature 406:959-964(2000).
DR EMBL; AE004798; AAG07184.1;
DR InterPro; IPR002453;
DR InterPro; IPR003010;
DR Pfam; PF00795; CN_hydrolase; 1.
DR PROSITE; PS00228; TUBULIN_B_AUTOREG; UNKNOWN_1.
KW Hypothetical protein
SQ SEQUENCE 264 AA; 29996 MW; 73AB525B907423A3 CRC64;

Query Match 52.6%; Score 41; DB 2; Length 264;
Best Local Similarity 61.5%; Pred. No. 31;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 OSVDFDGSYMN 15
| : ||| | : ||
Db 215 OSVDFDGSYMN 227

RESULT 8
Q9KY55 PRELIMINARY; PRT; 294 AA.
AC Q9KY55;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE SUCCINYL COA SYNTHETASE ALPHA CHAIN.
GN SUCD.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Brown S.P., Harris D.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [3]

RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RX MEDLINE-97000351; PubMed-8843436;
RA Redenbach M., Kieser H.M., Denapaita D., Eichner A., Cullum J.,
R Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL MOL. Microbiol. 21:77-96(1996).
DR EMBL; AL356832; CAB92672.1; -;
DR InterPro; IPR000303; -;
DR Pfam; PF00549; ligase-CoA; 1.
DR PROSITE; PS01216; SUCCINYL_COA_LIG_1; UNKNOWN_1.
DR PROSITE; PS00399; SUCCINYL_COA_LIG_2; 1.
SQ SEQUENCE 294 AA; 30238 MW; ECD4DC830CAE8F09 CRC64;

Query Match 52.6%; Score 41; DB 2; Length 294;
Best Local Similarity 72.7%; Pred. No. 34;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KASQSVDFDGD 11
DB 43 KAGTSVDFDGN 53

RESULT 9
ID Q924A1 PRELIMINARY; PRT; 400 AA.
AC Q924A1;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE TRAF PROTEIN.
GN TRAF.
OS Escherichia coli.
OC Bacteri; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
[1]
RN SEQUENCE FROM N.A.
RA Sampa G., Mizobuchi K.;
RT "Organization and diversification of plasmid genomes: complete
RT nucleotide sequence of the Colib-p9 genome.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB021078; BAA75169.1; -;
KW Plasmid.
SQ SEQUENCE 400 AA; 43180 MW; AB875F3869C7542A CRC64;

Query Match 52.6%; Score 41; DB 2; Length 400;
Best Local Similarity 77.8%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 DFDGDSYMN 15
DB 241 DFDGDKYHN 249

RESULT 10
ID Q9R2H5 PRELIMINARY; PRT; 400 AA.
AC Q9R2H5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE TRAF PROTEIN.
GN TRAF.
OS Salmonella typhimurium.
OG Plasmid R64.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;

RN SEQUENCE FROM N.A.
RP STRAIN=DRD-11;
RC Komano T., Narahara K., Yoshida T., Furuya N.;
RA "The transfer region of IncII plasmid R64: similarities between R64
RT tra genes and Legionella icm/dot genes.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=DRD-11;
RX MEDLINE-92011438; PubMed-1917882;
RA Furuya N., Komano T.;
RT "Determination of the nick site at origin of IncII plasmid R64: global
RT similarity of origin structures of IncII and IncP plasmids.";
RL J. Bacteriol. 173:6612-6617(1991).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=DRD-11;
RX MEDLINE-98053841; PubMed-9393692;
RA Furuya N., Komano T.;
RT "Mutational analysis of the R64 origin region: requirement for precise
RT location of the Nika-binding sequence.";
RL J. Bacteriol. 179:7291-7297(1997).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=DRD-11;
RX MEDLINE-98268996; PubMed-9603870;
RA Yoshida T., Furuya N., Ishikura M., Isobe T., Haino-Fukushima K.,
RA Ogawa T., Komano T.;
RT "Purification and characterization of thin pili of IncII plasmids
RT Colib-p9 and R64: formation of PiliV-specific cell aggregates by type
RT IV pili.";
RL J. Bacteriol. 180:2842-2848(1998).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=DRD-11;
RX MEDLINE-94132048; PubMed-8300611;
RA Pansegrau W., Schroder W., Lanka E.;
RT "Concerted action of three distinct domains in the DNA cleaving-
RT joining reaction catalyzed by relaxase (TraI) of conjugative plasmid
RT RP4.";
RL J. Biol. Chem. 269:2782-2789(1994).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=DRD-11;
RX MEDLINE-94285211; PubMed-8014987;
RA Pansegrau W., Lanka E., Barth P.T., Figurski D.H., Guiney D.G.,
RA Haas D., Helinski D.R., Schwab H., Stanisich V.A., Thomas C.M.;
RT "Complete nucleotide sequence of Birmingham IncP alpha plasmids.
RT Compilation and comparative analysis.";
RL J. Mol. Biol. 239:623-663(1994).
DR EMBL; AB027308; BAA77991.1; -;
KW Plasmid.
SQ SEQUENCE 400 AA; 43194 MW; 55685F2E137B9250 CRC64;

Query Match 52.6%; Score 41; DB 2; Length 400;
Best Local Similarity 77.8%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 DFDGDSYMN 15
DB 241 DFDGDKYHN 249

RESULT 11
ID Q9ZW06 PRELIMINARY; PRT; 972 AA.
AC Q9ZW06;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE PUMILIO-LIKE PROTEIN.

Query Match 51.3%; Score 40; DB 10; Length 171;
 Best Local Similarity 58.3%; Pred. No. 28;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 4 QSVDFDGDGYMN 15
 Db 138 KSVDSGDGYVS 149

RESULT 15
 Q9M7Q9 PRELIMINARY; PRT; 171 AA.
 AC Q9M7Q9;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE CALCIUM-BINDING PROTEIN.
 GN PCA23.
 OS Olea europaea (Common olive).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
 OC Lamiales; Oleaceae; Olea.
 OX NCBI_TaxID=4146;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20115491; PubMed=10648840;
 RX Ledesma A., Villalba M., Rodriguez R.;
 RT "Cloning, expression and characterization of a novel four EF-hand
 Ca(2+)-binding protein from olive pollen with allergenic activity.";
 RL FEBS Lett. 466:192-196(2000).
 CC -!- SIMILARITY: TO EF-HAND FAMILY.
 DR EMBL; AF078680; AAF31152.1; -.
 DR InterPro; IPR002048; -.
 DR InterPro; IPR003299; -.
 DR Pfam; PF00036; efhand; 4.
 DR PRINTS; PR01362; CALFLAGIN.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
 DR SMART; SM00054; EFh; 1.
 KW Calcium-binding.
 SQ SEQUENCE 171 AA; 18957 MW; 207B6F0468FAB83B CRC64;

Query Match 51.3%; Score 40; DB 10; Length 171;
 Best Local Similarity 58.3%; Pred. No. 28;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 4 QSVDFDGDGYMN 15
 Db 138 KSVDSGDGYVS 149

Search completed: June 28, 2001, 16:08:21
 Job time: 949 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2001, 16:14:35 ; Search time 362.28 Seconds
(without alignments)
1.171 Million cell updates/sec

Title: US-09-724-406-14
Perfect score: 31
Sequence: 1 AASNLES 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_0601.*

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2: /SIDS8/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SIDS8/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SIDS8/gcgdata/geneseq/geneseq/AA1983.DAT.*
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22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	31	100.0	7	16	AA70196
2	31	100.0	7	19	AAW83028
3	31	100.0	7	20	AA23773
4	31	100.0	7	20	AA18115
5	31	100.0	7	21	AA14745
6	31	100.0	7	21	AAW90895
7	31	100.0	7	21	AAV59260
8	31	100.0	7	21	AAV51137
9	31	100.0	15	15	AAW66144
10	31	100.0	41	21	AAV91015
11	31	100.0	103	21	AAV59263

12	31	100.0	103	21	AAV51140	Murine derived pro
13	31	100.0	106	14	AA33309	MAE15 light chain.
14	31	100.0	106	21	AA85197	Light chain amino
15	31	100.0	111	10	AA90541	Immunoglobulin L c
16	31	100.0	111	15	AA55123	Mouse anti-HIV mu5
17	31	100.0	111	15	AA55127	Mouse-human chimera
18	31	100.0	111	15	AA60302	Anti HIV antibody
19	31	100.0	111	15	AA60306	Chimeric anti HIV
20	31	100.0	111	20	AA23781	Light chain variab
21	31	100.0	111	20	AAV18123	Light chain sequen
22	31	100.0	111	21	AAV59267	Antibody 4H5 L cha
23	31	100.0	111	21	AAV51144	Murine derived pro
24	31	100.0	111	21	AAV51146	Murine derived pro
25	31	100.0	112	13	AA24575	Human x mouse modi
26	31	100.0	113	22	AA71895	Monoclonal antibody
27	31	100.0	115	11	AA04134	Anti-Leu 3a light
28	31	100.0	131	10	AA90543	Amino acids sequen
29	31	100.0	131	11	AA04132	Anti-Leu 3a light
30	31	100.0	131	14	AA32123	Anti-CD4 antibody
31	31	100.0	131	16	AA75355	Humanized antibody
32	31	100.0	131	16	AA70202	Humanized antibody
33	31	100.0	131	18	AAW34516	Variable kappa cha
34	31	100.0	131	20	AAV23779	Light chain variab
35	31	100.0	131	20	AAV23771	Light chain variab
36	31	100.0	131	20	AAV18126	Light chain sequen
37	31	100.0	131	20	AAV18118	Light chain sequen
38	31	100.0	132	16	AA70189	Mouse MAb 3B9 ligh
39	31	100.0	132	20	AAV23767	Light chain variab
40	31	100.0	132	20	AAV18120	Light chain sequen
41	31	100.0	218	18	AAW13563	Humanized anti-L-s
42	31	100.0	222	18	AAW01751	MH1 monoclonal ant
43	31	100.0	238	19	AAW83031	Anti-Fas humanised
44	31	100.0	238	19	AAW83032	Anti-Fas humanised
45	31	100.0	238	19	AAW83033	Anti-Fas humanised

ALIGNMENTS

RESULT 1
AA70196
ID AA70196 standard; Protein; 7 AA.
XX
AC AA70196;
XX
DT 20-SEP-1995 (first entry)
XX
DE MAb 3B9 light chain CDR.
XX
KW Chimeric antibody; humanized antibody; antibody engineering;
KW monoclonal antibody; MAb; interleukin-4; IL-4; allergy; CDR;
KW complementarity determining region.
XX
OS Mus sp.
XX
PN WO9507301-A.
XX
PD 16-MAR-1995.
XX
PF 07-SEP-1994; 94WO-US10308.
XX
PR 07-SEP-1993; 93US-0117366.
PR 14-OCT-1993; 93US-0136783.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PI Gross MS, Holmes SD, Sylvester DR;
XX
XX WPI; 1995-123387/16.
XX
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of IL-4-mediated

PT and IgE-mediated allergic conditions
 PS Disclosure; Page 55; 97pp; English.
 XX Spleen cells from mice immunized with human IL-4 were used to prepare
 CC hybridomas, which were screened for anti-IL-4 MAB secretion. Only
 CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy
 CC chains were cloned into pGEM7f+ and transformed into E. coli
 CC DH5-alpha. A light chain cDNA clone was sequenced (AA083490) that
 CC encoded the protein given in AAR70189. 3 CDRs (AAR70195-97) were
 CC identified.
 XX Sequence 7 AA;
 SQ

Query Match 100.0%; Score 31; DB 15; Length 7;
 Best Local Similarity 100.0%; Pred. NO. 3.4e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AASNLES 7
 Db | | | | | | |
 1 aasnles 7

RESULT 2
 AA083028
 ID AA083028 standard; Peptide; 7 AA.
 XX
 AC AA083028;
 XX
 DT 15-MAR-1999 (first entry)
 XX
 DE Anti-Fas MAB HFE7A light chain CDR-L2.
 XX
 KW HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
 KW apoptosis; autoimmune disease; Hashimoto's disease;
 KW systemic lupus erythematosus; graft versus host disease;
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 KW transplant rejection; therapy; complementarity determining region;
 KW CDR.
 XX Mus musculus.
 OS AU9859701-A.
 XX
 PN 08-OCT-1998.
 XX
 PD 30-MAR-1998; 98AU-0059701.
 XX
 PF 08-OCT-1997; 97JP-0276064.
 XX
 PR 01-APR-1997; 97JP-0082953.
 XX
 PR 25-JUN-1997; 97JP-0169088.
 XX
 XX (SANY) SANKYO CO LTD.
 XX
 XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
 PI Masahiko O, Nobufusa S, Shin Y, Tohru T;
 XX
 DR WPI; 1998-543440/47.
 XX
 XX New antibodies and proteins bind conserved epitope of Fas antigen -
 PT used to evaluate drugs in animal models and to treat Fas-associated
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 PT myocarditis, hepatitis and AIDS
 XX
 PS Claim 9; Page 185; 292pp; English.
 XX

CC This is the amino acid of complementarity determining region 2
 CC (CDR-L2) of the light chain (see AA083042) of murine anti-human Fas
 CC monoclonal antibody HFE7A. The invention relates to antibodies,
 CC especially humanised antibodies (see AA083031-37), recognising the
 CC Fas antigen. Such antibodies preferably comprise a heavy chain and
 CC a light chain including CDRs (see AA083024-29) from the heavy and
 CC light chains of HFE7A. Humanised antibodies are produced by CDR
 CC grafting. The antibodies are capable of inducing apoptosis in
 CC abnormal cells expressing Fas, and of inhibiting Fas-induced
 CC apoptosis in normal cells. They are used to evaluate, in animal
 CC models, treatments of diseases that involve Fas/Fas ligand
 CC interactions, and also to treat such diseases, including autoimmune
 CC disease (e.g. systemic lupus erythematosus, Hashimoto's disease,
 CC graft versus host disease, Sjogren syndrome, pernicious anaemia,
 CC Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, rheumatoid arthritis, autoimmune haemolytic anaemia,
 CC sterility, myasthenia gravis, multiple sclerosis, Basedow's
 CC disease, thrombopenia purpura and insulin-dependent diabetes),
 CC allergies, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
 CC glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and
 CC transplant rejection (all claimed).
 XX
 XX Sequence 7 AA;

Query Match 100.0%; Score 31; DB 19; Length 7;
 Best Local Similarity 100.0%; Pred. NO. 3.4e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AASNLES 7
 Db | | | | | | |
 1 aasnles 7

RESULT 3
 AAY23773
 ID AAY23773 standard; Peptide; 7 AA.
 XX
 AC AAY23773;
 XX
 DT 13-SEP-1999 (first entry)
 XX
 DE CDR of the light chain variable region of antibody 3B9.
 XX
 KW Light chain variable region; interleukin-4; IL-4; antibody 3B9;
 KW chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;
 KW immunoglobulin E-mediated allergic reaction; allergic rhinitis;
 KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
 KW rheumatoid arthritis; host-versus-graft disease; renal disease;
 KW allergy; complementarity determining region.
 XX
 OS Mus sp.
 XX
 PN US5928904-A.
 XX
 PD 27-JUL-1999.
 XX
 PF 07-JUN-1995; 95US-0483632.
 XX
 PR 07-JUN-1995; 95US-0483632.
 XX
 PR 07-SEP-1993; 93US-0117366.
 XX
 PR 14-OCT-1993; 93US-0136783.
 XX
 PR 07-SEP-1994; 94WO-US10308.
 XX
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 XX (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 XX Gross MS, Holmes SD, Sylvester DR;
 PI
 XX WPI; 1999-429500/36.
 DR
 DR N-PSDB; AAX85890.
 XX
 XX New DNA molecules encoding recombinant antibodies useful for

PT treating IL4-mediated conditions
 XX Example 3; Column 43-44; 50pp; English.
 XX
 CC The present sequence represents a complementarity determining region
 CC (CDR) of the light chain variable region of murine interleukin-4
 CC (IL-4) antibody 3B9. The specification describes chimeric and
 CC humanised IL-4 monoclonal antibodies. The antibodies of the
 CC invention are used in therapeutic and pharmaceutical compositions
 CC for treating IL-4 mediated and immunoglobulin E-mediated allergic
 CC reactions e.g. allergic rhinitis, conjunctivitis, atopic dermatitis,
 CC atopic asthma, anaphylactic shock, rheumatoid arthritis,
 CC host-versus-graft disease and renal disease. They are also useful
 CC in the diagnosis of an allergy or condition associated with excess
 CC IL-4 production through the measurement e.g. by ELISA of circulating
 CC endogenous IL-4 levels in humans.
 XX
 SQ Sequence 7 AA;

Query Match 100.0%; Score 31; DB 20; Length 7;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AASNLES 7
 Db 1 aasnles 7

RESULT 4
 AAY18115
 ID AAY18115 standard; peptide; 7 AA.
 XX
 AC AAY18115;
 XX
 XX 11-AUG-1999 (first entry)
 DT
 DE Light chain CDR for hIL-4 specific antibody.
 XX
 KW Antibody; Interleukin-4; IL4; immunoglobulin E; IgE mediated disease;
 KW allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;
 KW atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;
 KW autoimmune disease; graft versus host disease;
 KW complementarity determining region; CDR.
 XX
 OS Synthetic.
 XX
 XX US5914110-A.
 XX
 XX 22-JUN-1999.
 XX
 XX 07-JUN-1995; 95US-0483636.
 XX
 XX 07-JUN-1995; 95US-0483636.
 PR
 PR 07-SEP-1993; 93US-0117266.
 PR
 PR 14-OCT-1993; 93US-0136783.
 PR
 XX 07-SEP-1994; 94WO-US10308.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 XX Gross MS, Holmes SD, Sylvester DR;
 XX
 XX WPI; 1999-370482/31.
 DR
 DR N-PSDB; AAX79514.
 XX
 XX Recombinant IL4 antibodies
 PT
 PS Claim 7; Column 43; 50pp; English.
 XX
 CC This sequence represents a light chain complementarity determining region
 CC (CDR) from an antibody of the invention. The antibody is a chimeric or
 CC humanised interleukin-4 (IL4) monoclonal antibody for the treatment of

CC immunoglobulin E (IgE) mediated diseases. The antibodies are useful for
 CC the treatment of allergic disorders such as allergic rhinitis,
 CC conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock.
 CC The antibodies are also useful for regulating B and T cell proliferation
 CC and as such are useful in the treatment of autoimmune diseases and graft
 CC versus host disease.
 XX
 SQ Sequence 7 AA;

Query Match 100.0%; Score 31; DB 20; Length 7;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AASNLES 7
 Db 1 aasnles 7

RESULT 5
 AAB14745
 ID AAB14745 standard; peptide; 7 AA.
 XX
 AC AAB14745;
 XX
 XX 24-NOV-2000 (first entry)
 DT
 DE Mouse anti-Fas antibody HFE7A light chain CDR2.
 XX
 KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
 KW murine; complementarity determining region; CDR; human Fas;
 KW Fas ligand; apoptosis modulator; programmed cell death;
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;
 KW hepatitis; AIDS; graft rejection; light chain.
 XX
 OS Mus musculus.
 XX
 XX JP2000169393-A.
 XX
 XX 20-JUN-2000.
 XX
 XX 30-SEP-1999; 99JP-0278301.
 XX
 XX 30-SEP-1998; 98JP-0276883.
 XX
 XX (SANY) SANKYO CO LTD.
 XX
 XX WPI; 2000-485645/43.
 XX
 XX Preventive or treating agent for the diseases caused by an abnormality
 XX in the Fas/Fas ligand system e.g. autoimmune diseases, contains
 XX anti-Fas antibody -
 XX
 XX Claim 10; Page 63; 139pp; Japanese.

CC The invention relates to compositions for the prevention or treatment
 CC of diseases caused by an abnormality in the Fas/Fas ligand system
 CC containing an anti-Fas antibody as the active component. The anti-Fas
 CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
 CC or a humanised version of HFE7A containing identical CDRs
 CC (complementarity determining regions) to antibody HFE7A. Via its
 CC interaction with Fas, the antibody of the invention acts as a modulator
 CC of apoptosis. The compositions of the invention may therefore be used in
 CC the treatment or prevention of conditions such as autoimmune diseases,
 CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
 CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
 CC and organ graft rejection. Sequences AAB14744-B14746 represent CDRs 1-3
 CC of the light chain of the murine anti-human Fas monoclonal antibody
 CC HFE7A, which is produced by hybridoma HFE7A (FERM-BP-5828).

Sequence 7 AA;

Query Match 100.0%; Score 31; DB 21; Length 7;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
 | | | | | | |
 Db 1 aasnles 7

RESULT 6
 ID AAW90895 standard; peptide; 7 AA.
 XX AC AAW90895;
 XX 08-AUG-2000 (first entry)
 DT Murine anti-Fas antibody peptide fragment #5.
 DE Fas; antibody; murine; anti-inflammatory; anti-anemic; antidiabetic;
 XX anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiatic;
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 XX Mus musculus.
 OS
 XX
 XX EP990663-A2.
 XX 05-APR-2000.
 XX 29-SEP-1999; 99EP-0307711.
 XX 30-SEP-1998; 98JP-0276881.
 PR 30-SEP-1998; 98JP-0276882.
 XX (SANY) SANKYO CO LTD.
 XX PA Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 XX PI WPI; 2000-258930/23.
 XX
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems
 XX
 XX Disclosure; Page 98; 263pp; English.
 PS
 XX This invention describes a novel humanized anti-Fas antibody-like
 XX molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiatic and hepatotropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC

CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a murine anti-Fas antibody peptide fragment described in the method
 CC of the invention.
 XX
 XX Sequence 7 AA;

Query Match 100.0%; Score 31; DB 21; Length 7;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
 | | | | | | |
 Db 1 aasnles 7

RESULT 7
 ID AAY59260 standard; peptide; 7 AA.
 XX AAY59260;
 AC 17-APR-2000 (first entry)
 DT Antibody 4H5 L chain variable region CDR2 fragment.
 XX CD4 antigen; anti-human; antibody; 4H5; drug; CDR;
 KW complementarity determining region.
 XX Mus sp.
 OS
 XX JPI1332563-A.
 XX 07-DEC-1999.
 XX 26-MAY-1998; 98JP-0163034.
 XX 26-MAY-1998; 98JP-0163034.
 PR (ASAH) ASAH KASEI KOGYO KK.
 XX WPI; 2000-091351/08.
 XX An antibody and the nucleic acid coding the antibody -
 PT Claim 2; Page 14; 25pp; Japanese.

CC The invention provides an antibody having affinity to CD4 antigen. The
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and
 CC application for drugs. It is highly safe in human dose. Sequences
 CC AAY59259-61 represent the complementarity determining region (CDR)-1,
 CC CDR-2 and CDR-3 fragments in the L chain variable region of the
 CC antibody 4H5 respectively.
 XX
 XX Sequence 7 AA;

Query Match 100.0%; Score 31; DB 21; Length 7;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
 | | | | | | |
 Db 1 aasnles 7

RESULT 8

AA511137
ID AA511137 standard; Protein; 7 AA.

AC AA511137;

XX 31-MAR-2000 (first entry)

XX Murine CD4/CD34 recognizing antibody light chain CDR-2 region #1.

XX Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
KW HIV infection; autoimmune disease; complementarity determining region;
KW CDR-2; light chain; murine.

XX Mus sp.

XX WO9961629-A1.

XX 02-DEC-1999.

XX 24-MAY-1999; 99WO-JP02711.

XX 25-MAY-1998; 98JP-0159957.

XX 26-MAY-1998; 98JP-0163023.

XX (ASAH) ASAH KASEI KOGYO KK.

XX (ASAH) ASAH MEDICAL CO LTD.

XX Ono M, Soka T, Morimoto I, Miyamura K;

XX WPI; 2000-086720/07.

XX Devices containing antibodies recognising CD4 or CD34 and their use for
PT the separation of CD4 or CD34 positive cells

XX Claim 3; Page 77; 11pp; Japanese.

XX This invention describes a novel device (I) for separating cluster
CC differentiation (CD)-positive cells using a recombinant (chimeric or
CC single-chain) antibody recognising CD4 or CD34. The devices are useful
CC for the separation of CD4 or CD34 positive cells, which is useful for
CC the collection of hematopoietic undifferentiated cells, elimination of
CC lymphocytes from cells to be used in bone marrow transplantation, the
CC detection of leukemic cells and the production of medicinal
CC compositions for the treatment of HIV infection and autoimmune diseases.
CC This sequence represents a murine derived complementarity determining
CC region CDR-2 protein fragment which is used to illustrate the method of
CC the invention.

XX Sequence 7 AA;

Query Match 100.0%; Score 31; DB 21; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
Db |||||
1 aasnles 7

RESULT 9

ID AAR66144 standard; peptide; 15 AA.

XX AAR66144;

XX 12-JUL-1995 (first entry)

XX CD-4 antibody variable region complementary peptide.

XX CD-4 antibody variable region; complementary peptide;
KW extra-corporeal blood circulation; cell filter material.

XX Synthetic.

XX JP06269663-A.

XX 27-SEP-1994.

XX 17-MAR-1993; 93JP-0057206.

XX 17-MAR-1993; 93JP-0057206.

XX (TOYM) TOYODO KK.

XX WPI; 1994-346316/43.

XX Material for collecting cells positive for CD-4 antibody -
PT comprises nonwoven fabric having keto-alkyl halide functional gp
XX Example 2; Page 7; 9pp; Japanese.

XX AAR66140-R66146 are peptides complementary to the variable region
CC of the CD-4 antibody, these peptides are fixed onto a claimed
CC nonwoven fabric (average fibre dia. of 1-30 microns) coated with
CC keto-alkyl halide functional groups. This material can be used
CC as a filter for CD-4 positive cells in a medical treatment
CC involving the extra-corporeal circulation of blood.

XX Sequence 15 AA;

Query Match 100.0%; Score 31; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
Db |||||
9 aasnles 15

RESULT 10

AA511015

ID AA511015 standard; protein; 41 AA.

XX AA511015;

XX 05-SEP-2000 (first entry)

XX 1F7 antibody variable light chain L2 amino acid sequence SEQ ID NO:6.

XX 1F7 antibody; murine; monoclonal antibody; diagnosis; HIV; infection;
KW AIDS; anti-HIV; human immunodeficiency virus; detection;
KW acquired immunodeficiency syndrome.

XX Mus sp.

XX US6057421-A.

XX 02-MAY-2000.

XX 03-DEC-1997; 57US-0984277.

XX 30-NOV-1994; 94US-0351193.

XX (IMMP-) IMMOPHERON INC.

XX Muller S, Kohler H;

XX WPI; 2000-338622/29.

XX Variable heavy and light chain regions of murine monoclonal antibody
PT 1F7, useful for treating HIV infection and AIDS
XX Claim 1; Fig 8; 45pp; English.

XX The present invention describes the variable heavy and light chain
 CC regions (I) of murine monoclonal antibody (mAb) 1F7. AAY91014 to
 CC AAY91016 represent specifically claimed amino acid sequences of the
 CC variable light chain, and AAY91017 to AAY91019 represent specifically
 CC claimed amino acid sequence of the variable heavy chain. The antibodies
 CC are used for treatment of HIV (human immunodeficiency virus) infection
 CC and AIDS (acquired immunodeficiency syndrome). They are also used for
 CC detecting HIV in serum and for stimulating HIV antigen related and
 CC committed B cells to produce broadly reactive and neutralising antibodies
 CC by clonotypic stimulation.
 XX Sequence 41 AA;

Query Match 100.0%; Score 31; DB 21; Length 41;
 Best Local Similarity 100.0%; Pred. No. 2.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
 Db 12 aasnles 18
 |||||

RESULT 11
 AAY59263
 ID AAY59263 standard; protein; 103 AA.

XX AC AAY59263;
 XX DT 17-APR-2000 (first entry)
 XX DE Antibody 4H5 L chain variable region.
 XX KW CD4 antigen; anti-human; antibody; 4H5; drug.
 XX OS Mus sp.

XX PN JP11332563-A.
 XX PD 07-DEC-1999.
 XX PF 26-MAY-1998; 98JP-0163034.
 XX PR 26-MAY-1998; 98JP-0163034.
 XX PA (ASAH) ASAH KASEI KOGYO KK.
 XX DR WPI; 2000-091351/08.
 XX DR N-PSDB; AAZ58662.

XX An antibody and the nucleic acid coding the antibody -
 XX Claim 5; Page 15-16; 25pp; Japanese.

XX The invention provides an antibody having affinity to CD4 antigen. The
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and
 CC application for drugs. It is highly safe in human dose. The present
 CC sequence represents the L chain variable region of the antibody 4H5.

XX Sequence 103 AA;

Query Match 100.0%; Score 31; DB 21; Length 103;
 Best Local Similarity 100.0%; Pred. No. 7.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
 Db 46 aasnles 52
 |||||

RESULT 12

AAY51140
 ID AAY51140 standard; Protein; 103 AA.

XX AC AAY51140;
 XX DT 31-MAR-2000 (first entry)
 XX DE Murine derived protein fragment #2.
 XX KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
 KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
 KW HIV infection; autoimmune disease; murine.
 XX OS Mus sp.

XX PN WO9961629-A1.

XX PD 02-DEC-1999.

XX PF 24-MAY-1999; 99WO-JP02711.

XX PR 25-MAY-1998; 98JP-0159957.

XX PR 26-MAY-1998; 98JP-0163023.

XX PA (ASAH) ASAH KASEI KOGYO KK.
 XX PA (ASAH) ASAH MEDICAL CO LTD.

XX PI Ono M, Soka T, Morimoto I, Miyamura K;

XX DR WPI; 2000-086720/07.

XX DR N-PSDB; AAZ44204.

XX Devices containing antibodies recognising CD4 or CD34 positive cells
 PT the separation of CD4 or CD34 positive cells -

XX Claim 22; Page 79; 111pp; Japanese.

XX This invention describes a novel device (I) for separating cluster
 CC differentiation (CD)-positive cells using a recombinant (chimeric or
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful
 CC for the separation of CD4 or CD34 positive cells, which is useful for
 CC the collection of hematopoietic undifferentiated cells, elimination of
 CC lymphocytes from cells to be used in bone marrow transplantation, the
 CC detection of leukemic cells and the production of medicinal
 CC compositions for the treatment of HIV infection and autoimmune diseases.
 CC This sequence represents a murine derived protein fragment which is used
 CC to illustrate the method of the invention.

XX Sequence 103 AA;

Query Match 100.0%; Score 31; DB 21; Length 103;
 Best Local Similarity 100.0%; Pred. No. 7.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
 Db 46 aasnles 52
 |||||

RESULT 13

AAR33309

ID AAR33309 standard; Protein; 106 AA.

XX AC AAR33309;

XX DT 05-JUL-1993 (first entry)

XX DE MAE15 light chain.

XX KW Antibody; high affinity; FCEH; low affinity; FCEL;
 KW IgE receptor; histamine; mast cell; basophil; Kabat;
 KW CDR; murine; MAE11; MAE13; MAE15; MAE17.

XX The sequence is an L chain variable region from an immunoglobulin with
 CC anti-HIV neutralising activity. See AAN90491-3, and AAN90495.
 XX
 SQ Sequence 111 AA;

Query Match 100.0%; Score 31; DB 10; Length 111;
 Best Local Similarity 100.0%; Pred. No. 8.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
 |||||
 Db 54 aasnles 60

Search completed: June 28, 2001, 16:14:35
 Job time: 1323 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 28, 2001, 16:01:14 ; Search time 138.34 Seconds
(without alignments)
1.019 Million cell updates/sec

Title: us-09-724-406-14
Perfect score: 31
Sequence: 1 AASNLES 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 2014635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A.COMB.pcp.*
2: /cgn2_6/ptodata/2/iaa/5B.COMB.pcp.*
3: /cgn2_6/ptodata/2/iaa/6A.COMB.pcp.*
4: /cgn2_6/ptodata/2/iaa/6B.COMB.pcp.*
5: /cgn2_6/ptodata/2/iaa/PCTUS.COMB.pcp.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	31	100.0	7	2	US-08-483-636-18
2	31	100.0	7	2	US-08-483-632-18
3	31	100.0	41	3	US-08-984-277-6
4	31	100.0	106	3	US-08-466-151-6
5	31	100.0	111	1	US-08-491-845-8
6	31	100.0	111	1	US-08-491-845-8
7	31	100.0	111	2	US-08-483-636-73
8	31	100.0	111	2	US-08-483-632-73
9	31	100.0	115	4	US-08-513-968-51
10	31	100.0	131	2	US-08-483-636-14
11	31	100.0	131	2	US-08-483-632-14
12	31	100.0	131	2	US-08-483-632-14
13	31	100.0	131	2	US-08-483-632-58
14	31	100.0	131	3	US-08-589-939-3
15	31	100.0	131	4	US-08-579-378A-14
16	31	100.0	131	4	US-08-579-378A-18
17	31	100.0	132	2	US-08-483-632-2
18	31	100.0	132	2	US-08-483-636-2
19	31	100.0	218	5	PCT-US96-13152-2
20	28	90.3	7	2	US-08-650-262-11
21	28	90.3	98	3	US-08-881-037-75
22	28	90.3	108	2	US-08-650-262-2
23	28	90.3	120	1	US-08-111-080-24
24	28	90.3	120	1	US-08-211-980-24
25	28	90.3	120	5	PCT-US93-07967-24
26	27	87.1	6	1	US-08-137-1170-137
27	27	87.1	6	2	US-08-436-717-137

28	27	87.1	17	2	US-08-712-212-5	Sequence 5, Appl
29	27	87.1	17	5	PCT-US95-05160-5	Sequence 5, Appl
30	27	87.1	64	2	US-08-765-179B-10	Sequence 10, Appl
31	27	87.1	106	1	US-08-202-047-26	Sequence 26, Appl
32	27	87.1	106	3	US-08-964-690-26	Sequence 26, Appl
33	27	87.1	111	1	US-07-634-278-46	Sequence 46, Appl
34	27	87.1	111	1	US-07-634-278-46	Sequence 47, Appl
35	27	87.1	111	1	US-07-634-278-47	Sequence 30, Appl
36	27	87.1	111	1	US-08-111-080-30	Sequence 32, Appl
37	27	87.1	111	1	US-08-111-080-32	Sequence 46, Appl
38	27	87.1	111	1	US-08-477-728-46	Sequence 47, Appl
39	27	87.1	111	1	US-08-477-728-47	Sequence 11, Appl
40	27	87.1	111	1	US-08-275-053-11	Sequence 14, Appl
41	27	87.1	111	1	US-08-275-053-14	Sequence 30, Appl
42	27	87.1	111	1	US-08-211-980-30	Sequence 32, Appl
43	27	87.1	111	1	US-08-207-169A-4	Sequence 4, Appl
44	27	87.1	111	1	US-08-474-040-46	Sequence 46, Appl
45	27	87.1	111	1	US-08-474-040-47	Sequence 47, Appl

ALIGNMENTS

RESULT 1
US-08-483-636-18
; Sequence 18, Application US/08483636
; Patent No. 5914110
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,636
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

us-09-724-406-14.ra

Fri Jun 29 08:04:26 2001

US-08-483-636-18

Query Match 100.0%; Score 31; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
Db 1 AASNLES 7

RESULT 2

US-08-483-632-18
; Sequence 18, Application US/08483632
; Patent No. 5928904
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/483,632
; FILING DATE: 14-OCT-1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-483-632-18

Query Match 100.0%; Score 31; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
Db 1 AASNLES 7

RESULT 3

US-08-984-277-6
; Sequence 6, Application US/08984277
; Patent No. 6057421
; GENERAL INFORMATION:
; APPLICANT: Muller, Sybille
; APPLICANT: Kohler, Heinz
; TITLE OF INVENTION: VARIABLE HEAVY AND LIGHT CHAIN REGIONS OF MURINE
; TITLE OF INVENTION: MONOCLONAL ANTIBODY IF7
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDermott, Will & Emery
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/984,277
; FILING DATE: 3-DEC-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bucca, Daniel
; REGISTRATION NUMBER: 42,368
; REFERENCE/DOCKET NUMBER: 50200-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-756-8600
; TELEFAX: 202-756-8699
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; US-08-984-277-6

Query Match 100.0%; Score 31; DB 3; Length 41;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
Db 12 AASNLES 18

RESULT 4

US-08-466-151-6
; Sequence 6, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardiou, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/466,151

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/466163

FILING DATE: 06-Jun-1995

APPLICATION NUMBER: 08/405617

FILING DATE: 15-MAR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/185899

FILING DATE: 26-JAN-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/879495

FILING DATE: 07-MAY-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/744768

FILING DATE: 14-AUG-1991

ATTORNEY/AGENT INFORMATION:

NAME: Svoboda, Craig G.

REGISTRATION NUMBER: 39,044

REFERENCE/DOCKET NUMBER: P0718P2C1D1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-1489

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 106 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-08-466-151-6

Query Match 100.0%; Score 31; DB 3; Length 106;

Best Local Similarity 100.0%; Pred. No. 3.1; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7

Db 54 AASNLES 60

RESULT 5

US-08-491-845-8

Sequence 8, Application US/08491845

Patent No. 5773247

GENERAL INFORMATION:

APPLICANT: MAEDA, Hiroaki

APPLICANT: KIMACHI, Kazuhiko

APPLICANT: EDA, Yasuyuki

APPLICANT: SHIOSAKI, Kouichi

APPLICANT: OSATOMI, Kiyoshi

APPLICANT: TOKIYOSHI, Sachio

TITLE OF INVENTION: RECOMBINANT ANTI-HIV ANTIBODY AND

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Browdy and Neimark

STREET: 419 Seventh Street N.W. Ste. 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/491,845

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP93/00039

FILING DATE: 14-JAN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Browdy, Roger L.

REGISTRATION NUMBER: 25,618

REFERENCE/DOCKET NUMBER: MAEDA-5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 628-5197

TELEFAX: (202) 737-3528

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 111 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-491-845-8

Query Match 100.0%; Score 31; DB 1; Length 111;

Best Local Similarity 100.0%; Pred. No. 3.3;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7

Db 54 AASNLES 60

RESULT 6

US-08-491-845-16

Sequence 16, Application US/08491845

Patent No. 5773247

GENERAL INFORMATION:

APPLICANT: MAEDA, Hiroaki

APPLICANT: KIMACHI, Kazuhiko

APPLICANT: EDA, Yasuyuki

APPLICANT: SHIOSAKI, Kouichi

APPLICANT: OSATOMI, Kiyoshi

APPLICANT: TOKIYOSHI, Sachio

TITLE OF INVENTION: RECOMBINANT ANTI-HIV ANTIBODY AND

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Browdy and Neimark

STREET: 419 Seventh Street N.W. Ste. 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/491,845

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP93/00039

FILING DATE: 14-JAN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Browdy, Roger L.

REGISTRATION NUMBER: 25,618

REFERENCE/DOCKET NUMBER: MAEDA-5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 628-5197

TELEFAX: (202) 737-3528

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

; LENGTH: 111 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-491-845-16

Query Match 100.0%; Score 31; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
Db 54 AASNLES 60

RESULT 7
US-08-483-636-73
; Sequence 73, Application US/08483636
; Patent No. 5914110
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,636
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5090
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-483-636-73

Query Match 100.0%; Score 31; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
Db 54 AASNLES 60

RESULT 8
US-08-483-632-73
; Sequence 73, Application US/08483632
; Patent No. 5928904
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,632
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-483-632-73

Query Match 100.0%; Score 31; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
Db 54 AASNLES 60

RESULT 9
US-08-513-968-51
; Sequence 51, Application US/08513968
; Patent No. 6114143

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; GENERAL INFORMATION:
; APPLICANT: EDA, Yasuyuki
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: MAKIZUMI, Keiichi
; APPLICANT: SHIOSAKI, Kouichi
; APPLICANT: OSATOMI, Kiyoshi
; APPLICANT: KINACHI, Kazuhiko
; APPLICANT: HIGUCHI, Hirofumi
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-HIV MONOCLONAL ANTIBODY
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,968
; FILING DATE: 11-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 78913/1993
; FILING DATE: 11-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: EDA-1
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-513-968-51

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Query Match 100.0%; Score 31; DB 4; Length 115;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AASNLES 7
DB 58 AASNLES 64

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RESULT 10
US-08-483-636-14
; Sequence 14, Application US/08483636
; Patent No. 5914110
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA

```

```

; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,636
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-483-636-14

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Query Match 100.0%; Score 31; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AASNLES 7
DB 73 AASNLES 79

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RESULT 11
US-08-483-636-58
; Sequence 58, Application US/08483636
; Patent No. 5914110
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,636
; FILING DATE:
; CLASSIFICATION: 424

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-483-636-58

Query Match 100.0%; Score 31; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
Db 73 AASNLES 79

RESULT 12
US-08-483-632-14
; Sequence 14, Application US/08483632
; Patent No. 5928904
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,632
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
```

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; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-483-632-14

Query Match 100.0%; Score 31; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
Db 73 AASNLES 79

RESULT 13
US-08-483-632-58
; Sequence 58, Application US/08483632
; Patent No. 5928904
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,632
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
```


TITLE OF INVENTION: Humanized Antibodies Reactive with

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 28, 2001, 15:58:43 ; Search time 234.85 Seconds
(without alignments)
2.270 Million cell updates/sec

Title: US-09-724-406-14
Perfect score: 31
Sequence: 1 AASNLES 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	65	2 C38601	Ig kappa chain V r
2	31	100.0	65	2 B38601	Ig kappa chain V r
3	31	100.0	93	2 A38601	Ig kappa chain V r
4	31	100.0	110	1 KVM510	Ig kappa chain V r
5	31	100.0	111	1 KVM5C1	Ig kappa chain V r
6	31	100.0	111	1 KVM5A3	Ig kappa chain V r
7	31	100.0	111	1 KVM5S3	Ig kappa chain V r
8	31	100.0	111	1 KVM5S9	Ig kappa chain V r
9	31	100.0	112	2 S19971	Ig kappa chain V r
10	31	100.0	112	2 S19976	Ig kappa chain V r
11	31	100.0	131	2 PH1226	Ig kappa chain V r
12	31	100.0	463	2 B64160	hypothetical prote
13	31	100.0	942	2 T39624	6-phosphofructokin
14	31	100.0	1208	2 T00362	hypothetical prote
15	28	90.3	108	1 K1HUGL	Ig kappa chain V-I
16	28	90.3	112	2 S19972	Ig kappa chain V r
17	28	90.3	120	2 S06731	Ig kappa chain V r
18	28	90.3	122	2 S40370	Ig kappa chain pre
19	28	90.3	313	1 QMXRWT	capsomere protein
20	28	90.3	313	1 QMXRWN	nonstructural prot
21	28	90.3	632	2 D71941	ATP-dependent zinc
22	28	90.3	784	1 A55236	kinesin-related pr
23	27	87.1	81	2 S42193	Ig kappa chain V r
24	27	87.1	91	2 S25462	Ig kappa chain V r
25	27	87.1	95	2 S25177	Ig kappa chain V r
26	27	87.1	101	2 S59640	Ig kappa chain V r
27	27	87.1	102	2 PH1076	Ig light chain V r
28	27	87.1	102	2 PH1077	Ig light chain V r
29	27	87.1	107	2 S26343	Ig kappa chain V r

30	27	87.1	107	2 S26344	Ig kappa chain V r
31	27	87.1	108	1 K1HURU	Ig kappa chain V-I
32	27	87.1	108	1 KVM5S4	Ig kappa chain V r
33	27	87.1	111	1 KVM5S7	Ig kappa chain V r
34	27	87.1	111	1 KVM5S8	Ig kappa chain V r
35	27	87.1	111	1 KVM5S8	Ig kappa chain V r
36	27	87.1	111	1 KVM5S7	Ig kappa chain V r
37	27	87.1	111	1 KVM5A0	Ig kappa chain V r
38	27	87.1	111	2 S09963	Ig kappa chain V r
39	27	87.1	111	2 S09965	Ig kappa chain V-J
40	27	87.1	111	2 S09966	Ig kappa chain V-J
41	27	87.1	111	2 S09966	anti-glycoprotein
42	27	87.1	112	2 S45722	Ig kappa chain V r
43	27	87.1	115	2 S63596	Ig kappa chain V r
44	27	87.1	120	2 S46374	Ig kappa chain V-J
45	27	87.1	131	1 KVM5M6	Ig kappa chain pre

ALIGNMENTS

RESULT 1

C38601
Ig kappa chain V region (2B5) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 23-Jul-1999
C:Accession: C38601
R:Goshorn, S.C.; Retzel, E.; Jermerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A:Title: Common structural features among monoclonal antibodies binding the same anti
A:Reference number: A38601, MUID:91115823
A:Accession: C38601
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-65 <GOS>
A:Cross-references: G3:M57980; NID:g196406; PIDN:AAA63361.1; PID:g196407
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 31; DB 2; Length 65;
Best Local Similarity 100.0%; Pred. NO. 0.68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
Db 7 AASNLES 13

RESULT 2

B38601
Ig kappa chain V region (7D4) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 23-Jul-1999
C:Accession: B38601
R:Goshorn, S.C.; Retzel, E.; Jermerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A:Title: Common structural features among monoclonal antibodies binding the same anti
A:Reference number: A38601; MUID:91115823
A:Accession: B38601
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-65 <GOS>
A:Cross-references: G3:M57979; NID:g196404; PIDN:AAA63360.1; PID:g196405
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 31; DB 2; Length 65;
Best Local Similarity 100.0%; Pred. NO. 0.68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7

us-09-724-406-14.rpr

Fri Jun 29 08:04:27 2001

```
Db          7 AASNLES 13
          |||||
RESULT 3
A38601
Ig kappa chain V region (IG3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 23-Jul-1999
C:Accession: A38601
R:Coshorn, S.C.; Retzel, E.; Jermerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A:Title: Common structural features among monoclonal antibodies binding the same antigen
A:Reference number: A38601; MUID:91115823
A:Accession: A38601
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-93 <GOS>
A:Cross-references: GB:M57978; NID:g196402; PIDN:AAA63359.1; PID:g196403
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match          100.0%; Score 31; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
Db 35 AASNLES 41
          |||||

RESULT 4
KVMS10
Ig kappa chain V region (PC7210) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
C:Accession: D01937; A01937
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152
A:Accession: D01937
A:Molecule type: protein
A:Residues: 1-110 <WEI>
A:Cross-references: EMBL:Z25444; NID:g407832; PIDN:CAA80931.1; PID:g407833
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match          100.0%; Score 31; DB 1; Length 110;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
Db 54 AASNLES 60
          |||||

RESULT 5
KVMSC1
Ig kappa chain V region (CBPC 101) - mouse (tentative sequence)
C:Species: Mus musculus (house mouse)
C:Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 31-Mar-2000
C:Accession: A01936
R:McKean, D.J.; Bell, M.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978
A:Title: Mechanisms of antibody diversity: multiple genes encode structurally related molecules
A:Reference number: A93822; MUID:79012520
A:Accession: A01936

A:Molecule type: protein
A:Residues: 1-111 <MCK>
C:Comment: This chain was isolated from a myeloma protein.
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match          100.0%; Score 31; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
Db 54 AASNLES 60
          |||||

RESULT 6
KVMS43
Ig kappa chain V region (PC7043) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 21-Jan-2000
C:Accession: A01937; S42187; S42194; S42199; S42188; S42191; S42192
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152
A:Accession: A01937
A:Molecule type: protein
A:Residues: 1-111 <WEI>
R:Mo, J.A.; Bona, C.A.; Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
A:Title: Variable region gene selection of immunoglobulin G-expressing B cells with s
A:Reference number: S42176; MUID:94009207
A:Accession: S42187
A:Molecule type: DNA
A:Residues: 10-99 <MOJ>
A:Cross-references: EMBL:Z25444; NID:g407832; PIDN:CAA80931.1; PID:g407833
A:Note: V-kappa-21E; anti-collagen
A:Accession: S42194
A:Molecule type: DNA
A:Residues: 12-99 <MOJ>
A:Cross-references: EMBL:Z25458; NID:g407844; PIDN:CAA80945.1; PID:g407845
A:Note: V-kappa-21E; anti-collagen
A:Accession: S42190
A:Molecule type: DNA
A:Residues: 13-99 <MOF>
A:Cross-references: EMBL:Z25450; NID:g407838; PIDN:CAA80937.1; PID:g407839
A:Note: V-kappa-21E; anti-collagen
A:Accession: S42189
A:Molecule type: DNA
A:Residues: 15-99 <MOA>
A:Cross-references: EMBL:Z25448; NID:g407836; PIDN:CAA80935.1; PID:g407837
A:Note: V-kappa-21E; anti-collagen
A:Accession: S42188
A:Molecule type: DNA
A:Residues: 12-99 <MOZ>
A:Cross-references: EMBL:Z25446; NID:g407834; PIDN:CAA80933.1; PID:g407835
A:Note: V-kappa-21E; anti-collagen
A:Accession: S42191
A:Molecule type: DNA
A:Residues: 10-99 <MOY>
A:Cross-references: EMBL:Z25452; NID:g407840; PIDN:CAA80939.1; PID:g407841
A:Note: V-kappa-21E; anti-collagen
A:Accession: S42192
A:Molecule type: DNA
A:Residues: 10-99 <MOO>
A:Cross-references: EMBL:Z25454; NID:g407842; PIDN:CAA80941.1; PID:g407843
A:Note: V-kappa-21E; anti-collagen
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds.
```

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AASNLES 7
Db 54 AASNLES 60

RESULT 7
KVMS83
Ig kappa chain V region (PC7183) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
C:Accession: B01937; A01937
R:Weigert, M.; Garmatyan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152
A:Accession: B01937
A:Molecule type: protein
A:Residues: 1-111 <WEI>
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AASNLES 7
Db 54 AASNLES 60

RESULT 8
KVMS69
Ig kappa chain V region (PC7769) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
C:Accession: E01937; A01937
R:Weigert, M.; Garmatyan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152
A:Accession: E01937
A:Molecule type: protein
A:Residues: 1-111 <WEI>
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AASNLES 7
Db 54 AASNLES 60

Db 54 AASNLES 60
RESULT 9
SI9971
Ig kappa chain V region (CD4 mAb clone M-T310 and others) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: SI9971; SI9973
R:Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A:Description: Structural characterization of CD4 mAb.
A:Reference number: SI9963
A:Accession: SI9971
A:Molecule type: mRNA
A:Residues: 1-112 <WEI>
A:Cross-references: EMBL:X65091; NID:g52288; PIDN:CAA46219.1; PID:g52289
A:Experimental source: clone M-T310
A:Accession: SI9973
A:Molecule type: mRNA
A:Residues: 1-112 <WEI>
A:Cross-references: EMBL:X65092; NID:g52292; PIDN:CAA46220.1; PID:g52293
A:Experimental source: M-T404
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AASNLES 7
Db 54 AASNLES 60

RESULT 10
SI9976
Ig kappa chain V region (M-T413) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: SI9976
R:Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A:Description: Structural characterization of CD4 mAb.
A:Reference number: SI9963
A:Accession: SI9976
A:Molecule type: mRNA
A:Residues: 1-112 <WEI>
A:Cross-references: EMBL:X65093; NID:g52298; PIDN:CAA46221.1; PID:g52299
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AASNLES 7
Db 54 AASNLES 60
RESULT 11
PHI226
Ig kappa chain precursor V region (M-T310) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jan-2000
C:Accession: PHI226
R:Weissenhorn, W.; Scheuer, W.; Kaluza, B.; Schwirzke, M.; Reiter, C.; Flieger, D.; L

Gene 121, 271-278, 1992
A:Title: Combinatorial functions of two chimeric antibodies directed to human CD4 and on
A:Reference number: PH1224; MUID:93077041
A:Accession: PH1226
A:Molecule type: mRNA
A:Residues: 1-131 <WEI>
A:Cross-references: GB:S50265; NID:g260765; PIDN:AAB24320.1; PID:g260766
A:Note: This mouse sequence was hybridized and fused with a human constant region gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-131/Product: Ig light chain V region #status predicted <MAT>
F:36-114/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 1.5; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 1 AASNLES 7
|||||
DB 74 AASNLES 80

RESULT 12
B64160
hypothetical protein H10852 - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 26-Aug-1999
C:Accession: B64160
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.
Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.
Science 269, 456-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630
A:Accession: B64160
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-463 <TIGR>
A:Cross-references: GB:U27266; GB:I42023; NID:gl573854; PIDN:AAC22509.1; PID:gl573866; T
A:Note: best homolog was a hypothetical protein from Escherichia coli
C:Superfamily: multidrug-efflux transporter
C:Keywords: antibiotic resistance; transmembrane protein

Query Match 100.0%; Score 31; DB 2; Length 463;
Best Local Similarity 100.0%; Pred. No. 6.3; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 1 AASNLES 7
|||||
DB 94 AASNLES 100

RESULT 13
T39624
6-phosphofructokinase beta subunit - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Jan-2000
C:Accession: T39624
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.
submitted to the EMBL Data Library, March 1998
A:Reference number: Z21843
A:Accession: T39624
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-942 <WOO>
A:Cross-references: EMBL:AL022104; PIDN:CAAL7900.1; GSPDB:GN00067; SPDB:SPBPC16H5.02
A:Experimental source: strain 972h-; cosmid c16H5
C:Genetics:
A:Gene: SPDB:SPBPC16H5.02

A:Map position: 2
A:Superfamily: human 6-phosphofructokinase; 6-phosphofructokinase 1 homology
C:Superfamily: human 6-phosphofructokinase; 6-phosphofructokinase 1 homology

Query Match 100.0%; Score 31; DB 2; Length 942;
Best Local Similarity 100.0%; Pred. No. 14; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 1 AASNLES 7
|||||
DB 165 AASNLES 171

RESULT 14
T00362
hypothetical protein KIAA0675 - human
C:Species: Homo sapiens (man)
C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 02-Sep-2000
C:Accession: T00362
R:Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, R.
DNA Res. 5, 169-176, 1998
A:Title: Prediction of the coding sequences of unidentified human genes. X. The compl
A:Reference number: Z14142; MUID:98403880
A:Accession: T00362
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-1208 <ISH>
A:Cross-references: EMBL:AB014575; NID:g3327163; PIDN:BAA31650.1; PID:g3327164
A:Experimental source: brain; clone HK02566
C:Genetics:
A:Note: KIAA0675
C:Superfamily: RING finger homology
F:1144-1193/Domain: RING finger homology <RRN>

Query Match 100.0%; Score 31; DB 2; Length 1208;
Best Local Similarity 100.0%; Pred. No. 19; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 1 AASNLES 7
|||||
DB 896 AASNLES 902

RESULT 15
K1HUGL
Ig kappa chain V-I region (Gal) - human (tentative sequence)
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C:Accession: A01867
R:Laure, C.J.; Watanabe, S.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 354, 1503-1504, 1973
A:Title: The primary structure of a monoclonal IgM-immunoglobulin (macroglobulin Gal)
A:Reference number: A01867; MUID:75059122
A:Accession: A01867
A:Molecule type: protein
A:Residues: 1-108 <LAU>
A:Note: the C region of this chain has the Inv (3) marker
C:Comment: This chain was isolated from a Waldenström's macroglobulin.
C:Genetics:
A:Gene: GDB:IGKV1
A:Cross-references: GDB:136264
A:Map position: 2p12-2p12
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (h
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:16-90/Domain: immunoglobulin homology <IMM>
F:23-88/Disulfide bonds: #status predicted

Query Match 90.3%; Score 28; DB 1; Length 108;
Best Local Similarity 85.7%; Pred. No. 7.2;

Matches	6;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	AASNLES	7						
			1						
Db	50	AASNLOS	56						

Search completed: June 28, 2001, 15:58:44
Job time: 372 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2001, 15:54:35 ; Search time 105.36 Seconds
(without alignments)
2.276 Million cell updates/sec

Title: US-09-724-406-14
Perfect score: 31
Sequence: 1 AASNLES 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues
Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	31	100.0	110	1 KV3P_MOUSE	P01668 mus musculus
2	31	100.0	111	1 KV3L_MOUSE	P01664 mus musculus
3	31	100.0	111	1 KV3M_MOUSE	P01665 mus musculus
4	31	100.0	111	1 KV3N_MOUSE	P01666 mus musculus
5	31	100.0	111	1 KV3O_MOUSE	P01669 mus musculus
6	31	100.0	463	1 V1EO_HAEN	P44903 haemophilus
7	28	90.3	108	1 KVIG_HUMAN	P01599 homo sapien
8	28	90.3	313	1 VP9_WTVJ	P12326 wound tumor
9	28	90.3	313	1 VP9_WTVNJ	P131611 wound tumor
10	28	90.3	632	1 FTSH_HELPJ	Q92m66 helicobacte
11	28	90.3	784	1 KL68_DROME	P46867 drosophila
12	27	87.1	108	1 KV1B_HUMAN	P01594 homo sapien
13	27	87.1	108	1 KV3V_MOUSE	P01674 mus musculus
14	27	87.1	111	1 KV3H_MOUSE	P01660 mus musculus
15	27	87.1	111	1 KV3J_MOUSE	P01662 mus musculus
16	27	87.1	111	1 KV3K_MOUSE	P01663 mus musculus
17	27	87.1	111	1 KV3Q_MOUSE	P01667 mus musculus
18	27	87.1	111	1 KV3R_MOUSE	P01670 mus musculus
19	27	87.1	111	1 KV3S_MOUSE	P01671 mus musculus
20	27	87.1	111	1 KV3T_MOUSE	P01672 mus musculus
21	27	87.1	131	1 KV3I_MOUSE	P01661 mus musculus
22	27	87.1	177	1 PSS_BACSU	P39823 bacillus su
23	27	87.1	230	1 CUTI_FUSCC	Q99174 fusarium so
24	27	87.1	230	1 CUTI_FUSSO	P00590 fusarium so
25	27	87.1	260	1 UPPS_BACSU	Q31751 bacillus su
26	27	87.1	486	1 YN8U_YEAST	P53742 saccharomyc
27	27	87.1	662	1 UVRB_RICPR	Q9zdw2 rickettsia
28	26	83.9	112	1 KV3G_MOUSE	P01659 mus musculus
29	26	83.9	132	1 KV3F_MOUSE	P01658 mus musculus
30	26	83.9	456	1 RICH_HUMAN	P35790 homo sapien
31	26	83.9	1407	1 CYAA_DICDI	Q03100 dictyosteli
32	26	83.9	2017	1 MYSN_DROME	Q99323 drosophila
33	25	80.6	259	1 FLA2_NATMA	Q93718 natrialba m

RESULT 1

KV3P_MOUSE
ID KV3P_MOUSE STANDARD; PRT; 110 AA.
AC P01668;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 7210.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.

RX MEDLINE-79073152; PubMed-103003;

RA Weigert M., Garmaitan L., Loh E., Schilling J., Hood L.E.;

RT "Rearrangement of genetic information may produce immunoglobulin

RT diversity";

RL Nature 276:785-790 (1978).

DR PIR; D01937; KVM510.

DR InterPro: IPR003006; -

DR Pfam: PF000047; Ig: 1.

KW Immunoglobulin V region.

FT DOMAIN 1 23

FT DOMAIN 24 38 FRAMEWORK 1. COMPLEMENTARITY-DETERMINING 1.

FT DOMAIN 39 53 FRAMEWORK 2.

FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.

FT DOMAIN 61 92 FRAMEWORK 3.

FT DOMAIN 93 100 COMPLEMENTARITY-DETERMINING 3.

FT DOMAIN 101 110 FRAMEWORK 4.

FT DISULFID 23 92 BY SIMILARITY.

FT NON_TER 110 110

SQ SEQUENCE 110 AA; 11950 MW; 69FIA5CE886B1249 CRC64;

Query Match 100.0%; Score 31; DB 1; Length 110;

Best Local Similarity 100.0%; Pred. No. 0.65;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7

DB 54 AASNLES 60

RESULT 2

KV3L_MOUSE
ID KV3L_MOUSE STANDARD; PRT; 111 AA.
AC P01664;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION CBPC 101.
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

```

RN  SEQUENCE.
RX  MEDLINE=79012520; PubMed=99744;
RA  McKean D.J., Bell M., Potter M.;
RT  "Mechanisms of antibody diversity: multiple genes encode structurally
RT  related mouse kappa variable regions.";
RL  Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
CC  -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR  PIR; A01936; KVMSC1.
DR  InterPro: IPR003006; -.
DR  Pfam: PF00047; Ig; 1.
KW  Immunoglobulin V region.
FT  DOMAIN 1 23
FT  DOMAIN 24 38
FT  DOMAIN 39 53
FT  DOMAIN 54 60
FT  DOMAIN 61 92
FT  DOMAIN 93 101
FT  DOMAIN 102 111
FT  DISULFID 23 92
FT  NON_TER 111 111
SQ  SEQUENCE 111 AA; 11964 MW; E2BIAD98AD965962 CRC64;

Query Match 100.0%; Score 31; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AASNLES 7
DB 54 AASNLES 60

RESULT 3
KV3M_MOUSE
ID KV3M_MOUSE STANDARD; PRT; 111 AA.
AC P01665;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 7043.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR PIR; B01937; KVMSC3.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11952 MW; 2058BB50CE306D31 CRC64;

Query Match 100.0%; Score 31; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AASNLES 7
DB 54 AASNLES 60

RESULT 5
KV3Q_MOUSE
ID KV3Q_MOUSE STANDARD; PRT; 111 AA.
AC P01669;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 7769.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR PIR; E01937; KVMSC9.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12002 MW; 7A5FCB586C306D29 CRC64;

Query Match 100.0%; Score 31; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AASNLES 7
DB 54 AASNLES 60

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DB 54 AASNLES 60

RESULT 4
KV3N_MOUSE
ID KV3N_MOUSE STANDARD; PRT; 111 AA.
AC P01666;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 7183.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR PIR; B01937; KVMSC3.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11952 MW; 2058BB50CE306D31 CRC64;

Query Match 100.0%; Score 31; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AASNLES 7
DB 54 AASNLES 60

RESULT 5
KV3Q_MOUSE
ID KV3Q_MOUSE STANDARD; PRT; 111 AA.
AC P01669;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 7769.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR PIR; E01937; KVMSC9.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12002 MW; 7A5FCB586C306D29 CRC64;

Query Match 100.0%; Score 31; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AASNLES 7
DB 54 AASNLES 60

```

FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT DOMAIN 102 111
 FT DISULFID 23 92
 FT NON_TER 111 111
 SQ SEQUENCE 111 AA; 12011 MW; 6FAA345279356829 CRC64;

Query Match 100.0%; Score 31; DB 1; Length 111;
 Best Local Similarity 100.0%; Pred. No. 0.65;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
 DB 54 AASNLES 60

RESULT 6
 YIEO_HAEIN
 ID YIEO_HAEIN STANDARD; PRT; 463 AA.
 AC P44903;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE HYPOTHETICAL PROTEIN HI0852.
 GN HI0852.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Haemophilus.
 OX NCBI_TaxID=727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-RD / KW20 / ATCC 51907;
 RX MEDLINE=95350630; PubMed=7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA McInerney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus
 influenzae Rd.";
 RL Science 269:496-512(1995).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
 CC (PROBABLE).
 CC -!- SIMILARITY: STRONG. TO E.COLI YIEO.
 CC -!- SIMILARITY: BELONGS TO THE MAJOR FACILITATOR FAMILY (ALSO KNOWN
 CC AS THE DRUG RESISTANCE TRANSLOCASE FAMILY).
 CC -----
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 CC -----
 DR EMBL; U32766; AAC22509.1; -
 DR TIGR; HI0852; -
 KW Hypothetical protein; Transport; Transmembrane; Inner membrane.
 FT TRANSMEM 10 30 POTENTIAL.
 FT TRANSMEM 49 69 POTENTIAL.
 FT TRANSMEM 82 102 POTENTIAL.
 FT TRANSMEM 107 127 POTENTIAL.
 FT TRANSMEM 139 159 POTENTIAL.
 FT TRANSMEM 165 185 POTENTIAL.
 FT TRANSMEM 197 217 POTENTIAL.
 FT TRANSMEM 225 245 POTENTIAL.

FT TRANSMEM 267 287 POTENTIAL.
 FT TRANSMEM 298 318 POTENTIAL.
 FT TRANSMEM 328 348 POTENTIAL.
 FT TRANSMEM 354 374 POTENTIAL.
 FT TRANSMEM 393 413 POTENTIAL.
 FT TRANSMEM 429 449 POTENTIAL.
 SQ SEQUENCE 463 AA; 50002 MW; D725EFFD50F9F23F CRC64;

Query Match 100.0%; Score 31; DB 1; Length 463;
 Best Local Similarity 100.0%; Pred. No. 3.2;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
 DB 94 AASNLES 100

RESULT 7
 KVIG_HUMAN
 ID KVIG_HUMAN STANDARD; PRT; 108 AA.
 AC P01599;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-I REGION GAL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=75059122; PubMed=4215718;
 RA Laure C.J., Wataabe S., Hilschmann N.;
 RT "The primary structure of a monoclonal IgM-immunoglobulin
 RT (macroglobulin Gal.), I. The amino acid sequence of the L-chain of
 RL kappa-type, subgroup I.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 354:1503-1504(1973).
 CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
 CC MACROGLOBULIN.
 DR PIR; A01867; KIHUGL.
 DR HSSP; P01607; IREI.
 DR InterPro; IPR003006; -
 DR Pfam; PF00047; Ig; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 107
 FT DISULFID 23 88
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11814 MW; CIAD3CB0F600FF73 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 108;
 Best Local Similarity 85.7%; Pred. No. 3.6;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
 DB 50 AASNLES 56

RESULT 8
 VP9_WTV
 ID VP9_WTV STANDARD; PRT; 313 AA.
 AC P12326;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)

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Best Local Similarity 85.7%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

01-JUL-1993 (Rel. 26, Last annotation update)
DE STRUCTURAL PROTEIN P9 (CAPSOMERE PROTEIN P9) (PROTEIN PNS11).
GN S11.
OS Wound tumor virus (WTV).
OC Viruses; dsRNA viruses; Reoviridae; Phytoreovirus.
OX NCBI_TaxID=10987;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89263810; PubMed=2726499;
RA Dall D.J., Anzola J.V., Xu Z., Nuss D.L.;
RT "Complete nucleotide sequence of wound tumor virus genomic segment
S11".
RL Nucleic Acids Res. 17:3599-3599(1989).
CC -!- SIMILARITY: TO RICE DWARF VIRUS S9 AND RICE GALL DWARF VIRUS S10.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X14219; CAA324239.1;
DR PIR; S04139; QMWRWT.
SQ SEQUENCE 313 AA; 35606 MW; 6746F59840AD17F2 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 313;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNL5 7
DB 294 AASNL5 300

RESULT 9
VP9_WTVNJ STANDARD; PRT; 313 AA.
ID VP9_WTVNJ
AC P31611;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE STRUCTURAL PROTEIN P9 (CAPSOMERE PROTEIN P9) (PROTEIN PNS11).
OS Wound tumor virus (strain NJ) (WTV).
OC Viruses; dsRNA viruses; Reoviridae; Phytoreovirus.
OX NCBI_TaxID=31595;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92074261; PubMed=1962460;
RA Hillman B.I., Anzola J.V., Halpern B.T., Cavileer T.D., Nuss D.L.;
RT "First field isolation of wound tumor virus from a plant host:
minimal sequence divergence from the type strain isolated from an
insect vector".
RL Virology 185:896-900(1991).
CC -!- SIMILARITY: TO RICE DWARF VIRUS S9 AND RICE GALL DWARF VIRUS S10.
CC
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CC
CC EMBL; M77020; AAA48500.1;
DR PIR; C41705; QMWRWN.
KW Nonstructural protein.
SQ SEQUENCE 313 AA; 35551 MW; D9B904785C601C34 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 313;

QY 1 AASNL5 7
DB 294 AASNL5 300

RESULT 10
FTSH_HELPJ STANDARD; PRT; 632 AA.
ID FTSH_HELPJ
AC Q9ZM66;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CELL DIVISION PROTEIN FTSH HOMOLOG (EC 3.4.24.-).
GN FTSH OR JHP0356.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9912057; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.C., deTonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives G.F.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
gastric pathogen Helicobacter pylori".
RL Nature 397:176-180(1999)
CC -!- FUNCTION: SEEMS TO ACT AS AN ATP-DEPENDENT ZINC METALLOPEPTIDASE
CC (BY SIMILARITY).
CC -!- COFACTOR: BINDS ONE ZINC ION (POTENTIAL).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M41 (ZINC
CC METALLOPROTEASE).
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AE001471; AAD05932.1;
DR InterPro; IPR000642;
DR InterPro; IPR001939;
DR Pfam; PF00004; AAA; 1.
DR Pfam; PF01434; Peptidase_M41; 1.
DR PROSITE; PS00674; AAA; 1.
KW Cell division; ATP-binding; Transmembrane; Hydrolase; Metalloprotease;
KW Zinc.
FT DOMAIN 1 9 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 10 31 POTENTIAL.
FT DOMAIN 32 116 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 117 137 POTENTIAL.
FT DOMAIN 138 632 CYTOPLASMIC (POTENTIAL).
FT NP_BIND 210 217 ATP (POTENTIAL).
FT METAL 434 434 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 435 435 BY SIMILARITY.
FT METAL 438 438 ZINC (CATALYTIC) (BY SIMILARITY).
SQ SEQUENCE 632 AA; 69765 MW; 2FB67B43C51559FB CRC64;

Query Match 90.3%; Score 28; DB 1; Length 632;
Best Local Similarity 85.7%; Pred. No. 25;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNL5 7

Db 616 AANNLES 622

|||||

RESULT 11
KL68_DROME
ID KL68_DROME STANDARD; PRT; 784 AA.
AC P48867;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 15-JUL-1998 (Rel. 36, Last annotation update)
DE KINESIN-LIKE PROTEIN KL68D.
GN KLP68D OR KLP5.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Phrygotea; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95050960; PubMed=7525600;
RA Pesavento P.A., Stewart R.J., Goldstein L.S.B.;
RT "Characterization of the KLP68D kinesin-like protein in Drosophila;
RL Possible roles in axonal transport.";
RN J. Cell Biol. 127:1041-1048(1994).
[2]
RP SEQUENCE OF 220-342 FROM N.A.
RX MEDLINE=92020874; PubMed=1924306;
RA Stewart R.J., Pesavento P.A., Woerpel D.N., Goldstein L.S.B.;
RT "Identification and partial characterization of six members of the
RL kinesin superfamily in Drosophila.";
RN Proc. Natl. Acad. Sci. U.S.A. 88:8470-8474(1991).
CC -1- FUNCTION: PLUS-END DIRECTED MICROTUBULE MOTOR THAT MAY BE USED FOR
CC ANTEROGRADE AXONAL TRANSPORT AND COULD CONCEIVABLY MOVE CARGOES IN
CC FLY NEURONS DIFFERENT THAN THOSE MOVED BY KINESIN HEAVY CHAIN OR
CC OTHER PLUS-END DIRECTED MOTORS.
CC -1- TISSUE SPECIFICITY: EXPRESSED PRIMARILY IN THE CENTRAL NERVOUS
CC SYSTEM AND IN A SUBSET OF THE PERIPHERAL NERVOUS SYSTEM DURING
CC EMBRYOGENESIS.
CC -1- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. KINESIN
CC II SUBFAMILY.

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EMBL; U15974; AAA69929.1; -
EMBL; M74431; AAA28658.1; -
DR HSSP; P56536; 2KIN.
DR FlyBase; FBgn0004381; klp68D.
DR InterPro; IPR001752; -
DR Pfam; PF00225; kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR PROSITE; PS00057; KINESIN_MOTOR_DOMAIN2; 1.
KW Motor protein; Microtubules; ATP-binding; Coiled coil.
FT DOMAIN 16 275 MECHANOCHEMICAL (MOTOR).
FT DOMAIN 351 385 COILED COIL (POTENTIAL).
FT NP_BIND 106 113 COILED COIL (POTENTIAL).
FT NP_BIND 220 221 ATP (POTENTIAL).
FT CONFLICT 338 342 SS -> TC (IN REF. 2).
FT CONFLICT 338 342 GSRK -> VRGV (IN REF. 2).
SQ SEQUENCE 784 AA; 88193 MW; 94BB9BADF072DFC0 CRC64;

Query Match 90.38; Score 28; DB 1; Length 784;
Best Local Similarity 85.79; Pred. No. 32;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AANNLES 7
Db 751 AASNLD 757
|||||

RESULT 12
KVIB_HUMAN
ID KVIB_HUMAN STANDARD; PRT; 108 AA.
AC P01594;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION AU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72189444; PubMed=5028201;
RA Schiechl H., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RL immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
RN Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
[2]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=77022433; PubMed=1234024;
RA Fehnhamer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
RT Schwager P., Steigemann W., Schramm H.J.;
RL "The structure determination of the variable portion of the
RN Bence-Jones protein Au.";
CC Biophys. Struct. Mech. 1:139-146(1975).
CC -1- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY
CC MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V
CC REGION OF THE KAPPA CHAIN REI.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
CC PIR; A01862; KIHUA.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; -
DR Pfam; PF00047; Ig; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 107 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11939 MW; E8011187EE6F6B9 CRC64;

Query Match 87.18; Score 27; DB 1; Length 108;
Best Local Similarity 100.08; Pred. No. 6.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AANNLES 7
Db 51 AASNLD 56
|||||

RESULT 13
KV3V_MOUSE
ID KV3V_MOUSE STANDARD; PRT; 108 AA.
AC P01674;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 2154.
OS Mus musculus (Mouse).

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FT DISULFID 23 92 BY SIMILARITY.
 FT NON_TER 111
 SQ SEQUENCE 111 AA; 12099 MW; EC46C9D259213BE4 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 111;
 Best Local Similarity 100.0%; Pred. No. 6.7;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASNLES 7
 Db 55 ASNLES 60

RESULT 15
 KV3J_MOUSE STANDARD; PRT: 111 AA.
 ID KV3J_MOUSE
 AC P01662;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION ABPC 22/PC 9245.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;

RP SEQUENCE (ABPC 22).
 RX MEDLINE=79073152; PubMed=99744;
 RA McKean D.J., Bell M., Potter M.;
 RT "Mechanisms of antibody diversity: multiple genes encode structurally
 related mouse kappa variable regions.";
 RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
 RN [1]
 RN [2]

RP SEQUENCE (PC 9245).
 RX MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 diversity.";
 RL Nature 276:785-790(1978).
 CC -1- MISCELLANEOUS: THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.

DR InterPro: IPR003006;
 DR PIR: A01935; KVM5M6.
 DR PIR: PF00047; Ig: 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT DOMAIN 102 111
 FT DISULFID 23 92
 FT NON_TER 111
 SQ SEQUENCE 111 AA; 12041 MW; D7DF0609303453CE CRC64;

Query Match 87.1%; Score 27; DB 1; Length 111;
 Best Local Similarity 100.0%; Pred. No. 6.7;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASNLES 7
 Db 55 ASNLES 60

Search completed: June 28, 2001, 15:54:36
 Job time: 124 sec

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;

RP SEQUENCE.
 RX MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 diversity.";
 RL Nature 276:785-790(1978).
 DR PIR: A01940; KVM554.
 DR InterPro: IPR003006; -;
 DR PIR: PF00047; Ig: 1.

DR Immunoglobulin V region.
 KW DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT DOMAIN 102 108
 FT DISULFID 23 92
 FT NON_TER 108
 SQ SEQUENCE 108 AA; 11699 MW; D40921D18DAC4B9E CRC64;

Query Match 87.1%; Score 27; DB 1; Length 108;
 Best Local Similarity 100.0%; Pred. No. 6.5;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASNLES 7
 Db 55 ASNLES 60

RESULT 14
 KV3H_MOUSE STANDARD; PRT: 111 AA.
 ID P01660;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION PC 3741/TEPC 111.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;

RP SEQUENCE (PC 3741).
 RX MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 diversity.";
 RL Nature 276:785-790(1978).
 RN [1]

RP SEQUENCE (TEPC 111).
 RX MEDLINE=79012520; PubMed=99744;
 RA McKean D.J., Bell M., Potter M.;
 RT "Mechanisms of antibody diversity: multiple genes encode structurally
 related mouse kappa variable regions.";
 RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).

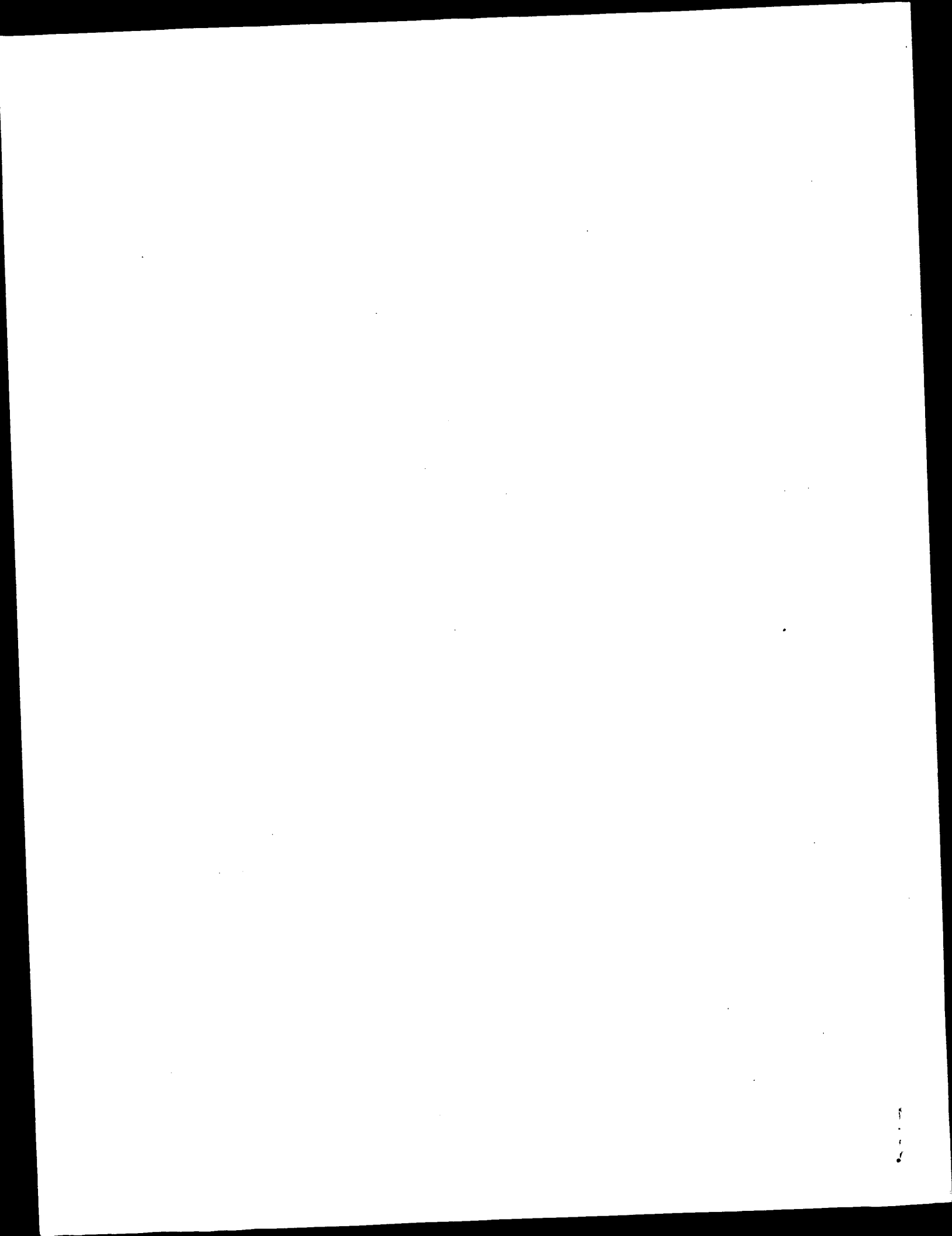
CC -1- MISCELLANEOUS: THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL.
 DR InterPro: IPR003006;
 DR PIR: A01934; KVM537.
 DR PIR: PF00047; Ig: 1.
 KW Immunoglobulin V region.

FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT DOMAIN 102 111
 FT DOMAIN 103 111

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OM protein - protein search, using sw model
Run on: June 28, 2001, 16:08:21 ; Search time 411.58 Seconds
(without alignments)
2.250 Million cell updates/sec

Title: US-09-724-406-14

Perfect score: 31
Sequence: 1 AASNLES 7

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues
Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL16:.*
1: sp-archaea:.*
2: sp-bacteria:.*
3: sp-fungi:.*
4: sp-human:.*
5: sp-invertebrate:.*
6: sp-mammal:.*
7: sp-mhc:.*
8: sp-organelle:.*
9: sp-phage:.*
10: sp-plant:.*
11: sp-rodent:.*
12: sp-unclassified:.*
13: sp-vertebrate:.*
14: sp-virus:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	942	3	042938
2	31	100.0	1208	4	075162
3	28	90.3	103	11	09JL80
4	28	90.3	204	5	09U2Y4
5	28	90.3	784	5	09VTN8
6	27	87.1	310	2	P94981
7	27	87.1	389	10	09SAF7
8	27	87.1	419	10	09M887
9	27	87.1	443	10	09L176
10	27	87.1	468	10	09LFX3
11	27	87.1	497	3	074901
12	27	87.1	576	14	09JGJ9
13	27	87.1	619	2	09F9H4
14	27	87.1	643	10	09LSX2
15	27	87.1	689	1	09HMT9
16	27	87.1	746	3	Q08754
17	27	87.1	826	13	09YHD5
18	27	87.1	832	5	016360
19	27	87.1	856	5	09V706

20	27	87.1	927	2	09PGG3
21	27	87.1	1195	13	09PUM2
22	27	87.1	1425	2	085862
23	27	87.1	2406	5	09N905
24	27	87.1	4880	11	09JLT1
25	27	87.1	5085	11	09JKS6
26	26	83.9	292	5	023983
27	26	83.9	297	2	050805
28	26	83.9	367	10	09SE32
29	26	83.9	367	10	09FPB1
30	26	83.9	408	4	094798
31	26	83.9	444	4	09UHX4
32	26	83.9	547	5	09VWD9
33	26	83.9	585	13	09FVN8
34	26	83.9	588	4	09H3W6
35	26	83.9	589	4	09HAZ5
36	26	83.9	589	4	09H3R4
37	26	83.9	589	4	09H0T8
38	26	83.9	595	4	09UMX0
39	26	83.9	601	4	09NKR5
40	26	83.9	624	4	09UHD9
41	26	83.9	624	4	09HAZ4
42	26	83.9	624	4	09UHD9
43	26	83.9	638	11	09QZM0
44	26	83.9	664	10	022834
45	26	83.9	750	5	001348
	26	83.9	801	5	09VTD3

ALIGNMENTS

RESULT 1
O42938 ID O42938 PRELIMINARY; PRT; 942 AA.
AC O42938
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE PROBABLE 6-PHOSPHOFRUCTOKINASE BETA SUBUNIT (EC 2.7.1.11)
GN SPEC16H5.02. (PHOSPHOFRUCTOKINASE 1) (PHOSPHOHEXOKINASE) (6PF-1-K BETA SUBUNIT).
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Wood V., Rajandream M.A., Barrell B.G., Skelton J., Churcher C.M.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -! CATALYTIC ACTIVITY: ATP + D-FRUCTOSE 6-PHOSPHATE = ADP + D-FRUCTOSE 1,6-BISPHOSPHATE.
CC -! PATHWAY: KEY CONTROL STEP OF GLYCOLYSIS.
CC -! SUBUNIT: HETEROOCTAMER OF 4 ALPHA AND 4 BETA CHAINS (BY SIMILARITY).
CC EMBL; AL022104; CAA17900.1; -.
DR HSSP; P00512; 3PEK
DR InterPro; IPR000023; -.
DR Pfam; PF00365; PFK; 3.
DR PRINTS; PR00476; PHFRCTKINASE.
DR PRODOM; PD000707; -. 2.
DR PROSITE; PS00433; PHOSPHOFRUCTOKINASE; 2.
KW Kinase; Transferase; Glycolysis; Repeat; Allosteric enzyme;
KW Phosphorylation; Magnesium
SQ SEQUENCE 942 AA; 102554 MW; C6052AF7C1DB75B4 CRC64;

Query Match 100.0%; Score 31; DB 3; Length 942;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7

us-09-724-406-14.rspt

Fri Jun 29 08:04:28 2001

Query Match 90.3%; Score 28; DB 11; Length 103;
 Best Local Similarity 85.7%; Pred. No. 17;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
 Db 46 AASNLES 52

RESULT 4
 Q9U2Y4 PRELIMINARY; PRT: 204 AA.

ID Q9U2Y4
 AC Q9U2Y4
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE Y113G7A.14 PROTEIN.

GN Y113G7A.14
 OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN SEQUENCE FROM N.A.

RP Lennard N.; Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.

RL [2] SEQUENCE FROM N.A.

RP MEDLINE=99069613; PubMed=9851916;

RA none;

RT "Genome sequence of the nematode C.elegans: A platform for

RL Science 282:2012-2018(1998).

DR EMBL: AL132858; CAB60484.1; -- 8968065DF2EA9C7E CRC64;

SQ SEQUENCE 204 AA; 23067 MW; 8968065DF2EA9C7E CRC64;

Query Match 90.3%; Score 28; DB 5; Length 204;
 Best Local Similarity 85.7%; Pred. No. 35;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
 Db 134 SASNLES 140

RESULT 5
 Q9VTN8 PRELIMINARY; PRT: 784 AA.

ID Q9VTN8
 AC Q9VTN8
 DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)

DE KLP68D PROTEIN.

GN KLP68D OR CG7293.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN SEQUENCE FROM N.A.

RP STRAIN=BERKELEY;

RC MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,

Db 165 AASNLES 171

RESULT 2
 Q75162 PRELIMINARY; PRT: 1208 AA.

ID Q75162
 AC Q75162
 DT 01-NOV-1998 (TREMBlrel. 08, Created)

DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)

DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)

DE KIAA0675 PROTEIN.

GN KIAA0675.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN SEQUENCE FROM N.A.

RP TISSUE=BRAIN;

RC MEDLINE=98403880; PubMed=9734811;

RA Ishikawa K., Nagase T., Suyama M., Miyajima N., Tanaka A., Kotani H.,

RA Nomura N., Ohara O.;

RT "Prediction of the coding sequences of unidentified human genes. X.

RT The complete sequences of 100 new cDNA clones from brain which can

RL code for large proteins in vitro.";

RL DNA Res. 5:169-176(1998).

CC -1- SIMILARITY: CONTAINS A RING (C3HC4-CLASS) ZINC FINGER.

DR EMBL: AB014575; BAA31650.1; --

DR HSSP: P28990; 1CHC.

DR InterPro: IPR001841; --

DR Pfam: PF00097; zf-C3HC4; 1.

DR SMART: SM00184; RING; 1.

KW Zinc-finger. 1208 AA; 138603 MW; 76945A63AF85207E CRC64;

SQ SEQUENCE 1208 AA; 138603 MW; 76945A63AF85207E CRC64;

Query Match 100.0%; Score 31; DB 4; Length 1208;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7
 Db 896 AASNLES 902

RESULT 3
 Q9JL80 PRELIMINARY; PRT: 103 AA.

ID Q9JL80
 AC Q9JL80
 DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)

DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).

DE Mus musculus (Mouse).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN SEQUENCE FROM N.A.

RP STRAIN=BALB/C;

RC Malkiel S., Liao L., Cunningham M.W., Diamond B.;

RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-

RT acetyl-glucosamine antibodies from mice with autoimmune myocarditis."

RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF206026; AAF69324.1; --

DR InterPro: IPR003006; --

DR Pfam: PF00047; Ig; 1.

DR SMART: SM00406; IGV; 1.

FT NON_TER 103 103

FT NON_TER 103 103

SQ SEQUENCE 103 AA; 11224 MW; EC87D653DB3AAB21 CRC64;

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.A., Bouck J., Brokstein P., Bottlier P.,
RA Burtis K.C., Busam D.R., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fostier C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrelli J.H., Gu Z., Kennison J.P., Ketchum K.A.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulo G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.A.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.L.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan W., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RA "The genome sequence of Drosophila melanogaster."
RT Science 287:2185-2193 (2000).
RL EMBL: AE003543; AAF50008.1; -;
DR HSPB: P17129; 3KAR.
DR FLYBase: FBgn0004381; Klp68D.
DR InterPro: IPR001752; -;
DR Pfam: PF00225; kinesin; 1.
DR PRINTS: PR00380; KINESINHEAVY.
DR PROSITE: PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR PROSITE: PS00667; KINESIN_MOTOR_DOMAIN2; 1.
DR SMART: SM00129; KISC; 1.
KW ATP-binding; Coiled coil; Microtubules; Motor protein.
SQ SEQUENCE 784 AA; 8820 MW; 7A3C6716D22BC05D CRC64;

Query Match 90.3%; Score 28; DB 5; Length 784;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLS 7
DB 751 AASNLS 757

RESULT 6
P94981 ID P94981 PRELIMINARY; PRT; 310 AA.
AC P94981;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DE HYPOTHETICAL 30.2 KDA PROTEIN.
GN RV1646 OR MTCY06H11.1.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV.
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Busham D., Brown D., Chillingworth T., Connor R.,

RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squires R., Sulston J.E.,
RA Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence."
RL Nature 393:537-544 (1998).
DR EMBL: Z85982; CAB06640.1; -;
DR Tuberculist; RV1646; -;
DR InterPro: IPR000084; -;
DR Pfam: PF00934; PE; 1.
DR ProDom: PD001223; -; 1.
KW Hypothetical protein.
SQ SEQUENCE 310 AA; 30219 MW; F51DFE4CC2D9EDAD CRC64;

Query Match 87.1%; Score 27; DB 2; Length 310;
Best Local Similarity 85.7%; Pred. No. 96;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AASNLS 7
DB 14 AAGNLS 20

RESULT 7
Q9SAF7 ID Q9SAF7 PRELIMINARY; PRT; 389 AA.
AC Q9SAF7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE F3F19-36 PROTEIN.
GN F3F19.26.
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lee J.M., Lenz C.,
RA Liu S., Li J., Kremenetskaia I., Luros J., Ngan I., Gonzalez A.,
RA Altafi H., Araujo R., Chao Q., Conn L., Conway A.B., Dunn P.,
RA Hansen N., Huizar L., Kim C., Palm C., Rowley D., Shinn P., Walker M.,
RA Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
RT "Arabidopsis thaliana chromosome 1 BAC F3F19 sequence."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Theologis A.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Theologis;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC007357; AAC31076.1; -;
DR InterPro: IPR001350; -;
DR InterPro: IPR001611; -;
DR InterPro: IPR003592; -;
DR Pfam: PF00560; LRR; 7.
DR PRINTS: PR00019; LEURICHRPT.
DR PROSITE: PS00572; GLYCOSYL_HYDROL_F1_1; UNKNOWN_1.
DR SMART: SM00370; LFR; 1.
SQ SEQUENCE 389 AA; 43216 MW; 1DC342A0BF4B7EBF CRC64;

Query Match 87.1%; Score 27; DB 10; Length 389;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;

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Sequence features of the regions of 4,251,695 bp covered by ninety Pl.
 RT TAC and BAC clones.
 RL DNA Res.: 7:217-221(2000).
 DR EMBL: AF001313; BAB03087.1; -.
 DR InterPro: IPR001360; -.
 DR InterPro: IPR001611; -.
 DR InterPro: IPR003592; -.
 DR Pfam: PF00560; LRR: 4.
 DR PRINTS: PR00019; LEURICHRPT.
 DR PROSITE: PS00572; GLYCOSYL_HYDROL_F1_1; UNKNOWN1.
 DR SMART: SM00370; LRR: 1.
 KW Receptor. 443 AA; 49318 MW; 1E2D37B3F9066F4C CRC64;
 SQ SEQUENCE

Query Match 87.1%; Score 27; DB 10; Length 443;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASNLES 7
 DB 105 ASNLES 110

RESULT 10
 Q9LFX3 PRELIMINARY; PRT; 468 AA.
 ID Q9LFX3
 AC Q9LFX3
 DT 01-OCT-2000 (TREMELrel. 15, Created)
 DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMELrel. 16, Last annotation update)
 DE T7N9.21.
 OS Arabidopsis thaliana (Mouse-ear cross).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; euroids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=3702;
 OX [1]
 RN SEQUENCE FROM N.A.
 RP Chinn S., Brooks S., Buehler E., Chao O., Johnson-Hopson C., Kim C.,
 RA Khan P., Altafi H., Bei Q., Chin C., Chlou J., Choi E., Conn L.,
 RA Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Lee J.,
 RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
 RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
 RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
 RA Ecker J.R.;
 FT "Genomic sequence for Arabidopsis thaliana BAC T7N9 from chromosome
 I."
 RT Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RL [2]
 RN SEQUENCE FROM N.A.
 RP Ecker J.R.;
 RA Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RL [3]
 RN SEQUENCE FROM N.A.
 RP Ecker J.R.;
 RA Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 RL [4]
 RN SEQUENCE FROM N.A.
 RP Ecker J.R.;
 RA Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 RL [5]
 RN SEQUENCE FROM N.A.
 RP Ecker J.R.;
 RA Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 RL [6]
 RN SEQUENCE FROM N.A.
 RP Cheuk R., Shinn P., Brooks S., Buehler E., Chao O., Johnson-Hopson C.,
 RA Khan S., Kim C., Altafi H., Bei Q., Chin C., Chlou J., Choi E., Lam B.,
 RA Conn L., Conway A., Gonzalez A., Hansen N., Howng B., Koo T., Lam B.,
 RA Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N.,
 RA Nguyen M., Pham P., Sakano H., Schwartz J., Southwick A.,
 RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.,
 RA Ecker J.R.

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASNLES 7
 DB 106 ASNLES 111

RESULT 8
 Q9M887 PRELIMINARY; PRT; 419 AA.
 ID Q9M887
 AC Q9M887
 DT 01-OCT-2000 (TREMELrel. 15, Created)
 DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMELrel. 16, Last annotation update)
 DE PUTATIVE RAD23.
 GN FlbB3.17.
 OS Arabidopsis thaliana (Mouse-ear cross).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; euroids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=3702;
 OX [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN-CV. COLUMBIA;
 RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.,
 RA Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
 RA Bowman C.L., White O., Nierman W.C., Fraser C.M.;
 RA "Arabidopsis thaliana chromosome III BAC F16B3 genomic sequence."
 RT Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AC021640; AAF32461.1; -.
 DR InterPro: IPR000449; -.
 DR InterPro: IPR002965; -.
 DR Pfam: PF00240; ubiquitin; 1.
 DR PRINTS: PR00627; UBA; 2.
 DR PROSITE: PS0053; UBQUITIN.2; 1.
 DR SEQUENCE 419 AA; 44247 MW; CAA13BC4FFEB1E25 CRC64;

Query Match 87.1%; Score 27; DB 10; Length 419;
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AASNLES 7
 DB 183 AGSNLES 189

RESULT 9
 Q9LI76 PRELIMINARY; PRT; 443 AA.
 ID Q9LI76
 AC Q9LI76
 DT 01-OCT-2000 (TREMELrel. 15, Created)
 DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMELrel. 16, Last annotation update)
 DE SIMILARITY TO ELICITOR-INDUCIBLE RECEPTOR EIR.
 OS Arabidopsis thaliana (Mouse-ear cross).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; euroids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=3702;
 OX [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN-COLUMBIA;
 RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RL [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN-COLUMBIA;
 RX PubMed=10907853;
 RA Nakamura Y.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. II."

RA Theologis A., Ecker J.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC000348; AAF79860.1; -;
 SQ SEQUENCE 468 AA; 53589 MW; F140B6E374024FEB CRC64;

Query Match
 Best Local Similarity 87.1%; Score 27; DB 10; Length 468;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AASNLE 6
 |||||
 Db 78 AASNLE 83

RESULT 11
 074901
 ID 074901 PRELIMINARY; PRT; 497 AA.
 AC 074901
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DE HYPOPHETICAL 55.1 KDA PROTEIN.
 GN SPCC613.01 OR SPCC757.14.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972H-;
 RA Bothe G., Pohl T., Lyne M., Rajandream M.A., Barrell B.G., Bothe G., Pohl T.;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 1-260 FROM N.A.
 RC STRAIN=972H-;
 RA Lyne M., Rajandream M.A., Barrell B.G., Bothe G., Pohl T.;
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL031644; CAA21053.1; -;
 DR EMBL; AL031825; CAA21239.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 497 AA; 55125 MW; 63D113F831A602C7 CRC64;

Query Match
 Best Local Similarity 87.1%; Score 27; DB 3; Length 497;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AASNLES 7
 |||||
 Db 62 ATSNLES 68

RESULT 12
 09JGJ9
 ID 09JGJ9 PRELIMINARY; PRT; 576 AA.
 AC 09JGJ9;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DE 64-KDA READTHROUGH PROTEIN (FRAGMENT).
 GN RT.
 OS soil-borne wheat mosaic virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Furovirus.
 OX NCBI_TaxID=28375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JAPANESE;
 RX MEDLINE=20238044; PubMed=10772992;
 RA Shiraki Y., Suzuki N., French R.C.;
 RT "Similarity and divergence among viruses in the genus Furovirus.";
 RL Virology 270:201-207(2000).

DR EMBL; AB033690; BAA94800.1; -;
 FT NON_TER 1
 SQ SEQUENCE 575 AA; 63984 MW; 8DF91221FD61E1F7 CRC64;

Query Match
 Best Local Similarity 87.1%; Score 27; DB 14; Length 576;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AASNLES 7
 |||||
 Db 453 AENLES 459

RESULT 13
 09F9H4
 ID 09F9H4 PRELIMINARY; PRT; 619 AA.
 AC 09F9H4;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DE OUTER MEMBRANE PROTEIN A.
 GN OMPA.
 OS Rickettsia felis (Rickettsia azadi).
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
 OC Rickettsiaceae; Rickettsieae; Rickettsia.
 OX NCBI_TaxID=42862;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bouyer D.H., Stenos J., Crocquet-Valdes P.A., Foil L.D., Walker D.H.;
 RT "The identification and characterization of a previously undiscovered
 rOmpA-encoding gene in Rickettsia felis";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF191026; AAG17185.1; -;
 SQ SEQUENCE 619 AA; 60547 MW; 1AA12066EEFA1B CRC64;

Query Match
 Best Local Similarity 100.0%; Score 27; DB 2; Length 619;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLE 6
 |||||
 Db 508 AASNLE 513

RESULT 14
 09LSX2
 ID 09LSX2 PRELIMINARY; PRT; 643 AA.
 AC 09LSX2;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DE EMB|CAB8628.1.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RX MEDLINE=20181125; PubMed=10718197;
 RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
 RT features of the regions of 3,076,755 bp covered by sixty P1 and TAC
 RT clones";
 RL DNA Res. 7:31-63(2000).
 DR EMBL; AB025638; BAA97418.1; -;
 DR InterPro; IPR001471; -;
 DR ProDom; PD001423; -; 1.
 SQ SEQUENCE 643 AA; 73049 MW; 58B44A6C4A18DA21 CRC64;

us-09-724-406-14.rspt

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Query Match 87.1%; Score 27; DB 10; Length 643;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASNLES 7
 Db 541 ASNLES 546

RESULT 15
 Q9HMT9 PRELIMINARY; PRT; 689 AA.
 ID Q9HMT9
 AC Q9HMT9;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE EXCISION NUCLEASE CHAIN B.
 GN UVRB OR VNG2390G.
 OS Halobacterium sp. (strain NRC-1).
 OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
 OC Halobacterium.
 OX NCBI_TaxID=64091;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20504483; PubMed=11016950;
 RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
 RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
 RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
 RA Leithausen B., Keller K., Cruz R., Danson M.J., Hough D.W., Dale H.,
 RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Spudich J.L., Jung K.-H.,
 RA Isenbarger T.A., Peck R.F., Fohlschroder M., Dennis P.P., Omer A.D.,
 RA Alam M., Freitas T., Hou S., Daniels C.J., Hood L., Dassarma S.,
 RA Ehardt H., Lowe T.M., Liang P., Riley M., Hood L.,
 RT "Genome sequence of Halobacterium species NRC-1.",
 RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
 DR EMBL; AE005120; AAG20482.1; -;
 DR InterPro; IPR001410; -;
 DR InterPro; IPR001650; -;
 DR InterPro; IPR001943; -;
 DR Pfam; PF00271; helicase_C; 1.
 DR Pfam; PF02151; UVR; 1.
 SQ SEQUENCE 689 AA; 77507 MW; BED16C96A94E93B8 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 689;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLE 6
 Db 645 AASNLE 650

Search completed: June 28, 2001, 16:08:22
 Job time: 950 sec

1

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	54	100.0	111	15	AAR55123	Mouse anti-HIV mu5
2	54	100.0	111	15	AAR55127	Mouse-human chimera
3	54	100.0	111	15	AAR60302	Anti HIV antibody
4	54	100.0	111	15	AAR60306	Chimeric anti HIV
5	54	100.0	113	22	AAW1895	Monoclonal antibody
6	54	100.0	218	18	AAW13563	Humanized anti-L-s
7	54	100.0	222	18	AAW01751	MH1 monoclonal ant
8	51	94.4	110	15	AAR60810	Light chain variab
9	51	94.4	111	15	AAR53930	Variable light cha
10	51	94.4	112	17	AAW00830	Anti-human FasL an
11	51	94.4	112	18	AAW19016	

12	48	88.9	246	18	AAW09434
13	48	88.9	247	18	AAW09443
14	48	88.9	281	19	AAW82311
15	48	88.9	288	19	AAW82314
16	48	88.9	288	19	AAW82316
17	48	88.9	483	19	AAW82317
18	48	88.9	531	19	AAW82315
19	48	88.9	539	21	AAW43749
20	48	88.9	554	21	AAW50823
21	45	83.3	9	16	AAW50822
22	44	81.5	9	16	AAW5477
23	44	81.5	9	16	AAW54578
24	44	81.5	9	17	AAW011449
25	44	81.5	106	14	AAW44172
26	44	81.5	106	14	AAW33309
27	44	81.5	111	10	AAW85197
28	44	81.5	112	10	AAW90341
29	44	81.5	131	13	AAW24557
30	44	81.5	131	13	AAW90543
31	44	81.5	131	17	AAW011443
32	43.5	80.6	131	19	AAW44168
33	42	77.8	132	14	AAW37716
34	42	77.8	9	18	AAW27346
35	42	77.8	107	18	AAW27353
36	42	77.8	112	16	AAW79158
37	42	77.8	112	16	AAW79156
38	42	77.8	112	18	AAW27358
39	42	77.8	112	18	AAW27527
40	42	77.8	132	12	AAW10920
41	42	77.8	237	20	AAW3873
42	41	75.9	240	20	AAW73875
43	41	75.9	112	12	AAW13089
44	40	74.1	215	16	AAW64202
45	40	74.1	9	19	AAW83029
	40	74.1	9	21	AAW14746

ALIGNMENTS

RESULT	1
AA55123	
ID	AA55123 standard; Protein; 111 AA.
XX	
AC	AA55123;
XX	
DT	27-JAN-1995 (first entry)
XX	
DE	Mouse anti-HIV mu5.5 light chain variable region.
XX	
KW	Immunoglobulin; heavy chain; anti-HIV antibody; neutralisation;
KW	human immunodeficiency virus; variable region; VH chain; murine.
XX	
OS	Mus musculus.

JP06125783-A.
10-MAY-1994.

JP06125783-A.
10-MAY-1994.
28-DEC-1991; 91JP-0359808.
28-DEC-1991; 91JP-0359808.
(KAGA-) 2H KAGAKU KESSEI-RYOHO KENKYUSHO.
WPI: 1994-187942/23.
N-PSDB; AAQ65558.
Mouse-human chimeric anti-HIV antibody heavy and light chains -
and recombinant antibody consisting of the H- and L-chains,
useful in AIDS therapy
Claim 5; Fig 12; 22pp; Japanese.
Murine monoclonal antibodies mu 39.1 and mu 5.5 both neutralise HIV.
The heavy and light chain variable regions from these antibodies
were sequenced (AAR55120-R55123). The murine anti-HIV CDRs were
introduced into human framework regions to construct chimeric
antibodies (AAR55124-R55127).

Query Match 100.0%; Score 54; DB 15; Length 111;
Best Local Similarity 100.0%; Pred. No. 0.016; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0

QY 1 QQSNEPWT 9
DB 93 qqsnepwt 101

RESULT 3
ID AAR60302 standard; Protein; 111 AA.
XX AAR60302;
XX 09-MAR-1995 (first entry)
XX Anti HIV antibody light chain variable region.
DE Antibody; heavy chain; light chain; human immunodeficiency virus;
KW HIV; acquired immune deficiency syndrome; AIDS: treatment;
KW prophylaxis; Mus musculus; Homo sapiens.
XX Mus musculus.
XX Key Location/Qualifiers
PH 1..23 /label= Framework region 1.
FT Region 24..38 /label= CDR1.
FT Region 39..53 /label= Framework region 2.
FT Region 54..60 /label= CDR2.
FT Region 61..92 /label= Framework region 3.
FT Region 93..101 /label= CDR3.
FT Region 102..111 /label= Framework region 4.
FT
XX W09415969-A.
XX
XX 21-JUL-1994.
XX

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XX PF 28-DEC-1991; 91JP-0359808.
XX PR 28-DEC-1991; 91JP-0359808.
XX XX (KAGA-) ZH KAGAKU KESSEI-RYOHO KENKYUSHO.
XX XX WPI; 1994-187942/23.
XX XX N-PSDB; AQA65554.
XX DR Mouse-human chimeric anti-HIV antibody heavy and light chains -
XX PT and recombinant antibody consisting of the H- and L-chains,
XX PT useful in AIDS therapy
XX XX Example 3; Fig 4; 22pp; Japanese.
XX PS Murine monoclonal antibodies mu 39.1 and mu 5.5 both neutralise HIV.
XX CC The heavy and light chain variable regions from these antibodies
XX CC were sequenced (AAR55120-R55123). The murine anti-HIV CDRs were
XX CC introduced into human framework regions to construct chimeric
XX CC antibodies (AAR55124-R55127).
XX XX
XX XX Sequence 111 AA;
XX PS
XX PS Query Match 100.0%; Score 54; DB 15; Length 111;
XX PS Best Local Similarity 100.0%; Pred. No. 0.016; 0; Gaps 0;
XX PS Matches 9; Conservative 0; Mismatches 0;
QY 1 QOSNEDPWT 9
DB 93 qqsneDPWT 101
XX XX
RESULT 2
ID AAR55127 standard; Protein; 111 AA.
XX AC AAR55127;
XX XX
XX 30-JAN-1995 (first entry)
XX XX Mouse-human chimeric anti-HIV mu5.5-derived light chain V region.
XX DE Immunoglobulin; heavy chain; anti-HIV antibody; neutralisation;
XX KW human immunodeficiency virus; variable region; VL chain; murine;
XX KW chimeric; humanised.
XX XX
XX OS Chimeric Mus musculus.
XX OS Chimeric Homo sapiens.
XX XX
XX PH Location/Qualifiers
XX FT 1..23
XX FT /label= FR1
XX FT /note= "human"
XX FT 24..38
XX FT /label= CDR1
XX FT /note= "murine"
XX FT 39..53
XX FT /label= FR2
XX FT 54..60
XX FT /label= CDR2
XX FT /note= "murine"
XX FT 61..92
XX FT /label= FR3
XX FT /note= "human"
XX FT 93..101
XX FT /label= CDR3
XX FT /note= "murine"
XX FT 102..111
XX FT /label= FR4
XX FT /note= "human"
XX XX

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PF 14-JAN-1993; 93WO-JP000039.
 XX 14-JAN-1993; 93AU-0032671.
 PR 14-JAN-1993; 93WO-JP000039.
 XX
 PA (KAGA) CHERO SERO THERAPEUTIC RES INST.
 PI Eda Y, Kimachi K, Maeda H, Osatomi K, Shiosaki K;
 PI Tokiyoshi S;
 XX WPI: 1994-249145/30.
 DR N-PSDB; AAQ70372.
 XX
 PT Recombinant chimeric anti HIV antibody - useful for the treatment
 PT and prevention of HIV
 XX Claim 15; Figure 4; 51pp; Japanese.
 XX The recombinant antibody light chain has neutralising activity
 CC against HIV. Chimeric antibodies comprising both mouse and human
 CC sequences are useful in the treatment/prevention of AIDS caused by
 CC HIV.
 XX
 SQ Sequence 111 AA;

Query Match 100.0%; Score 54; DB 15; Length 111;
 Best Local Similarity 100.0%; Pred. No. 0.016;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QQSNEPWT 9
 Db 93 qqsneqpw 101
 |||||

RESULT 4
 AAR60306
 ID AAR60306 standard; Protein; 111 AA.
 AC AAR60306;
 XX
 DT 13-MAR-1995 (first entry)
 DE Chimeric anti HIV antibody light chain variable region.
 XX Antibody; heavy chain; light chain; human immunodeficiency virus;
 KW HIV; acquired immune deficiency syndrome; AIDS: treatment;
 KW prophylaxis; Mus musculus; Homo sapiens.
 XX Chimeric Homo sapiens.
 OS Chimeric Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Region 1..23
 FT /label= Framework region 1.
 FT Region 24..38
 FT /label= CDR1.
 FT /note= "Mouse derived amino acid sequence."
 FT Region 39..53
 FT /label= Framework region 2.
 FT Region 54..60
 FT /label= CDR2.
 FT /note= "Mouse derived amino acid sequence."
 FT Region 61..92
 FT /label= Framework region 3.
 FT Region 93..101
 FT /label= CDR3.
 FT /note= "Mouse derived amino acid sequence."
 FT Region 102..111
 FT /label= Framework region 4.
 PN W09415969-A.
 XX

PD 21-JUL-1994.
 XX 14-JAN-1993; 93WO-JP000039.
 PF 14-JAN-1993; 93AU-0032671.
 PR 14-JAN-1993; 93WO-JP000039.
 XX
 PA (KAGA) CHERO SERO THERAPEUTIC RES INST.
 PI Eda Y, Kimachi K, Maeda H, Osatomi K, Shiosaki K;
 PI Tokiyoshi S;
 XX WPI: 1994-249145/30.
 DR N-PSDB; AAR60306.
 XX
 PT Recombinant chimeric anti HIV antibody - useful for the treatment
 PT and prevention of HIV
 XX Claim 14; Figure 12; 51pp; Japanese.
 XX The recombinant antibody light chain has neutralising activity
 CC against HIV. Chimeric antibodies comprising both mouse and human
 CC sequences are useful in the treatment/prevention of AIDS caused by
 CC HIV.
 XX
 SQ Sequence 111 AA;

Query Match 100.0%; Score 54; DB 15; Length 111;
 Best Local Similarity 100.0%; Pred. No. 0.016;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QQSNEPWT 9
 Db 93 qqsneqpw 101
 |||||

RESULT 5
 AAB71895
 ID AAB71895 standard; protein; 113 AA.
 AC AAB71895;
 XX
 DT 09-MAY-2001 (first entry)
 DE Monoclonal antibody ST40 light chain.
 XX Antibody; ST40; molecular mimetic; CD4; human immunodeficiency virus;
 KW HIV; infection.
 XX Unidentified.
 OS
 FT WO200109191-A1.
 FT 08-FEB-2001.
 XX
 FT 02-AUG-2000; 2000WO-GB02972.
 XX
 FT 02-AUG-1999; 99EP-0401968.
 XX
 FT (SYNT-) SYNT:EM SA.
 XX
 FT Casset F, Granier C, Kaczorek M, Lahana R, Rees A, Roux F;
 PI WPI: 2001-168699/17.
 DR
 XX
 PT Designing molecular mimetics to mimic a parent molecule activity,
 PT useful e.g. therapeutically and diagnostically, uses computational
 PT screening to identify active chemical groups by accessibility within
 XX the parent molecule -
 XX Example 1; Fig 1; 85pp; English.
 XX

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CC The present sequence was used in a method for designing a mimetic which
 CC exhibits an activity associated with a parent molecule. Such mimetics
 CC may be smaller than the parent molecule and correspondingly easier and
 CC cheaper to make, since the active region of the parent molecule is
 CC normally relatively small. The method is useful where the parent molecule
 CC is a binding domain or the hypervariable region of an antibody or other
 CC member of the immunoglobulin superfamily. It is useful when the parent
 CC molecule is an antibody and the mimetic a peptide, especially an antibody
 CC which binds CD4 and a peptide which binds CD4. The mimetics designed and
 CC produced are useful diagnostically to detect cells bearing CD4 on their
 CC surfaces or may be included in pharmaceuticals e.g. to treat conditions
 CC in which CD4 is implicated (e.g. HIV).

XX SQ Sequence 113 AA;
 XX Query Match 100.0%; Score 54; DB 22; Length 113;
 XX Best Local Similarity 100.0%; Pred. No. 0.016; Indels 0; Gaps 0;
 XX Matches 9; Conservative 0; Mismatches 0;

QY 1 QQSNEPWT 9
 Db |||||

RESULT 6
 AAW13563
 ID AAW13563 standard; Protein: 218 AA.
 AC AAW13563;
 XX 03-JUN-1997 (first entry)
 DT Humanised anti-L-selectin antibody Hudreg 55 light chain.
 DE L-selectin; humanised antibody; Hudreg 55; acute organ damage;
 XX organ failure; poly-trauma; haemorrhagic-traumatic shock.
 KW Chimeric Mus sp.;
 XX Chimeric Homo sapiens.
 OS WO9706822-A1.
 XX 27-FEB-1997.
 XX 14-AUG-1996; 96WO-US13152.
 XX 27-DEC-1995; 95US-0578953.
 PR 17-AUG-1995; 95EP-0112895.
 PR 19-SEP-1995; 95EP-0114696.
 XX (BOEF) BOEHRINGER MANNHEIM GMBH.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 XX Co M, Haselbeck A, Martin U, Schumacher G;
 PI WPI: 1997-165036/15.
 XX N-PSDB; AAT61280.

DR Using anti-selectin antibody to prevent acute organ damage and
 XX multiple organ failure - during extracorporeal circulation or
 XX following polytrauma, e.g. haemorrhagic-traumatic shock
 XX Disclosure: Page 32-33; 52pp; English.

XX Humanised anti-L-selectin antibody Hudreg 55 comprises 2 light
 XX chains each having the sequence given in AAW13563 and 2 heavy chains
 XX each having the sequence given in AAW13564. These are encoded by the
 XX cDNA clones given in AAT61280 and AAT61281. Hudreg 55 can be used to
 XX prevent multiple organ failure associated with polytrauma and for
 XX the prevention of acute organ damage associated with extracorporeal
 XX blood circulation. The antibody inhibits interaction between the
 XX carbohydrate-recognising domain of the selectin and the

CC corresponding cell surface receptor.

XX SQ Sequence 218 AA;
 XX Query Match 100.0%; Score 54; DB 18; Length 218;
 XX Best Local Similarity 100.0%; Pred. No. 0.032; Indels 0; Gaps 0;
 XX Matches 9; Conservative 0; Mismatches 0;

QY 1 QQSNEPWT 9
 Db |||||

RESULT 7
 AAW01751
 ID AAW01751 standard; Protein: 222 AA.
 AC AAW01751;
 XX 21-AUG-1997 (first entry)
 DT MH1 monoclonal antibody kappa chain.
 DE CDR; light chain; antigen binding site; antigen free animal;
 XX germfree animal; immunoreactive; thrombotic event.
 KW Mus musculus.
 XX Location/Qualifiers
 XX Key 19...39
 XX Domain /label= CDR1
 XX Domain 63..68
 XX Domain /label= CDR2
 XX Domain 99..104
 XX Domain /label= CDR3

WO9640986-A1.

XX 19-DEC-1996.
 XX 29-APR-1996; 96WO-US07891.
 XX 07-JUN-1995; 95US-0486420.
 XX (AMBI-) AMERICAN BIOGENETIC SCI INC.
 XX Dimitrijevic N, Dimitrijevic N;
 XX WPI: 1997-052360/05.
 XX N-PSDB; AAT59338.

DR Calibrator comprising lyophilised compen contg. DesAABB fibrin
 XX polymers, buffer and stabilising agent - for use in soluble fibrin
 XX assays used for evaluating pre-disposition to thrombotic event
 XX Disclosure: Page 96; 120pp; English.

XX The present sequence represents the MH1 monoclonal antibody kappa
 XX (light) chain, which was produced in antigen free (germfree) mice. A new
 XX invention contemplates the production and use of recombinantly produced
 XX derivatives of monoclonal antibody MH1 and fusion proteins containing a
 XX portion of MH1 that bind to the same epitope recognised by monoclonal
 XX antibody MH1, such as single chain antigen binding proteins comprising
 XX the antigen binding site of monoclonal antibody MH1. A calibrator for
 XX use in an in vitro assay for detecting the presence of soluble
 XX crosslinked and soluble non-crosslinked DesAABB fibrin polymers, is
 XX claimed. This calibrator can be used in kits which use an antibody that
 XX specifically binds to an epitope which recognises the MH1 monoclonal
 XX antibody. This calibrator is useful for evaluating predisposition to a
 XX thrombotic event, supporting a diagnosis of an occurrence of a
 XX thrombotic event or monitoring a thrombotic event in a mammal.
 XX The lyophilised calibrator exhibits excellent immunoreactive stability

CC in storage in the lyophilised state and after reconstitution.
 XX
 SQ Sequence 222 AA;

Query Match 100.0%; Score 54; DB 18; Length 222;
 Best Local Similarity 100.0%; Pred. No. 0.032;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QOSNEDPWT 9
 Db 97 qqsndpwt 105
 ||:|||||

RESULT 8
 AAR60810
 ID AAR60810 standard; Protein; 110 AA.
 AC AAR60810;
 DT 06-DEC-1994 (first entry)
 DE Light chain variable region of antibody HCMV16.
 KW Antibody; humanised antibody; variable region; immune response;
 KW cytomegalovirus; glycoprotein; complementarity determining region;
 KW CDR; heavy chain; light chain; ds.
 XX
 OS Mus musculus.
 PN WO9409136-A.
 XX
 PD 28-APR-1994.
 XX
 PF 15-OCT-1993; 93WO-GB02134.
 XX
 PR 15-OCT-1992; 92GB-0021654.
 XX
 PA (KETT-) KETTOCK LODGE CAMPUS 2.
 XX
 PI Carr FJ, Hamilton AA, Harris WJ;
 DR WPI; 1994-151321/18.
 DR N-PSDB; AAQ73749.
 XX

New humanised monoclonal antibodies against Human Cytomegalovirus
 specificity or affinity, for treatment or prevention of HCMV
 infection.
 Disclosure; Figure 2; 53pp; English.
 Human monoclonal antibodies may be made specific for a pathogen by
 substituting the complementarity determining regions (CDR's) from
 the murine antibody variable domains which show desirable binding
 properties to that pathogen, into the human immunoglobulin heavy and
 light chain variable domains. These "humanised" antibodies should
 elicit a considerably reduced immune response in humans compared to
 chimeric antibodies as they contain considerably less murine
 components and their half life in the circulation should approach
 that of natural human antibodies. This sequence is taken from a
 donor monoclonal antibody HCMV16, specific for the human
 cytomegalovirus gH glycoprotein from which CDR's were taken to
 construct humanised antibodies. Humanised antibodies are described
 in AAQ63902-063908.

SQ Sequence 110 AA;
 Query Match 94.4%; Score 51; DB 15; Length 110;
 Best Local Similarity 88.9%; Pred. No. 0.053;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QOSNEDPWT 9
 Db 97 qqsndpwt 105
 ||:|||||

RESULT 10
 AAR60830
 ID AAR60830 standard; Protein; 112 AA.

QY 1 QOSNEDPWT 9
 Db 93 qqsndpwt 101
 ||:|||||

RESULT 9
 AAR53930
 ID AAR53930 standard; Protein; 111 AA.
 AC AAR53930;
 DT 05-DEC-1994 (first entry)
 DE Light chain variable region of humanised antibody 16HuVK.
 KW Antibody; humanised antibody; variable region; immune response;
 KW cytomegalovirus; glycoprotein; complementarity determining region;
 KW CDR; heavy chain; light chain.
 XX
 OS Homo sapiens.
 OS Mus musculus.
 PN WO9409136-A.
 XX
 PD 28-APR-1994.
 XX
 PF 15-OCT-1993; 93WO-GB02134.
 XX
 PR 15-OCT-1992; 92GB-0021654.
 XX
 PA (KETT-) KETTOCK LODGE CAMPUS 2.
 XX
 PI Carr FJ, Hamilton AA, Harris WJ;
 DR WPI; 1994-151321/18.
 DR N-PSDB; AAQ63908.
 XX

New humanised monoclonal antibodies against Human Cytomegalovirus
 specificity or affinity, for treatment or prevention of HCMV
 infection.
 Example 1; Figure 5; 53pp; English.
 Human monoclonal antibodies may be made specific for a pathogen by
 substituting the complementarity determining regions (CDR's) from
 the murine antibody variable domains which show desirable binding
 properties to that pathogen, into the human immunoglobulin heavy and
 light chain variable domains. These "humanised" antibodies should
 elicit a considerably reduced immune response in humans compared to
 chimeric antibodies as they contain considerably less murine
 components and their half life in the circulation should approach
 that of natural human antibodies. This sequence is a humanised heavy
 chain variable region comprising CDR's from the donor monoclonal
 antibody HCMV16, specific for the human cytomegalovirus gH
 glycoprotein. The framework region of the human heavy chain has been
 modified. Humanised antibodies are described in AAQ63902-Q63908.

SQ Sequence 111 AA;
 Query Match 94.4%; Score 51; DB 15; Length 111;
 Best Local Similarity 88.9%; Pred. No. 0.054;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QOSNEDPWT 9
 Db 93 qqsndpwt 101
 ||:|||||

RESULT 10
 AAR60830
 ID AAR60830 standard; Protein; 112 AA.

us-09-724-406-16.rag

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hepatitis B virus; HBV; hepatitis C virus; HCV; apoptosis;
liver cell; glutamate oxaloacetate; pyruvate transaminase.

XX AC AAW00830;
XX DT 19-MAY-1997 (first entry)
XX DE Variable light chain of anti-human Fas ligand antibody NOK-4.
XX DE Variable region; light chain; human; Fas ligand; monoclonal;
KW antibody; NOK-4; hybridoma; inhibition; apoptosis; assay;
KW diagnosis; disease; hepatitis; infectious mononucleosis;
KW systemic lupus erythematosus.
XX KW Mus musculus.
XX OS WO9629350-A1.
XX PN 26-SEP-1996.
XX PD 21-MAR-1996; 96WO-JP00734.
XX PF 27-OCT-1995; 95JP-0303492.
XX PR 20-MAR-1995; 95JP-0087420.
XX PA (SUME) SUMITOMO ELECTRIC IND CO.
XX PI Kayagaki N, Nakata M, Okumura K, Yagita H;
XX PI WPI: 1996-443140/44.
XX DR N-PSDB; AAT39556.
XX DR Monoclonal antibody specifically recognising the Fas ligand - useful
XX PT for the detection of Fas ligands either on cell surface or in
XX PT solution
XX PS Claim 26; Page 88; 133pp; Japanese.
XX CC The present sequence is the light chain variable region of the
XX CC anti-human Fas ligand monoclonal antibody (MAB) NOK-4. NOK-4 is
XX CC produced by the hybridoma NOK-4 (FERM BP-5047), which was prepared
XX CC by immunising mice with transformed human Fas ligand expressing COS
XX CC cells, and fusing spleen cells isolated from the mice with myeloma
XX CC P3x63Ag8.653 (ATCC CRL-1580) cells. The MAB recognises the human
XX CC Fas ligand on the cell surface or in solution, and can be used to
XX CC inhibit the apoptosis inducing cell surface Fas ligand/Fas
XX CC reaction. The MAB can also be used for a Fas ligand assay in
XX CC biological samples (e.g. human blood), especially for disease
XX CC diagnosis, e.g. hepatitis, infectious mononucleosis and systemic
XX CC lupus erythematosus.
XX SQ Sequence 112 AA;
Query Match 94.4%; Score 51; DB 17; Length 112;
Best Local Similarity 88.9%; Pred. No. 0.054; Indels 0; Gaps 0;
Matches 8; Conservative 1; Mismatches 0;
QY 1 QQSNEPWT 9
DB 93 qgnnedpwt 101
RESULT 11
AAW19016
ID AAW19016 standard; Protein; 112 AA.
XX AC AAW19016;
XX DT 14-JAN-1998 (first entry)
XX DE Anti-human FasL antibody (NOK4) light chain variable region.
XX DE Light chain; variable region; mouse; murine; human; Fas ligand;
KW FasL; monoclonal antibody; MAB; hybridoma; treatment; hepatitis;
KW

Mus sp.
WO9715326-A1.
01-MAY-1997.
24-OCT-1996; 96WO-JP03089.
27-OCT-1995; 95JP-0303491.
(SUME) SUMITOMO ELECTRIC IND CO.
Kayagaki N, Nakata M, Okumura K, Seino K, Yagita H;
WPI: 1997-258767/23.
N-PSDB; AAT69540.
Anti-human Fas Ligand antibody to treat hepatitis - controls
apoptosis in liver cells and improves liver function
Claim 6; Page 38; 51pp; Japanese.
The present sequence is the light chain variable region of the
murine anti-human Fas ligand (FasL) monoclonal antibody (MAB) NOK4,
which is expressed by the hybridoma NOK4 (FERM BP-5044). The MAB
can be used in the preparation of a composition for the effective
oral or parenteral treatment of hepatitis, including hepatitis
caused by hepatitis B or C virus. The composition controls apoptosis
in liver cells caused by the binding of FasL to Fas expressing liver
cells, and improves liver function by improving blood glutamate
oxaloacetate and pyruvate transaminase levels. The composition is
given in a dosage of 0.0001-1000, preferably 0.01-600 mg/day.
Spleen cells from mice immunised with FasL expressing COS cells
were fused with mouse myeloma cells to produce hybridomas. The
hybridomas were screened for anti-FasL activity, and the active
clones NOK1-5 isolated.
XX SQ Sequence 112 AA;
Query Match 94.4%; Score 51; DB 18; Length 112;
Best Local Similarity 88.9%; Pred. No. 0.054; Indels 0; Gaps 0;
Matches 8; Conservative 1; Mismatches 0;
QY 1 QQSNEPWT 9
DB 93 qgnnedpwt 101
RESULT 12
AAW09434
ID AAW09434 standard; Protein; 246 AA.
XX AC AAW09434;
XX DT 23-SEP-1997 (first entry)
XX DE Anti-CD19 antibody B43 single chain variable region.
XX DE CD19; antibody; variable region; B43; SJ25C1; BLY3; targeting;
KW cytotoxin conjugate; cancer treatment; leukaemia; B cell lymphoma;
KW variable; heavy; light chain.
XX OS Synthetic.
XX XX Key Location/Qualifiers
FH Domain 1..117 /label= heavy_chain
FT Region 1..26 /label= FRL
FT FT

XX	Modified single chain anti-CD19 antibody B43.
DE	CD19; antibody; variable region; B43; SJ25C1; BLX3; targeting;
XX	cytotoxin conjugate; cancer treatment; leukaemia; B cell lymphoma;
KW	variable; heavy, light chain.
KW	Synthetic.
XX	
OS	
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FH	Location/Qualifiers
FT	1..117
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FT	32..45
FT	/label= FR2
FT	46..62
FT	/label= CDR2
FT	63..94
FT	/label= FR3
FT	95..117
FT	/label= CDR3
FT	118..132
FT	/label= linker
FT	133..246
FT	/label= light_chain
FT	133..155
FT	/label= FR1
FT	156..170
FT	/label= CDR1
FT	171..185
FT	/label= FR2
FT	186..192
FT	/label= CDR2
FT	193..224
FT	/label= FR3
FT	225..246
FT	/label= CDR3
FT	Misc-difference 247
FT	/note= "additional C-terminal Cys residue"
XX	
PN	WO9636360-A1.
XX	
PD	21-NOV-1996.
XX	
PF	15-MAY-1996; 95WO-US06941.
XX	
PR	17-MAY-1995; 95US-0443408.
XX	
PA	(MINU) UNIV MINNESOTA.
XX	
PI	Bejcek BE, Kersey JH, Uckun FM, Wang D;
XX	
DR	WPI; 1997-042642/04.
XX	
PT	DNA encoding a single chain variable region polypeptide which binds
PT	CD19 - used in the treatment of leukaemia and B-cell lymphoma
PS	Disclosure; Page 108-109; 143pp; English.
XX	
CC	AAW09443 represents a modified single chain variable region polypeptic
CC	(heavy chain-linker-light chain) of anti-CD19 antibody B43. The modifi
CC	polypeptide has an additional C-terminal Cys residue, as compared to
CC	the unmodified polypeptide (no further information is given in the
CC	specification). Single chain polypeptides were conjugated to at least
CC	one cytotoxic agent and used to target the agent(s) to cancerous cells
CC	expressing CD19. The immunoconjugates can be used treatment of cancer,
XX	especially leukaemia and B-cell lymphoma.
XX	
XX	Sequence 247 AA:

us-09-724-406-16.rag

Fri Jun 29 08:04:29 2001

AAW82316
ID AAW82316 standard; Protein; 288 AA.
XX
AC AAW82316;
XX
DT 26-FEB-1999 (first entry)
XX
DE Mouse OKT3 variant antibody protein.
XX
KW OKT3; monoclonal antibody; MAB; point mutation; transplant rejection;
organ recipient; diagnosis; tumour; therapy.
XX
OS Mus sp.
OS Synthetic.
XX
PN DEL9721700-Cl.
XX
PD 19-NOV-1998.
XX
PF 23-MAY-1997; 97DE-1021700.
XX
PR 23-MAY-1997; 97DE-1021700.
XX
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI Kipriyanov S, Little M, Moldenhauer G;
XX
XX WPI; 1998-596150/51.
DR N-PSDB; AAV73335.
XX
PT Monoclonal antibody OKT3 with point-mutation - where cysteine is
replaced by another polar amino acid, useful for controlling
transplant rejection, and in tumour diagnostics and therapy
XX
PS Claim 3; Fig 2; 8pp; German.
XX
CC This sequence represents a monoclonal antibody (MAB) derived from OKT3
with a point-mutation where Cys at position H100A is replaced with
another polar amino acid, in this example Ser. The MAB is used in
CC lowering or eliminating the transplant rejection in an organ recipient,
CC and for diagnostic methods for tumours and tumour therapy.
XX
SQ Sequence 288 AA;

Query Match 88.9%; Score 48; DB 19; Length 288;
Best Local Similarity 88.9%; Pred. No. 0.5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSNEDPWT 9
DB 243 qgstedpwt 251

Search completed: June 28, 2001, 16:14:36
Job time: 1324 sec

Query Match 88.9%; Score 48; DB 18; Length 247;
Best Local Similarity 88.9%; Pred. No. 0.43; 1; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Gaps 0;

QY 1 QOSNEDPWT 9
DB 225 qgstedpwt 233

RESULT 14
AAW82314
ID AAW82314 standard; Protein; 281 AA.
XX
AC AAW82314;
XX
DT 26-FEB-1999 (first entry)
XX
DE Human ScFvCD19 protein.
XX
KW ScFvCD19; anti-CD19; single chain; antibody; B-cell marker; CD19; T cell;
retroviral vector; gene therapy; tumour-associated antigen; cancer.
XX
OS Homo sapiens.
XX
PN DEL9720152-AL.
XX
PD 05-NOV-1998.
XX
PF 02-MAY-1997; 97DE-1020152.
XX
PR 02-MAY-1997; 97DE-1020152.
XX
PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
PI Bargou R, Schroeder A, Schwenkenbecher J;
XX
XX WPI; 1998-584686/50.
DR N-PSDB; AAV73323.
XX
PT Retroviral vector system for gene therapy - by expression of
therapeutic gene in T cells
XX
PS Claim 8; Page 5; 10pp; German.
XX
CC This sequence represents a novel human recombinant anti-CD19 single chain
antibody. ScFvCD19 which recognizes the extracellular domain of the
B-cell marker CD19. This sequence is used in a retroviral vector system
for gene transfer and expression in primary human T cells which involves
a retroviral vector containing CDNA corresponding to a therapeutic gene,
a promoter selected from the SV40 immediate early promoter or the human
IL-2 or MHC I promoter and a selectable marker, and a packaging cell
line (i.e. a modified retroviral packaging line for enhanced transfer
into primary human T lymphocytes). This vector system in which the CDNA
encodes a single-chain antibody (scfv) specific for a tumour-associated
antigen can be used for gene therapy of cancer, especially by isolating
T cells from the patient's blood, stimulating the T cells in vitro,
introducing the retroviral vector into the T cells and returning the T
cells to the patient, preferably by intravenous injection.

Query Match 88.9%; Score 48; DB 19; Length 281;
Best Local Similarity 88.9%; Pred. No. 0.49;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

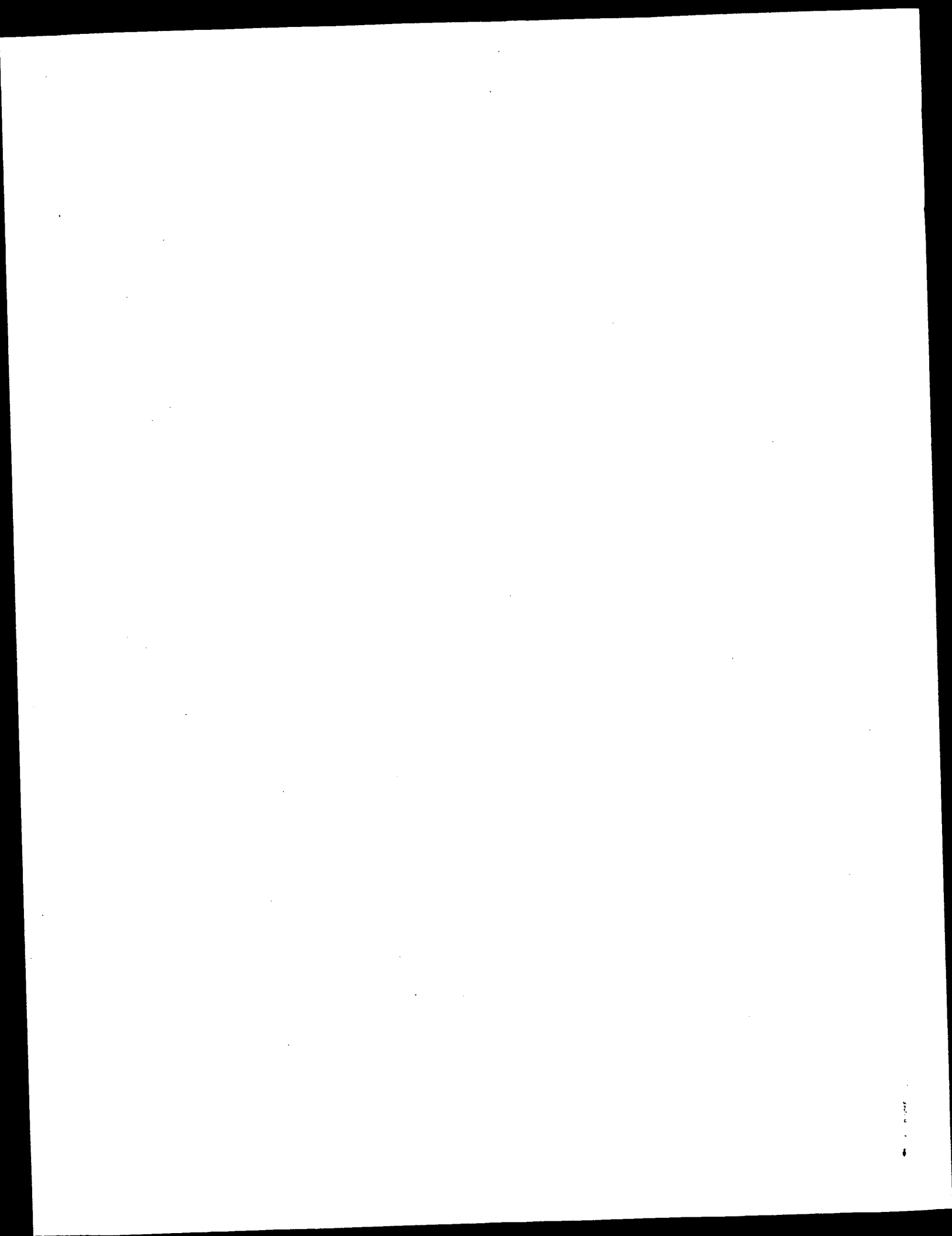
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DB 253 qgstedpwt 261

RESULT 15

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Page 9



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2001, 16:01:14 ; Search time 138.34 Seconds
(without alignments)
1.311 Million cell updates/sec

Title: US-09-724-406-16
Perfect score: 54
Sequence: 1 QOSNEDPWT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	111	1	US-08-491-845-8
2	54	100.0	111	1	US-08-491-845-16
3	54	100.0	115	4	US-08-513-968-51
4	54	100.0	131	4	US-08-579-378A-14
5	54	100.0	131	4	US-08-579-378A-18
6	54	100.0	218	5	PCT-US96-13152-2
7	51	94.4	112	3	US-09-065-059-13
8	45	83.3	9	5	PCT-US94-14106-42
9	44	81.5	9	5	PCT-US94-14106-43
10	44	81.5	106	3	US-08-466-151-6
11	40	74.1	111	2	US-08-887-352B-5
12	40	74.1	111	2	US-08-887-352B-6
13	40	74.1	111	3	US-08-887-352B-5
14	40	74.1	111	4	US-09-109-207C-5
15	40	74.1	111	4	US-09-109-207C-6
16	40	74.1	114	2	US-08-887-352B-8
17	40	74.1	114	2	US-08-887-352B-9
18	40	74.1	114	2	US-08-887-352B-10
19	40	74.1	114	2	US-09-109-207C-8
20	40	74.1	114	4	US-09-109-207C-9
21	40	74.1	114	4	US-09-109-207C-10
22	40	74.1	218	2	US-08-887-352B-13
23	40	74.1	218	2	US-08-887-352B-15
24	40	74.1	218	2	US-08-887-352B-17
25	40	74.1	218	2	US-08-887-352B-19
26	40	74.1	218	2	US-08-887-352B-24
27	40	74.1	218	3	US-08-466-151-9

28	40	74.1	218	4	US-09-109-207C-13	Sequence 13, Appl
29	40	74.1	218	4	US-09-109-207C-15	Sequence 15, Appl
30	40	74.1	218	4	US-09-109-207C-17	Sequence 17, Appl
31	40	74.1	218	4	US-09-109-207C-19	Sequence 19, Appl
32	40	74.1	218	4	US-09-109-207C-24	Sequence 24, Appl
33	40	74.1	218	4	US-09-282-505-1	Sequence 1, Appl
34	40	74.1	218	4	US-09-054-255-1	Sequence 1, Appl
35	40	74.1	218	4	US-08-887-352B-22	Sequence 22, Appl
36	40	74.1	248	2	US-08-887-352B-23	Sequence 23, Appl
37	40	74.1	248	4	US-09-109-207C-22	Sequence 22, Appl
38	40	74.1	248	4	US-08-483-632-20	Sequence 20, Appl
39	39	72.2	9	2	US-08-483-632-20	Sequence 20, Appl
40	39	72.2	111	1	US-07-634-278-54	Sequence 54, Appl
41	39	72.2	111	1	US-07-634-278-55	Sequence 55, Appl
42	39	72.2	111	1	US-08-477-728-54	Sequence 54, Appl
43	39	72.2	111	1	US-08-477-728-55	Sequence 55, Appl
44	39	72.2	111	1	US-08-477-728-55	Sequence 55, Appl
45	39	72.2	111	1	US-08-477-728-55	Sequence 55, Appl

ALIGNMENTS

RESULT 1
US-08-491-845-8
; Sequence 8, Application US/08491845
; Patent No. 5773247
; GENERAL INFORMATION:
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: EDA, Yasuyuki
; APPLICANT: SHIOSAKI, Kouichi
; APPLICANT: OSATOMI, Kiyoshi
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: RECOMBINANT ANTI-HIV ANTIBODY AND
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/491,845
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00039
; FILING DATE: 14-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: MAEDA-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-491-845-8

Query Match 100.0%; Score 54; DB 1; Length 111;

us-09-724-406-16.rai

Fri Jun 29 08:04:30 2001

Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNEDPWT 9
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DB 93 QOSNEDPWT 101

RESULT 2
US-08-491-845-16
; Sequence 16, Application US/08491845
; Patent No. 5773247
; GENERAL INFORMATION:
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: EDA, Yasuyuki
; APPLICANT: SHIOSAKI, Kouichi
; APPLICANT: OSATOMI, Kiyoshi
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: RECOMBINANT ANTI-HIV ANTIBODY AND
; TITLE OF INVENTION: PROCESS FOR PREPARING THE SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/491,845
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00039
; FILING DATE: 14-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: MAEDA=5
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-491-845-16

Query Match 100.0%; Score 54; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNEDPWT 9
| | | | | | | | | |
DB 93 QOSNEDPWT 101

RESULT 3
US-08-513-968-51
; Sequence 51, Application US/08513968
; Patent No. 6114143
; GENERAL INFORMATION:
; APPLICANT: EDA, Yasuyuki
; APPLICANT: MAEDA, Hiroaki

APPLICANT: MAKIZUMI, Keiichi
APPLICANT: SHIOSAKI, Kouichi
APPLICANT: OSATOMI, Kiyoshi
APPLICANT: KIMACHI, Kazuhiko
APPLICANT: HIGUCHI, Hirofumi
APPLICANT: TOKIYOSHI, Sachio
TITLE OF INVENTION: ANTI-HIV MONOCLONAL ANTIBODY
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,968
FILING DATE: 11-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 78913/1993
FILING DATE: 11-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: EDA=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-513-968-51

Query Match 100.0%; Score 54; DB 4; Length 115;
Best Local Similarity 100.0%; Pred. No. 0.0078;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNEDPWT 9
| | | | | | | | | |
DB 97 QOSNEDPWT 105

RESULT 4
US-08-579-378A-14
; Sequence 14, Application US/08579378A
; Patent No. 6210671
; GENERAL INFORMATION:
; APPLICANT: Co. Man Sung
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: L-Selectin
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/579,378A
; FILING DATE: 27-DEC-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/160,074
; FILING DATE: 30-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/983,946
; FILING DATE: 01-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95112895.8
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95114696.8
; FILING DATE: 19-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebescheutz, Joe O.
; REGISTRATION NUMBER: 37,505
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-579-378A-14

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Query Match      100.0%; Score 54; DB 4; Length 131;
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QY 1 QOSNEDPWT 9
Db 113 QOSNEDPWT 121

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RESULT 5
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; Patent No. 6210671
; GENERAL INFORMATION:
; APPLICANT: Co. Man Sung
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/579,378A
; FILING DATE: 27-DEC-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/160,074
; FILING DATE: 30-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/983,946
; FILING DATE: 01-DEC-1992

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95112895.8
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95114696.8
; FILING DATE: 19-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebescheutz, Joe O.
; REGISTRATION NUMBER: 37,505
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-579-378A-18

```

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Query Match      100.0%; Score 54; DB 4; Length 131;
Best Local Similarity 100.0%; Pred. No. 0.009;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 QOSNEDPWT 9
Db 113 QOSNEDPWT 121

```

```

RESULT 6
PCT-US96-13152-2
; Sequence 2, Application PC/TUS9613152
; GENERAL INFORMATION:
; APPLICANT: Martin, Ulrich, et al.
; TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ f
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Computer Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/13152
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/578,953
; FILING DATE: 27-Dec-95
; APPLICATION NUMBER: EP 95 112 895.8
; FILING DATE: 17-Aug-95
; APPLICATION NUMBER: EP 95 114 969.9
; FILING DATE: 19-Sep-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Norman D. Hanson
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218
; TYPE: amino acid

```

APPLICANT: PROCESS FOR GENERATING SPECIFIC ANTIBODIES
 TITLE OF INVENTION: 61
 NUMBER OF SEQUENCES: 61
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII (TEXT)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/14106
 FILING DATE:
 CLASSIFICATION:
 INFORMATION FOR SEQ. ID NO. 42:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 AMINO ACIDS
 TYPE: AMINO ACID
 TOPOLOGY: LINEAR
 MOLECULE TYPE: PEPTIDE
 FRAGMENT TYPE: INTERNAL
 PCT-US94-14106-42

```
Query Match      83.3%; Score 45; DB 5; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.4e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```

1 QQSNEPWT 9
1 QQSNEPWT 9

```

```

1  RESULT      9
2  ; Sequence 14106-43
3  ; Sequence 43, Application PC/TUS9414106
4  ; GENERAL INFORMATION:
5  ;
6  ; APPLICANT:      Process for Generating Specific Antibodies
7  ;
8  ; TITLE OF INVENTION:
9  ;
10 ; NUMBER OF SEQUENCES: 61
11 ;
12 ; COMPUTER READABLE FORM:
13 ;
14 ; MEDIUM TYPE: Floppy disk
15 ;
16 ; COMPUTER: IBM PC compatible
17 ;
18 ; OPERATING SYSTEM: PC-DOS/MS-DOS
19 ;
20 ; SOFTWARE: ASCII (text)
21 ;
22 ; CURRENT APPLICATION DATA:
23 ;
24 ; APPLICATION NUMBER: PCT/US94/14106
25 ;
26 ; FILING DATE:
27 ;
28 ; CLASSIFICATION:
29 ;
30 ; INFORMATION FOR SEQ ID NO: 43:
31 ;
32 ; SEQUENCE CHARACTERISTICS:
33 ;
34 ; LENGTH: 9 amino acids
35 ;
36 ; TYPE: amino acid
37 ;
38 ; TOPOLOGY: linear
39 ;
40 ; MOLECULE TYPE: peptide
41 ;
42 ; FRAGMENT TYPE: internal
43 ;
44 ; PCT-US94-14106-43

```

Query Match	81.5%	Score 44;	DB 5;	Length 9;
Best Local Similarity	88.9%;	pred. No. 1.4e+05;		
Matches	8;	Conservative	1;	Mismatches 0;
Indels				0;
Gaps				0;

1 QQSNEPWT 9
| | | | | : |
1 QQSNEPFT 9

RESULT 10
US-08-466-151-6
; Sequence 6, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.

```

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-13152-2

Query Match          100.0%; Score 54; DB 5; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.016;
Conservative 9; Mismatches 0; Indels 0; Gaps 0;

```

Query Match	100.0%;	Score 54;	DB 5;	Length 218;
Best Local Similarity	100.0%;	Pred. NO.	0.016;	
Conservative	0;	Mismatches	0;	Indels

QY 1 QQSNEPWT 9
|||||
93 QQSNEPWT 101

RESULT 7
US-09-065-059-13
; Sequence 13, Application US/09065059
; Patent No. 6068841
GENERAL INFORMATION:

GENERAL INFORMATION:
APPLICANT: SEINO, Ken-ichiro
APPLICANT: KAYAGAKI, NO. 606884uhiko
APPLICANT: YAGITA, Hideo
APPLICANT: OKUMURA, KO
APPLICANT: NAKATA, Motomi
TITLE OF INVENTION: THERAPEUTIC AGENT FOR HEPATITIS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDermott, Will & Emery
STREET: 99 Canal Center Plaza
CITY: Alexandria
STATE: Virginia
COUNTRY: USA

```

: ZIP: 22314
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: REGISTRATION NUMBER: US/09/065,059

```

FILING DATE: 424
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Bucca Ph.D., Daniel
 REGISTRATION NUMBER: P-42, 368
 REFERENCE/POCKET NUMBER: 50356-151
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-518-5100
 TELEFAX: 703-684-1124
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 112 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 ns-09-065-059-13

```

Query Match          94.4%; Score 51; DB 3; Length 112;
Best Local Similarity 88.9%; pred. No. 0.026;
Matches            8; Conservative 1; Mismatches 0; Gaps 0;

```

1 QQSNEPWT 9
||:|||||
93 QONNEDPWT 101

RESULT 8
PCT-US94-14106-42
; Sequence 42, Application PC/TUS9414106
: GENERAL INFORMATION:

```

; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-466-151-6

```

```

Query Match      81.5%; Score 44; DB 3; Length 106;
Best Local Similarity 88.9%; Pred. NO. 0.42;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 QQSNEPWT 9
Db 93 QQSNEPWT 101

```

```

RESULT 11
US-08-887-352B-5
; Sequence 5, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:

```

```

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-887-352B-5

```

```

Query Match      74.1%; Score 40; DB 2; Length 111;
Best Local Similarity 77.8%; Pred. NO. 2.2;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 QQSNEPWT 9
Db 93 QQSNEPWT 101

```

```

RESULT 12
US-08-887-352B-6
; Sequence 6, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-887-352B-6

```

```

Query Match      74.1%; Score 40; DB 2; Length 111;

```

us-09-724-406-16.ra1

Fri Jun 29 08:04:30 2001

```
Best Local Similarity 77.8%; Pred. No. 2.2;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNEDPWT 9
DB 93 QOSHEDPYT 101

RESULT 13
US-08-466-151-2
; Sequence 2, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-466-151-2

Query Match 74.1%; Score 40; DB 3; Length 111;
Best Local Similarity 77.8%; Pred. No. 2.2;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNEDPWT 9
DB 93 QOSHEDPYT 101

US-09-109-207C-5
; Sequence 5, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypept
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 5
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-109-207C-5

Query Match 74.1%; Score 40; DB 4; Length 111;
Best Local Similarity 77.8%; Pred. No. 2.2;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNEDPWT 9
DB 93 QOSHEDPYT 101

RESULT 15
US-09-109-207C-6
; Sequence 6, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypept
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 6
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-111
; OTHER INFORMATION: F(ab) light chain sequence derived from MAEL1
US-09-109-207C-6

Query Match 74.1%; Score 40; DB 4; Length 111;
Best Local Similarity 77.8%; Pred. No. 2.2;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

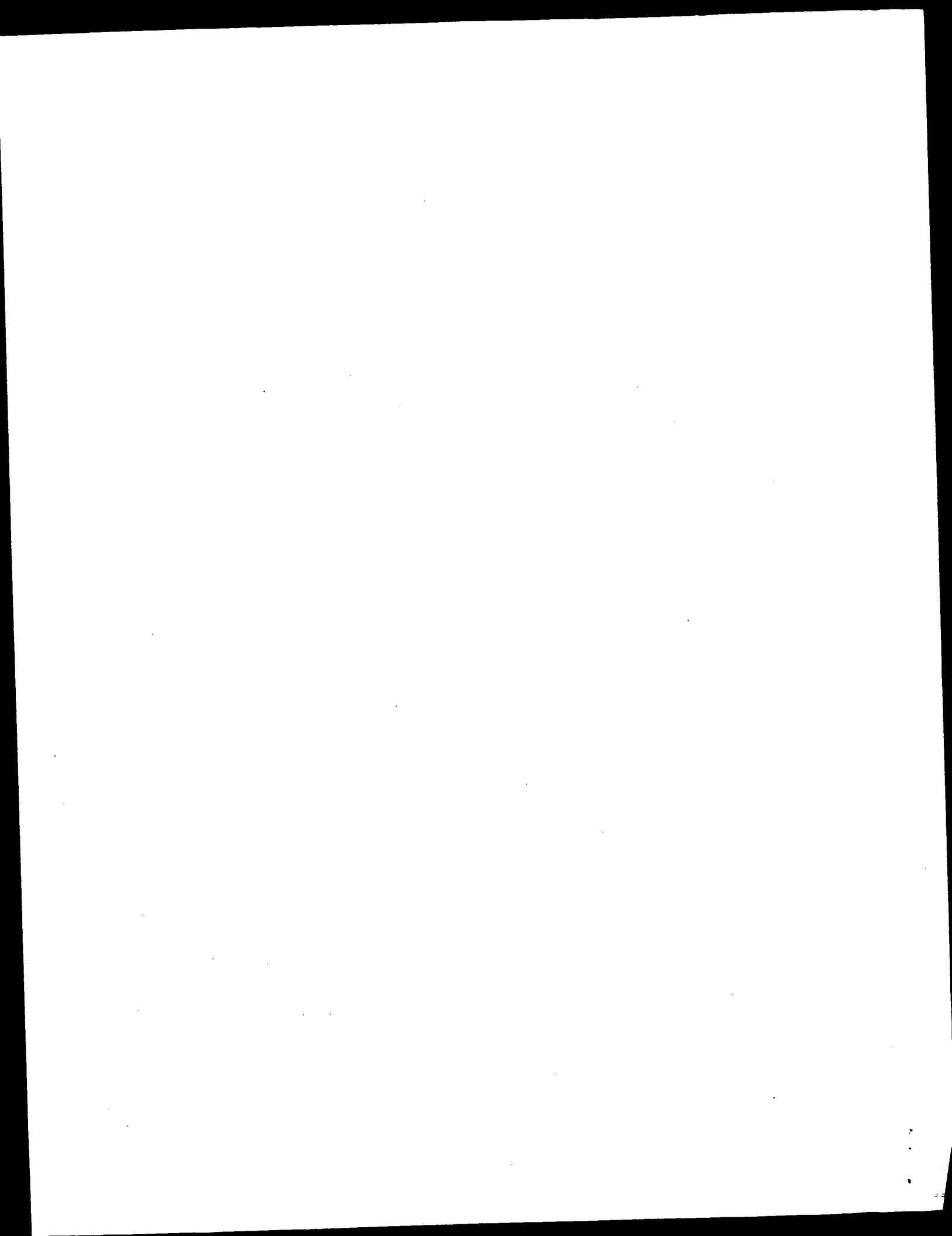
QY 1 QOSNEDPWT 9
DB 93 QOSHEDPYT 101

Search completed: June 28, 2001, 16:01:14
Job time: 522 sec
```

```
Query Match 74.1%; Score 40; DB 3; Length 111;
Best Local Similarity 77.8%; Pred. No. 2.2;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 QOSNEDPWT 9
DB 93 QOSHEDPYT 101
```

```
RESULT 14
US-09-109-207C-5
```

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 28, 2001, 15:58:44 ; Search time 234.85 Seconds
(without alignments)
2.919 Million cell updates/sec

Title: US-09-724-406-16
Perfect score: 54
Sequence: 1 QOSNEDPWT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*

1: pir1:*

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	111	1	KVMS08
2	54	100.0	111	1	KVMS69
3	51	94.4	131	1	KVMSM6
4	45	83.3	107	2	S26344
5	45	83.3	111	1	KVMS37
6	45	83.3	111	1	KVMS37
7	45	83.3	111	2	S09966
8	45	83.3	111	2	A33936
9	44	81.5	107	2	S26343
10	44	81.5	111	1	KVMS43
11	44	81.5	132	1	KVMS32
12	42	77.8	824	2	A86783
13	41	75.9	96	2	B49442
14	41	75.9	111	1	KVMS83
15	40	74.1	65	2	C38601
16	40	74.1	111	2	S09965
17	40	74.1	112	2	S19572
18	40	74.1	127	2	S04574
19	39	72.2	109	2	PH0093
20	39	72.2	111	1	KVMS80
21	39	72.2	704	2	S76120
22	39	72.2	2059	2	D82671
23	38	70.4	81	2	S42193
24	37	68.5	111	2	D45722
25	37	68.5	130	2	S40368
26	37	68.5	483	2	T19720
27	37	68.5	671	2	A55164
28	36	66.7	65	2	B38601
29	36	66.7	93	2	A38601

30	36	66.7	109	2	S31998
31	36	66.7	482	2	S65766
32	36	66.7	549	2	T50295
33	36	66.7	805	2	T19936
34	36	66.7	971	1	T01634
35	36	66.7	994	1	T08CR3
36	36	66.7	1171	2	T12936
37	36	66.7	1279	2	A47363
38	36	66.7	1287	2	T46032
39	35	64.8	107	2	JL0139
40	35	64.8	110	1	KVMS10
41	35	64.8	204	2	T36466
42	35	64.8	299	2	T35561
43	35	64.8	403	2	E84935
44	35	64.8	519	2	S36808
45	35	64.8	567	2	F64453

ALIGNMENTS

RESULT 1

KVMS08
Ig kappa chain V region (PC6308) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
R:Accession: C01937; A01937
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152
A:Accession: C01937
A:Molecule type: protein
A:Residues: 1-111 <WEI>
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status Predicted

Query Match
Best Local Similarity 100.0%; Score 54; DB 1; Length 111;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QOSNEDPWT 9
DB 93 QOSNEDPWT 101

RESULT 2

KVMS69
Ig kappa chain V region (PC7769) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
R:Accession: E01937; A01937
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152
A:Accession: E01937
A:Molecule type: protein
A:Residues: 1-111 <WEI>
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status Predicted

Query Match

100.0%; Score 54; DB 1; Length 111;

us-09-724-406-16.rpr

Fri Jun 29 08:04:31 2001

Query Match 94.4%; Score 51; DB 1; Length 131;
 Best Local Similarity 88.9%; Pred. No. 0.031; Indels 0; Gaps 0;
 Matches 8; Conservative 1; Mismatches 0

QY 1 QQSNEPWT 9
 ||:|||||
 Db 113 QQNEDPWT 121

RESULT 4
 S26344
 Ig kappa chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
 C:Accession: S26344
 R:Stark, S.E.; Caton, A.J.
 J. Exp. Med. 174, 613-624, 1991
 A:Title: Antibodies that are specific for a single amino acid interchange in a protein
 A:Reference number: S26309; MUID:91341421
 A:Accession: S26344
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-107 <STA>
 A:Cross-references: EMBL:X59209; NID:g52336; PIDN:CAA41919.1; PID:g1334074
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-93/Domain: immunoglobulin homology <IMM>

Query Match 83.3%; Score 45; DB 2; Length 107;
 Best Local Similarity 88.9%; Pred. No. 0.3; Indels 0; Gaps 0;
 Matches 8; Conservative 1; Mismatches 0

QY 1 QQSNEPWT 9
 |||||:|
 Db 92 QQSNEPWT 100

RESULT 5
 KWS37
 Ig kappa chain V regions (PC3741, T111) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 21-Jan-2000
 C:Accession: A93204; A93822; A01934
 R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
 Nature 276, 785-790, 1978
 A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
 A:Reference number: A93204; MUID:79073152
 A:Contents: PC3741
 A:Accession: A93204
 A:Molecule type: protein
 A:Residues: 1-111 <WEI>
 R:McKean, D.J.; Bell, M.; Potter, M.
 Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978
 A:Title: Mechanisms of antibody diversity: multiple genes encode structurally related
 A:Reference number: A93822; MUID:79012520
 A:Contents: T111
 A:Accession: A93822
 A:Molecule type: protein
 A:Residues: 1-111 <MCK>
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer
 F:16-94/Domain: immunoglobulin homology <IMM>
 F:23-92/Disulfide bonds: #status predicted

Query Match 83.3%; Score 45; DB 1; Length 111;
 Best Local Similarity 88.9%; Pred. No. 0.32; Indels 0; Gaps 0;
 Matches 8; Conservative 1; Mismatches 0

QY 1 QQSNEPWT 9
 |||||:|
 Db 93 QQSNEPWT 101

RESULT 3
 KWSM6
 Ig kappa chain precursor V regions (M63, AB22, PC9245, PC4050) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 21-Jan-2000
 C:Accession: B90412; B90374; B93822; C93204; D93204; PH1078; A01935
 R:Bursstein, V.; Schechter, I.
 Biochemistry 17, 2392-2400, 1978
 A:Title: Primary structures of N-terminal extra peptide segments linked to the variable
 A:Reference number: A90412; MUID:78235887
 A:Contents: M63
 A:Accession: B90412
 A:Molecule type: protein
 A:Residues: 1-35 <BUR>
 R:McKean, D.; Potter, M.; Hood, L.
 Biochemistry 12, 760-771, 1973
 A:Title: Mouse immunoglobulin chains. Pattern of sequence variation among kappa chains
 A:Reference number: A90374; MUID:73140225
 A:Contents: M63
 A:Accession: B90374
 A:Molecule type: protein
 A:Residues: 21-46, Q' 48-53, B' 55-57, Z' 59-86, F' 88-131 <MCK>
 A:Note: this sequence has since been revised in reference A93822
 R:McKean, D.J.; Bell, M.; Potter, M.
 Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978
 A:Title: Mechanisms of antibody diversity: multiple genes encode structurally related
 A:Reference number: A93822; MUID:79012520
 A:Contents: M63; AB22
 A:Accession: B93822
 A:Molecule type: protein
 A:Residues: 1-53; 69-107 <MC2>
 A:Accession: C93822
 A:Molecule type: protein
 A:Residues: 21-119, Y' 121-131 <MC3>
 R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
 Nature 276, 785-790, 1978
 A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
 A:Reference number: A93204; MUID:79073152
 A:Contents: PC9245; PC4050
 A:Accession: C93204
 A:Molecule type: protein
 A:Residues: 21-119, Y' 121-131 <WEI>
 A:Accession: D93204
 A:Molecule type: protein
 A:Residues: 21-119, Y' 121-123, A' 125-129, L' 131 <WE2>
 R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
 J. Exp. Med. 176, 761-779, 1992
 A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B
 A:Reference number: PH0971; MUID:92381444
 A:Accession: PH1078
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 21-122 <TIL>
 A:Experimental source: B cell, strain [NZB x NZW]F1, clone 17p.73
 C:Comment: The M63 precursor sequence is shown.
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-20/Domain: signal sequence #status experimental <SIG>
 F:21-131/Domain: Ig kappa chain precursor V region #status experimental <MAT>
 F:36-114/Domain: immunoglobulin homology <IMM>
 F:43-112/Disulfide bonds: #status predicted

QY 1 QOSNEDPWT 9
 |||||:|
 Db 93 QOSNEDPYT 101

RESULT 6
 KVMSC1

Ig kappa chain V region (CBPC 101) - mouse (tentative sequence)
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 31-Mar-2000
 C:Accession: A01936
 R:McKean, D.J.; Bell, M.; Potter, M.
 Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978
 A:Title: Mechanisms of antibody diversity: multiple genes encode structurally related mo
 A:Reference number: A93822; MUID:79012520
 A:Accession: A01936
 A:Molecule type: protein
 A:Residues: 1-111 <MCK>

C:Comment: This chain was isolated from a myeloma protein.
 hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer
 F:16-94/Domain: immunoglobulin homology <IMM>
 F:23-92/Disulfide bonds: #status predicted

Query Match 83.3%; Score 45; DB 1; Length 111;
 Best Local Similarity 88.9%; Pred. No. 0.32;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNEDPWT 9
 |||||:|
 Db 93 QOSNEDPYT 101

RESULT 7

Ig kappa chain V-J region (IE10) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 21-Jan-2000
 C:Accession: S09966
 R:Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
 Eur. J. Immunol. 20, 771-777, 1990
 A:Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodie
 A:Reference number: S09955; MUID:90269328
 A:Accession: S09966
 A:Molecule type: mRNA
 A:Residues: 1-111 <REI>
 A:Cross-references: EMBL:X51854; NID:955397; PIDN:CAA36147.1; PID:9930231
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 83.3%; Score 45; DB 2; Length 111;
 Best Local Similarity 88.9%; Pred. No. 0.32;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNEDPWT 9
 |||||:|
 Db 93 QOSNEDPYT 101

RESULT 8

Ig kappa chain V region (VM201) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000
 C:Accession: A33936
 R:Meek, K.; Johansson, B.; Schulman, J.; Bona, C.; Capra, J.D.
 Proc. Natl. Acad. Sci. U.S.A. 86, 4664-4668, 1989
 A:Title: Nucleotide changes in sequential variants of influenza virus hemagglutinin gene

A:Reference number: A33936; MUID:89282831
 A:Accession: A33936
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-111 <MEE>

A:Cross-references: GB:J04575; NID:9623194; PIDN:AAA60448.1; PID:9623196
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:14-94/Domain: immunoglobulin homology <IMM>

Query Match 83.3%; Score 45; DB 2; Length 111;
 Best Local Similarity 88.9%; Pred. No. 0.32;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNEDPWT 9
 |||||:|
 Db 93 QOSNEDPYT 101

RESULT 9

Ig kappa chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
 C:Accession: S26343
 R:Stark, S.E.; Caton, A.J.
 J. Exp. Med. 174, 613-624, 1991
 A:Title: Antibodies that are specific for a single amino acid interchange in a protei
 A:Reference number: S26309; MUID:91341421
 A:Accession: S26343
 A:Molecule type: preliminary
 A:Residues: 1-107 <STA>
 A:Cross-references: EMBL:X59207; NID:952334; PIDN:CAA41917.1; PID:91334073
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-93/Domain: immunoglobulin homology <IMM>

Query Match 81.5%; Score 44; DB 2; Length 107;
 Best Local Similarity 88.9%; Pred. No. 0.46;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNEDPWT 9
 |||||:|
 Db 92 QOSNEDPPT 100

RESULT 10
 KVMSC43

Ig kappa chain V region (PC7043) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 21-Jan-2000
 C:Accession: A01937; S42187; S42194; S42190; S42189; S42188; S42191; S42192
 R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
 Nature 276, 785-790, 1978
 A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
 A:Reference number: A03204; MUID:79073152
 A:Accession: A01937
 A:Molecule type: protein
 A:Residues: 1-111 <WEI>

R:Mo, J.A.; Bona, C.A.; Holmdahl, R.
 Eur. J. Immunol. 23, 2503-2510, 1993
 A:Title: Variable region gene selection of immunoglobulin G-expressing B cells with s
 A:Reference number: S42176; MUID:94009207
 A:Accession: S42187
 A:Molecule type: DNA
 A:Residues: 10-99 <MOJ>

A:Cross-references: EMBL:225444; NID:9407832; PIDN:CAA80931.1; PID:9407833
 A:Note: V-kappa-2IE; anti-collagen
 A:Accession: S42194
 A:Molecule type: DNA

Query Match 75.9%; Score 41; DB 2; Length 96;
 Best Local Similarity 88.9%; Pred. No. 1.4;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSNEDPWT 9
 DB 85 QOSNEDPLT 93
 ||||| |

RESULT 14
 KVM83
 Ig kappa chain V region (PC7183) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
 C:Accession: B01937; A01937
 R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
 Nature 276, 785-790, 1978
 A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
 A:Reference number: A93204; MUID:79073152
 A:Accession: B01937
 A:Molecule type: protein
 A:Residues: 1-111 <WEI>
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 12-mer complexes.
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-94/Domain: immunoglobulin homology <IMM>
 F:23-92/Disulfide bonds: #status predicted

Query Match 75.9%; Score 41; DB 1; Length 111;
 Best Local Similarity 88.9%; Pred. No. 1.7;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSNEDPWT 9
 DB 93 QOSNEDPLT 101
 ||||| |

RESULT 15
 C38601
 Ig kappa chain V region (2B5) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 23-Jul-1999
 C:Accession: C38601
 R:Goshorn, S.C.; Retzel, E.; Jemerson, R.
 J. Biol. Chem. 266, 2134-2142, 1991
 A:Title: Common structural features among monoclonal antibodies binding the same antigen
 A:Reference number: A38601; MUID:91115823
 A:Accession: C38601
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-65 <GOS>
 A:Cross-references: GB:M57980; NID:g196406; PIDN:AAA63361.1; PID:g196407
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 74.1%; Score 40; DB 2; Length 65;
 Best Local Similarity 88.9%; Pred. No. 1.4;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSNEDPWT 9
 DB 46 QOSNEDPRT 54
 ||||| |

Search completed: June 28, 2001, 15:58:44
 Job time: 372 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2001, 15:54:36 ; Search time 105.36 Seconds
(without alignments)
2.926 Million cell updates/sec

Title: US-09-724-406-16
Perfect score: 54
Sequence: 1 QQSNEPWT 9

Scoring table: BLQSOM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	111	1	P01667 mus musculus
2	54	100.0	111	1	P01669 mus musculus
3	51	94.4	131	1	P01661 mus musculus
4	45	83.3	111	1	P01660 mus musculus
5	45	83.3	111	1	P01664 mus musculus
6	44	81.5	111	1	P01665 mus musculus
7	44	81.5	132	1	P01658 mus musculus
8	42	77.8	111	1	P01662 mus musculus
9	41	75.9	111	1	P01654 mus musculus
10	39	72.2	111	1	P01656 mus musculus
11	39	72.2	111	1	P01663 mus musculus
12	38	70.4	111	1	P01659 mus musculus
13	38	70.4	112	1	P01657 mus musculus
14	37	68.5	671	1	P01655 mus musculus
15	36	66.7	417	1	P41889 schizosacch
16	36	66.7	417	1	P54998 rhodococcus
17	36	66.7	482	1	Q16581 homo sapien
18	36	66.7	971	1	Q00273 epizootic h
19	36	66.7	994	1	P08504 escherichia
20	36	66.7	1004	1	Q03277 sclara copr
21	36	66.7	1270	1	Q08211 homo sapien
22	36	66.7	1287	1	Q28141 bos taurus
23	36	66.7	1380	1	O70133 mus musculus
24	35	64.8	110	1	P01668 mus musculus
25	35	64.8	403	1	P57158 buchera ap
26	35	64.8	567	1	Q58628 methanococc
27	35	64.8	1023	1	O27179 methanobact
28	35	64.8	1102	1	P55019 pseudopleur
29	35	64.8	1592	1	Q93009 homo sapien
30	34	63.0	204	1	P53855 saccharomyc
31	34	63.0	232	1	P05379 thermus aqu
32	34	63.0	232	1	P27983 simian immu
33	34	63.0	374	1	Q58365 methanococc
					P18632 cryptomeria

34 34 63.0 436 1 60A_DROVI Q24735 drosophila
35 34 63.0 572 1 TC17_MOUSE Q61751 mus musculus
36 34 63.0 576 1 TC17_MOUSE Q62975 rattus norv
37 34 63.0 605 1 TC17_MOUSE Q60765 homo sapien
38 34 63.0 605 1 VCLA_GOSHI P09799 gossypium h
39 34 63.0 632 1 NTP1_MXVL Q9q814 myxoma viru
40 34 63.0 632 1 NTP1_SFVKA Q9q822 Shope fibro
41 34 63.0 906 1 CBL_HUMAN P22681 Shope sapien
42 33.5 62.0 885 1 CHB_SERMA Q54468 serratia ma
43 33 61.1 322 1 VP40_NPVHZ P36345 heliothis z
44 33 61.1 378 1 RSL_PROSP P14128 providencia
45 33 61.1 403 1 SHBG_MOUSE P97497 mus musculus

ALIGNMENTS

RESULT 1
KV3Q_MOUSE
ID KV3Q_MOUSE STANDARD; PRT; 111 AA.
AC P01667;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE IG KAPPA CHAIN V-III REGION PC 6308.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR PIR: C01937; KWS08.
DR InterPro: IPR003006;
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12071 MW; 7A4ADE4D6C256D29 CRC64;

Query Match 100.0%; Score 54; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSNEPWT 9
Db 93 QQSNEPWT 101

RESULT 2
KV3Q_MOUSE
ID KV3Q_MOUSE STANDARD; PRT; 111 AA.
AC P01669;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE IG KAPPA CHAIN V-III REGION PC 7769.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

Fri Jun 29 08:04:32 2001

EN SEQUENCE.
 RP MEDLINE=79073152; PubMed-103003;
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 RT diversity";
 RL Nature 276:785-790(1978).
 DR PIR: E01937; KVM569.
 DR InterPro: IPR003006; -.
 DR Pfam: PF00047; Ig: 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT DOMAIN 102 111
 FT DISULFID 23 92
 FT NON_TER 111 111
 SQ SEQUENCE 111 AA; 12011 MW; 6FAA345279356829 CRC64;

Query Match 100.0%; Score 54; DB 1; Length 111;
 Best Local Similarity 100.0%; Pred. No. 0.0035;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNEPWT 9
 DB 93 QOSNEPWT 101
 |||||

RESULT 3
 KV3H_MOUSE STANDARD; PRT; 131 AA.
 ID KV3H_MOUSE
 AC P01661;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION MOPC 63 PRECURSOR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE OF 1-35.
 RX MEDLINE=78235887; PubMed-98179;
 RA Burstein Y., Schechter I.;
 RT "Primary structures of N-terminal extra peptide segments linked to
 RT the variable and constant regions of immunoglobulin light chain
 RT precursors: implications for the organization and controlled
 RT expression of immunoglobulin genes";
 RL Biochemistry 17:2392-2400(1978).
 RN [2]
 RP SEQUENCE OF 21-131.
 RX MEDLINE=73140225; PubMed-4691517;
 RA McKean D.J., Potter M., Hood L.E.;
 RT "Mouse immunoglobulin chains. Pattern of sequence variation among
 RT kappa chains with limited sequence differences";
 RL Biochemistry 12:760-771(1973).
 RN [3]
 RP REVISIONS.

QY MEDLINE=79012520; PubMed-99744;
 RA McKean D.J., Bell M., Potter M.;
 RT "Mechanisms of antibody diversity: multiple genes encode structurally
 RT related mouse kappa variable regions";
 RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
 DR PIR: A01935; KVM56.
 DR InterPro: IPR003006; -.
 DR Pfam: PF00047; Ig: 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 131 IG KAPPA CHAIN V-III REGION MOPC 63.

Query Match 94.4%; Score 51; DB 1; Length 131;
 Best Local Similarity 88.9%; Pred. No. 0.014;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNEPWT 9
 DB 113 QOSNEPWT 121
 |||||

RESULT 4
 KV3H_MOUSE STANDARD; PRT; 111 AA.
 ID KV3H_MOUSE
 AC P01660;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION PC 3741/TEPC 111.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE (PC 3741).
 RX MEDLINE=79073152; PubMed-103003;
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 RT diversity";
 RL Nature 276:785-790(1978).
 RN [2]
 RP SEQUENCE (TEPC 111).
 RX MEDLINE=75012520; PubMed-99744;
 RA McKean D.J., Bell M., Potter M.;
 RT "Mechanisms of antibody diversity: multiple genes encode structurally
 RT related mouse kappa variable regions";
 RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
 CC -!- MISCELLANEOUS: THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL.

DR PIR: A01934; KVM537.
 DR InterPro: IPR003006; -.
 DR Pfam: PF00047; Ig: 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT DOMAIN 102 111
 FT DISULFID 23 92
 FT NON_TER 111 111
 SQ SEQUENCE 111 AA; 12099 MW; EC46C9D259213BE4 CRC64;

Query Match 83.3%; Score 45; DB 1; Length 111;
 Best Local Similarity 88.9%; Pred. No. 0.15;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSNEPWT 9
 DB 93 QOSNEPWT 101
 |||||

RESULT 5
KV3L_MOUSE
ID KV3L_MOUSE STANDARD; PRT; 111 AA.
AC P01664;
DT 21-JUL-1986 (Rel. 01, Created)
DE 21-JUL-1986 (Rel. 01, Last sequence update)
DE IG KAPPA CHAIN V-III REGION CBPC 101.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN NCBI_TaxID=10090;
RP SEQUENCE.
RX MEDLINE=79012520; PubMed=95744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
CC 1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A01936; KVMSC1.
DR InterPro: IPR003006;
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111
SQ SEQUENCE 111 AA; 11964 MW; E2B1AD98AD965962 CRC64;

Query Match 83.3%; Score 45; DB 1; Length 111;
Best Local Similarity 88.9%; Pred. No. 0.15;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QOSNEPWT 9
Db 93 QOSNEPWT 101
|||||:|

RESULT 6
KV3M_MOUSE
ID KV3M_MOUSE STANDARD; PRT; 111 AA.
AC P01665;
DT 21-JUL-1986 (Rel. 01, Created)
DE 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 7043.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN NCBI_TaxID=10090;
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gattaman L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR PIR; A01937; KVMSC3.
DR InterPro: IPR003006;
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
SQ SEQUENCE 111 AA; 11964 MW; E2B1AD98AD965962 CRC64;

Query Match 81.5%; Score 44; DB 1; Length 132;
Best Local Similarity 44.4%; Pred. No. 0.27;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QOSNEPWT 9
Db 113 ZZSBEPWT 121
:|:|:|

FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 102 111 FRAMEWORK 4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111
SQ SEQUENCE 111 AA; 12002 MW; 7A5PCB586C306D29 CRC64;

Query Match 81.5%; Score 44; DB 1; Length 111;
Best Local Similarity 88.9%; Pred. No. 0.22;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QOSNEPWT 9
Db 93 QOSNEPWT 101
|||||:|

RESULT 7
KV3F_MOUSE
ID KV3F_MOUSE STANDARD; PRT; 132 AA.
AC P01658;
DT 21-JUL-1986 (Rel. 01, Created)
DE 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION MOPC 321 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN NCBI_TaxID=10090;
RP SEQUENCE OF 1-37.
RX MEDLINE=78235887; PubMed=98179;
RA Birstein Y., Schechter I.;
RT "Primary structures of N-terminal extra peptide segments linked to
RT the variable and constant regions of immunoglobulin light chain
RT precursors: implications on the organization and controlled
RT expression of immunoglobulin genes.";
RL Biochemistry 17:2392-2400(1978).
RN [1]
RP SEQUENCE OF 21-132.
RX MEDLINE=73140224; PubMed=4120629;
RA McKean D.J., Potter M., Hood L.E.;
RT "Mouse immunoglobulin chains. Partial amino acid sequence of a kappa
RT chain.";
RL Biochemistry 12:749-759(1973).
CC 1- MISCELLANEOUS: THE PARTIAL SEQUENCE OF THE C REGION OF THIS
CC BENCE-JONES PROTEIN WAS ALSO DETERMINED. IT DIFFERS FROM THAT
CC REPORTED FOR MOUSE MOPC 21 ONLY IN THE TRANSPOSITION OF TWO NEARBY
CC RESIDUES.
DR PIR; A01933; KVMSC2.
DR InterPro: IPR003006;
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region; Bence-Jones protein; Signal.
FT SIGNAL 1 20
FT CHAIN 21 132 IG KAPPA CHAIN V-III REGION MOPC 321.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 59 73 FRAMEWORK 2.
FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 81 112 FRAMEWORK 3.
FT DOMAIN 113 121 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 122 131 FRAMEWORK 4.
FT DISULFID 43 112 BY SIMILARITY.
FT NON_TER 132 132
SQ SEQUENCE 132 AA; 14523 MW; 9F3B809BB773FBE9 CRC64;

Query Match 81.5%; Score 44; DB 1; Length 132;
Best Local Similarity 44.4%; Pred. No. 0.27;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QOSNEPWT 9
Db 113 ZZSBEPWT 121
:|:|:|

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RESULT 8
KV3J_MOUSE
ID KV3J_MOUSE STANDARD; PRT; 111 AA.
AC P01662;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION ABPC 22/PC 9245.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
OX [1]
RN SEQUENCE (ABPC 22); PubMed=99744;
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
[2]
RN SEQUENCE (PC 9245).
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gattaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
CC -1- MISCELLANEOUS: THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.
DR PIR: A01935; KVM56.
DR InterPro: IPR003006;
DR Pfam: PF00047; ig: 1.
DR Immunoglobulin V region.
KW DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12041 MW; D7DF0609303453CE CRC64;

Query Match 77.8%; Score 42; DB 1; Length 111;
Best Local Similarity 77.8%; Pred. No. 0.51; Indels 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 0;

Qy 1 QQSNEPWT 9
Db 93 QONNEDPYT 101

RESULT 9
KV3N_MOUSE
ID KV3N_MOUSE STANDARD; PRT; 111 AA.
AC P01666;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 7183.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
OX [1]
RN SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gattaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).

Query Match 72.2%; Score 39; DB 1; Length 111;
Best Local Similarity 77.8%; Pred. No. 1.8; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 2;

Qy 1 QQSNEPWT 9
Db 93 QQSKEVPWT 101

RESULT 10
KV3A_MOUSE
ID KV3A_MOUSE STANDARD; PRT; 111 AA.
AC P01654;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 2880/PC 1229.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
OX [1]
RN SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gattaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
CC -1- MISCELLANEOUS: THE PC 2880 AND PC 1229 SEQUENCES ARE IDENTICAL.
DR PIR: A01930; KVM580.
DR InterPro: IPR003006;
DR Pfam: PF00047; ig: 1.
DR Immunoglobulin V region.
KW DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11980 MW; AFEAC6A9D26FC12D CRC64;

Query Match 75.9%; Score 41; DB 1; Length 111;
Best Local Similarity 88.9%; Pred. No. 0.77; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 1;

Qy 1 QQSNEPWT 9
Db 93 QQSNEPWT 101

RESULT 11
KV3C_MOUSE
ID KV3C_MOUSE STANDARD; PRT; 111 AA.

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AC P01656;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION MOPC 70.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=67056897; PubMed=4162931;
 RA Gray W.R., Dreyer W.J., Hood L.E.;
 RT "Mechanism of antibody synthesis: size differences between mouse
 RT kappa chains."
 RL Science 155:465-467(1967).
 CC -I- MISCELLANEOUS; THIS IS A BENGE-JONES PROTEIN.
 DR PIR: A01930; KWSM80.
 DR InterPro: IPR003006; -.
 DR Pfam: PF00047; Ig; 1.
 DR Immunoglobulin V region; Bence-Jones protein.
 KW DOMAIN 1 23
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT DOMAIN 102 111
 FT DISULFID 23 92
 FT NON_TER 111 111
 SQ SEQUENCE 111 AA; 11904 MW; 4FE7ABC9DF0FC125 CRC64;

Query Match 72.2%; Score 39; DB 1; Length 111;
 Best Local Similarity 77.8%; Pred. No. 1.8;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOSNEDPWT 9
 III I III
 Db 93 QOSKEVFWT 101

RESULT 12
 KV3K_MOUSE STANDARD; PRT; 111 AA.
 AC P01663;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION PC 4050.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 RT diversity."
 RL Nature 276:785-790(1978).
 DR PIR: A01935; KWSM6.
 DR InterPro: IPR003006; -.
 DR Pfam: PF00047; Ig; 1.
 DR Immunoglobulin V region.
 KW DOMAIN 1 23
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT DOMAIN 102 111
 FT DISULFID 23 92
 FT NON_TER 111 111
 SQ SEQUENCE 111 AA; 11904 MW; 4FE7ABC9DF0FC125 CRC64;

FT NON_TER 111 111
 SQ SEQUENCE 111 AA; 12005 MW; 39D87619313453CB CRC64;
 Query Match 70.4%; Score 38; DB 1; Length 111;
 Best Local Similarity 77.8%; Pred. No. 2.7;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSNEDPWT 9
 III I III
 Db 93 QONNEDPLT 101

RESULT 13
 KV3G_MOUSE STANDARD; PRT; 112 AA.
 ID KV3G_MOUSE
 AC P01659;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION TEPC 124.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=73140225; PubMed=4691517;
 RA McKean D.J., Potter M., Hood L.E.;
 RT "Mouse immunoglobulin chains. Pattern of sequence variation among
 RT kappa chains with limited sequence differences."
 RL Biochemistry 12:760-771(1973).
 DR PIR: A01933; KWSM32.
 DR InterPro: IPR003006; -.
 DR Pfam: PF00047; Ig; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT DOMAIN 102 111
 FT DISULFID 23 92
 FT NON_TER 112 112
 SQ SEQUENCE 112 AA; 12339 MW; 7CFD328DBE8E9D71 CRC64;

Query Match 70.4%; Score 38; DB 1; Length 112;
 Best Local Similarity 44.4%; Pred. No. 2.7;
 Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSNEDPWT 9
 III I III
 Db 93 ZZSBZAPWT 101

RESULT 14
 CUT9_SCHPO STANDARD; PRT; 671 AA.
 ID CUT9_SCHPO
 AC P41889; O14231;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE CUT9 PROTEIN.
 GN CUT9 OR SPAC6F12.15C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.

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RT "Characterization of the desulfurization genes from Rhodococcus sp.
RT strain IGTS8."
RL J. Bacteriol. 176:6707-6716(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96031556; PubMed=7574582;
RA Piddington C.S., Kovacevich B.R., Rambosek J.;
RT "Sequence and molecular characterization of a DNA region encoding the
RT dibenzothiophene desulfurization operon of Rhodococcus sp. strain
RT IGTS8."
RL Environ. Microbiol. 61:468-475(1995).
CC -!- FUNCTION: PART OF A PATHWAY TO REMOVE COVALENTLY BOUND SULFUR FROM
CC DIBENZOTHIOPHENE (DBT) WITHOUT BREAKING CARBON-CARBON BONDS.
CC SULFUR DIOXYGENASE WHICH CONVERTS DBT TO DBT-SULFONE (DBT02 OR DBT
CC 5,5-DIOXIDE)
CC -!- PATHWAY: FIRST STEP IN PATHWAY FROM DBT TO 2-HBP.
CC -!- SIMILARITY: SOME, TO ACYL COENZYME A DEHYDROGENASES.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
CC EMBL; U08850; AAA56673.1; -
CC EMBL; L37363; AAA99484.1; -
CC InterPro: IPR001552; -
CC Pfam; PF00441; Acyl-CoA_dh; 3.
CC KW Oxidoreductase; Plasmid.
CC FT CONFLICT 56 56 G -> A (IN REF. 2).
CC FT CONFLICT 251 251 A -> R (IN REF. 2).
CC SQ SEQUENCE 417 AA; 45027 MW; CDBCF0054AE2FD0 CRC64;

Query Match 66.7%; Score 36; DB 1; Length 417;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QSNEDPWT 9
Db 290 QOATEDPYT 298

Search completed: June 28, 2001, 15:54:37
Job time: 125 sec

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RX MEDLINE=95096177; PubMed=7798319;
RA Samejima I., Yanagida M.;
RT "Bypassing anaphase by fission yeast cut9 mutation: requirement of
RT cut9+ to initiate anaphase."
RL J. Cell Biol. 127:1655-1670(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=972;
RA Badcock K., Churcher C.M., Barrell B.G., Rajandream M.A., Wood V.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: MAY PLAY A PIVOTAL ROLE IN THE CONTROL OF ANAPHASE.
CC COMPONENT OF THE 20S CYCLOSOME/ANAPHASE-PROMOTING COMPLEX (APC),
CC WHICH IS NECESSARY FOR CYCLIN DESTRUCTION.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
CC -!- SIMILARITY: CONTAINS 10 TPR REPEATS.
CC
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; D31844; BAA06630.1; -
CC EMBL; 298533; CAB11098.1; -
CC InterPro: IPR001440; -
CC Pfam; PF00515; TPR; 5.
CC KW Cell division; Cell cycle; Mitosis; Repeat; TPR repeat;
CC Nucleolar protein.
CC FT REPEAT 117 149 TPR 1.
CC FT REPEAT 150 184 TPR 2.
CC FT REPEAT 200 233 TPR 3.
CC FT REPEAT 339 372 TPR 4.
CC FT REPEAT 373 406 TPR 5.
CC FT REPEAT 407 440 TPR 6.
CC FT REPEAT 441 474 TPR 7.
CC FT REPEAT 475 508 TPR 8.
CC FT REPEAT 515 549 TPR 9.
CC FT REPEAT 550 583 TPR 10.
CC FT MUTAGEN 412 412 G->D: IN TEMPERATURE SENSITIVE MUTANT.
CC FT MUTAGEN 535 535 A->T: IN TEMPERATURE SENSITIVE MUTANT.
CC FT CONFLICT 103 103 A -> C (IN REF. 1).
CC SQ SEQUENCE 671 AA; 75888 MW; 5300382396270BE2 CRC64;

Query Match 68.5%; Score 37; DB 1; Length 671;
Best Local Similarity 85.7%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QSNEDPW 8
Db 509 QSNKPW 515

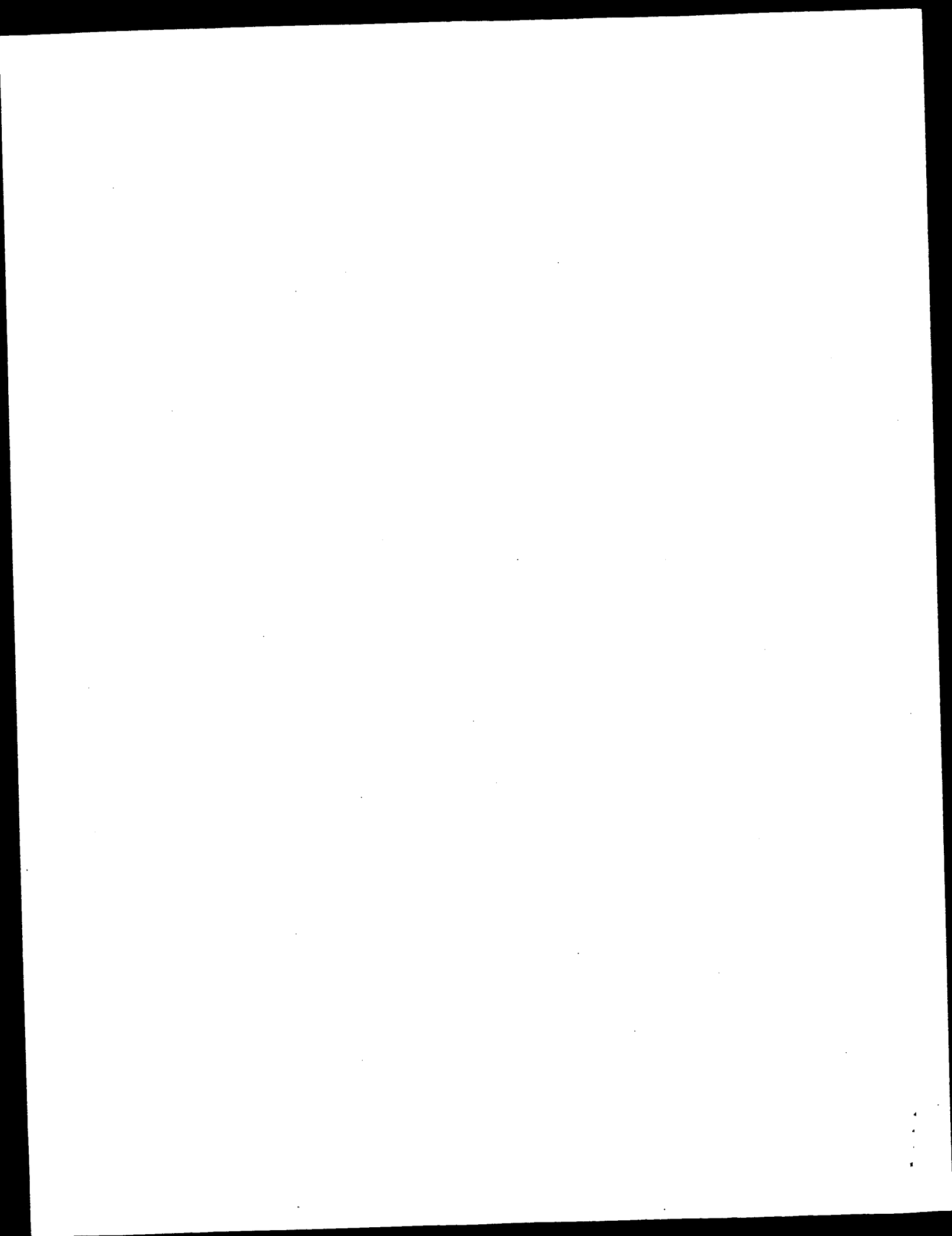
RESULT 15
SOXC_RHOSO
ID SOXC_RHOSO STANDARD; PRT; 417 AA.
AC P54998;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE DIBENZOTHIOPHENE DESULFURIZATION ENZYME C (DBT SULFUR DIOXYGENASE).
GN SOXC OR DS2C.
OS Rhodococcus sp. (strain IGTS8).
OG Plasmid.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.
OX NCBI_TaxID=1831;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=95050232; PubMed=7961424;
RA Denome S.A., Oldfield C., Nash L.J., Young K.D.;

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us-09-724-406-16.rsp

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RT Synecocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
 region from map positions 64% to 92% of the genome.;
 RL DNA Res. 2:153-166(1995).
 RN [3]

RP SEQUENCE FROM N.A.
 RX MEDLINE=97061201; PubMed=8905231;
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hiroseawa M., Sugliura M., Nakazaki N., Naruo K., Okumura S.,
 RA Hosouchi T., Matsuno A., Muraki A., Watanabe A., Yamada M., Yasuda M.,
 RA Shimo S., Takeuchi C., Wada T., Watanabe A.,
 RA Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 Synecocystis sp. strain PCC6803. II. Sequence determination of the
 entire genome and assignment of potential protein-coding regions.";
 RL DNA Res. 3:109-136(1996).
 DR EMBL: D63999; BAA10098.1;
 DR InterPro: IPR002692;
 DR Pfam: PF01804; Penicill.amidase; 1. 9F13B0DFA2278B63 CRC64;
 DR SEQUENCE 704 AA; 77956 MW; 9F13B0DFA2278B63 CRC64;
 SQ

Query Match 72.2%; Score 39; DB 2; Length 704;
 Best Local Similarity 66.7%; Pred. No. 31; Indels 0; Gaps 0;
 Matches 6; Conservative 1; Mismatches 2;

QY 1 QOSNEPWT 9
 DB 429 QNSNDPWT 437

RESULT 4
 Q9L5D6 PRELIMINARY; PRT; 720 AA.

ID Q9L5D6
 AC Q9L5D6
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE GLUTARYL 7-AMINOCEPHALOSPORANIC ACID ACYLASE
 OS Brevundimonas diminuta (Pseudomonas diminuta)
 OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
 OC Brevundimonas
 OX NCBI_TaxID=293;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-KAC-1;
 RA Kim D.-W., Kang S.-M., Yoon K.-H.;
 RT "Isolation of new Pseudomonas diminuta KAC-1 strain producing glutaryl
 7-aminocephalosporanic acid acylase.";
 RT 7-aminocephalosporanic acid acylase;
 RL Korean J. Microbiol. 37:200-205(1999).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN-KAC-1;
 RA Kim D.-W., Kang S.-M., Yoon K.-H.;
 RT "Cloning and the nucleotide sequence of a Pseudomonas diminuta KAC-1
 glutaryl 7-aminocephalosporanic acid acylase gene.";
 RT Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AF251710; AAF64242.1;
 DR InterPro: IPR002692;
 DR Pfam: PF01804; Penicill.amidase; 1. AD624797845CC39B CRC64;
 DR SEQUENCE 720 AA; 79779 MW; AD624797845CC39B CRC64;
 SQ

Query Match 72.2%; Score 39; DB 2; Length 720;
 Best Local Similarity 66.7%; Pred. No. 32; Indels 0; Gaps 0;
 Matches 6; Conservative 1; Mismatches 2;

QY 1 QOSNEPWT 9
 DB 439 QNSNDPWT 447

RESULT 5
 O86089

KW DNA replication; DNA-binding; DNA-directed DNA polymerase.
 SQ SEQUENCE 1104 AA; 125786 MW; 3E609827CEF3E40B CRC64;

Query Match 75.9%; Score 41; DB 14; Length 1104;
 Best Local Similarity 85.7%; Pred. No. 21; Indels 0; Gaps 0;
 Matches 6; Conservative 1; Mismatches 0;

QY 3 SNEDPWT 9
 DB 828 SNODPWT 834

RESULT 2
 Q9M4T2 PRELIMINARY; PRT; 263 AA.

ID Q9M4T2
 AC Q9M4T2
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE ARL2.
 GN Phaseolus acutifolius (teary bean).
 OS Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Eukaryota; Viridiplantae; Embryophyta; core eucotids; Rosidae; eurosids I;
 OC Magnoliophyta; eudicotyledons; core eucotids; Rosidae; eurosids I;
 OC Fabales; Fabaceae; Papilionoideae; Phaseolus.
 OX NCBI_TaxID=33129;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Gerhardt I.R., Pappas G., Chrispeels M.J., Grossi de Sa M.F.;
 RT "Insecticidal arcelin genes of the common bean are subject to
 divergent selection.";
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF25724; AAF71744.1;
 DR InterPro: IPR000985;
 DR InterPro: IPR001220;
 DR Pfam: PF00138; lectin_legA; 1.
 DR Pfam: PF00139; lectin_legB; 1.
 DR SEQUENCE 263 AA; 29025 MW; 36ED84DAFA8ECF9C CRC64;
 SQ

Query Match 72.2%; Score 39; DB 10; Length 263;
 Best Local Similarity 100.0%; Pred. No. 11; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0;

QY 3 SNEDPW 8
 DB 63 SNEDPW 68

RESULT 3
 Q55592 PRELIMINARY; PRT; 704 AA.

ID Q55592
 AC Q55592
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DT 7-BETA-(4-CARBXYBUTANAMIDO)CEPHALOSPORANIC ACID ACYLASE.
 DE SLR0378.
 GN Synecocystis sp. (strain PCC 6803).
 OS Bacteria; Cyanobacteria; Chroococcales; Synecocystis.
 OC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.
 OX NCBI_TaxID=1148;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-PCC6803;
 RA Tabata S.;
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]

RP SEQUENCE FROM N.A.
 RX MEDLINE=96127529; PubMed=8590279;
 RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
 RA Sugliura M., Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium

ID O86089 PRELIMINARY; PRT; 720 AA.
 AC O86089;
 DT 01-NOV-1998 (TREMblrel. 08, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 DE CEPHALOSPORIN ACYLASE.
 GN CAL.
 OS Pseudomonas sp. 130.
 OC Bacteria; Proteobacteria.
 OX NCBI_TaxID=81841;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=130.
 RX MEDLINE=99339939; PubMed=10411632;
 RA Li Y., Chen J., Jiang W., Mao X., Zhao G., Wang E.;
 RT "In vivo post-translational processing and subunit reconstitution of
 RL cephalosporin acylase from Pseudomonas sp. 130.";
 RL Eur. J. Biochem. 262:713-719(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=130;
 RA Li Y., Zhang Q., Yang Y., Zhao G., Wang E.;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF085353; AAC34685.2;
 DR InterPro: IPR002692;
 DR Pfam: PF01804; Penicil_amidase; 1.
 KW Porin.
 SQ SEQUENCE 720 AA; 79672 MW; C2EF964F5081D8CB CRC64;

Query Match 72.2%; Score 39; DB 2; Length 720;
 Best Local Similarity 56.7%; Pred. No. 32;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 QOSNDPWT 9
 | | | | |
 DB 439 QNSNDPWT 447

RESULT 6
 Q9PD50 PRELIMINARY; PRT; 2059 AA.
 ID Q9PD50;
 AC Q9PD50;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 DE SURFACE PROTEIN.
 GN XF1529.
 OS Xylella fastidiosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
 OX Xylella.
 OX NCBI_TaxID=2371;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=9A5C;
 RX MEDLINE=20365717; PubMed=10910347;
 RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
 RA Alvarado R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
 RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
 RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrier H.,
 RA Coutinho N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
 RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
 RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
 RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
 RA Garner M., Goldman G.H., Goldman M.H.S., Gomes S.B., Gruber A.,
 RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
 RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
 RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
 RA Machado M.A., Madelira A.M.B.N., Madelira H.M.F., Marino C.L.,
 RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
 RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
 RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
 RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,

de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
 RA Pexoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
 RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
 RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
 RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
 RA da Silva J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
 RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsunako M.H.,
 RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
 RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
 RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
 RL Nature 406:151-159(2000).
 DR EMBL: AF003982; AAF84338.1;
 SQ SEQUENCE 2059 AA; 204035 MW; EBA6A71B5DD24E10 CRC64;

Query Match 72.2%; Score 39; DB 2; Length 2059;
 Best Local Similarity 75.0%; Pred. No. 96;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 QSNEDPWT 9
 | | | | |
 DB 68 QCSNDPWT 75

RESULT 7
 Q9V5E3 PRELIMINARY; PRT; 350 AA.
 ID Q9V5E3;
 AC Q9V5E3;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 DE PROBABLE SERINE PROTEASE CG12133 (EC 3.4.21.-).
 GN CG12133.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celisner S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
 RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champagne M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Bottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., DeCher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fostler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali B., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasako P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Furl V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

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Fri Jun 29 08:04:33 2001

Best Local Similarity 62.5%; Pred. No. 50; Mismatches 5; Conservative 2; Indels 1; Gaps 0;

Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 "The genome sequence of *Drosophila melanogaster*.";
 Science 287:2185-2195(2000).
 -1- SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY.
 CC -1- SIMILARITY: TO CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1).
 CC EMBL: AE003831; INFM; AAF58868.1; -;
 DR HSP: Q61955; INFM; CG12133.
 DR Flybase; FBgn0033469; -;
 DR InterPro: IPR001254; -;
 DR InterPro: IPR001314; -;
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PROSITE: PS00134; TRYPsin_HIS; 1.
 DR PROSITE: PS00135; TRYPsin_SER; 1.
 DR SMART: SM00020; TRYP_SPC; 1.
 DR Hydrolyase; Serine protease.
 KW SEQUENCE 350 AA; 39380 MW; F922E2AFCD0E960 CRC64;
 SQ

Query Match 68.5%; Score 37; DB 5; Length 350;
 Best Local Similarity 75.0%; Pred. No. 36; Mismatches 1; Indels 0; Gaps 0;
 Matches 6; Conservative 1;

QY 2 QSNEDPWT 9
 DB 69 QSNQFPWT 76

RESULT 8
 ID Q18453 PRELIMINARY; PRT; 483 AA.

AC Q18453; 1996 (TREMELrel. 01, Created)
 DT 01-NOV-1998 (TREMELrel. 05, Last sequence update)
 DT 01-JAN-1998 (TREMELrel. 05, Last sequence update)
 DT 01-MAR-2001 (TREMELrel. 16, Last annotation update)
 DE C34E11.1 PROTEIN.
 GN C34E11.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Rhabditoides;
 CC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA McMurray A.;
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-94150718; PubMed-7906398;
 RA Wilson R., Anisovich R., Anderson K., Baynes C., Berks M., Coulson A., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Fulton L., Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister N., Latreille P., Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R., Smalton N., Smith A., Sonhammer E., Staden K., Sulston J., Thierri-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
 "2.2 Mb of contiguous nucleotide sequence from chromosome III of *C. elegans*.";
 RL Nature 368:32-38(1994).
 DR EMBL: Z67754; CAA91751.1; -;
 DR InterPro: IPR01026; -;
 DR Pfam: PF01417; ENTH; 1.
 DR SMART: SM00273; ENTH; 1.
 SQ SEQUENCE 483 AA; 52797 MW; 7F483D478A16203B CRC64;

Query Match 68.5%; Score 37; DB 5; Length 483;

RESULT 9
 Q83900 PRELIMINARY; PRT; 515 AA.

AC Q83900; 1996 (TREMELrel. 01, Created)
 DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
 DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
 DT 01-MAR-2001 (TREMELrel. 16, Last annotation update)
 DE PIIIA PROTEIN.
 OS Ovine adenovirus.
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Adenovirus.
 OX NCBI_TaxID=37367;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-OAV287;
 RX MEDLINE-95297141; PubMed-7778275;
 RA Vratil S., Boyle D., Kocherhans R., Both G.W.;
 RT "Sequence of ovine adenovirus homologs for 100K hexon assembly, 33K, pVIII, and fiber genes: early region E3 is not in the expected location.";
 RT Virology 209:400-408(1995).
 RL EMBL: U40839; AAA84974.1; -;
 DR InterPro: IPR003479; -;
 DR Pfam: PF02455; Hex_IIIa; 1.
 DR PIR: P02455; Hex_IIIa; 1.
 SQ SEQUENCE 515 AA; 58390 MW; BED9F7C3EC7E8F5B CRC64;

Query Match 68.5%; Score 37; DB 14; Length 515;
 Best Local Similarity 71.4%; Pred. No. 53; Mismatches 5; Conservative 2; Indels 0; Gaps 0;

QY 2 QSNEDPW 8
 DB 265 RNNEDPW 271

RESULT 10
 Q9NE92 PRELIMINARY; PRT; 2656 AA.

AC Q9NE92; 2000 (TREMELrel. 15, Created)
 DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMELrel. 16, Last annotation update)
 DE HYPOOETHETICAL PROTEIN L787.06.
 GN L787.06.
 OS Leishmania major.
 OC Eukaryota; Eudlenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-FRIEDLIN;
 RA Robben J., Aert R., Volckaert G., Ivens A.C., Quail M., Rajadream M.A., Barrell B.G.;
 RA Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-FRIEDLIN;
 RC MEDLINE-98148435; PubMed-9477341;
 RX Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M., Smith D.F.;
 RT "A physical map of the Leishmania major Friedlin genome.";
 RL Genome Res. 8:135-145(1998).
 DR EMBL: AL163492; CAB86690.1; -;
 DR InterPro: IPR001515; -;
 DR PRODOM: PD003823; -; 1.
 SQ SEQUENCE 2656 AA; 288578 MW; 3B281E0713819D0F CRC64;

Query Match 68.5%; Score 37; DB 5; Length 2656;
 Best Local Similarity 55.6%; Pred. No. 2.9e+02;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 QOSNEDPWT 9
 Db 1506 QEAESPWT 1514

RESULT 11
 ID Q9HB70 PRELIMINARY; PRT; 54 AA.
 AC Q9HB70;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DE PNAS-111.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yu W.-O., Chai Y.-B., Sun B.-Z., Zhu F., Liu X.-S., Li Z., Lu F.,
 RA Yan W., Yang H., Zhao Z.-L.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF275806; AAG23818.1; -;
 SQ SEQUENCE 54 AA; 6630 MW; 16150F0DFE98A32D CRC64;

Query Match 66.7%; Score 36; DB 4; Length 54;
 Best Local Similarity 44.4%; Pred. No. 7.9;
 Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 QOSNEDPWT 9
 Db 9 ERNNQNPWT 17

RESULT 12
 ID Q9WPN9 PRELIMINARY; PRT; 208 AA.
 AC Q9WPN9;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DE NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
 GN NEF.
 OS Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11723;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SVSN;
 RA Beer B.E., Bailes E., Goeken R., Dapolito G., Coulbaly C., Norley S.,
 RA Kurth R., Gautier J.P., Gautier-Hion A., Vallet D., Sharp P.M.,
 RA Hirsch V.M.;
 RT "Simian immunodeficiency virus from sun-tailed monkeys (Cercopithecus solatus) - evidence for host-dependent evolution within the C. l'hoesti superspecies";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES. IT SEEMS TO DOWN REGULATE THE CD4(T4) ANTIGEN. NEF PROTEIN ACCELERATES VIRULENT PROGRESSION OF AIDS BY ITS INTERACTION WITH CELLULAR PROTEINS INVOLVED IN SIGNAL TRANSDUCTION AND HOST CELL ACTIVATION. NEF HAS BEEN SHOWN TO BIND SPECIFICALLY TO A SUBSET OF THE SRC KINASE FAMILY (BY SIMILARITY).
 CC EMBL; AF131870; AAD39759.1; -;
 DR InterPro: IPR001556; -;
 DR Pfam: PF00469; F-protein; 1.
 KW AIDS; GTP-binding; Myristate.

SQ SEQUENCE 208 AA; 24132 MW; B7C385035D8E1BAF CRC64;

Query Match 66.7%; Score 36; DB 14; Length 208;
 Best Local Similarity 75.0%; Pred. No. 32;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 QOSNEDPWT 3
 Db 165 QGVNEDPW 172

RESULT 13
 ID Q9NX20 PRELIMINARY; PRT; 251 AA.
 AC Q9NX20;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DE 28.4 KDA PROTEIN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,
 RA Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T.,
 RA Nakamura Y., Isegai T., Sugano S.;
 RL "NEDO human cDNA sequencing project";
 RT Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PHOCHROMOCYTOMA;
 RA Peng Y., Li Y., Tu Y., Xu S., Han Z., Fu G., Chen Z.;
 RT "A novel gene expressed in human pheochromocytoma";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK000491; BAA91202.1; -;
 DR EMBL; AF183428; AAG09697.1; -;
 DR InterPro: IPR000114; -;
 DR Pfam: PF00252; Ribosomal_L16; 1.
 DR PRINTS: PR00060; RIBOSOMALL16.
 SQ SEQUENCE 251 AA; 28449 MW; 8A42A67DA80A6FEF CRC64;

Query Match 66.7%; Score 36; DB 4; Length 251;
 Best Local Similarity 44.4%; Pred. No. 39;
 Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 QOSNEDPWT 9
 Db 206 ERNNQNPWT 214

RESULT 14
 ID Q9FM84 PRELIMINARY; PRT; 252 AA.
 AC Q9FM84;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DE GENOMIC DNA, CHROMOSOME 5, p1 CLONE:MCD7.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RX MEDLINE=98290546; PubMed=9628582;
 RA Sato S., Kaneko T., Kotani H., Nakamura Y., Asamizu E., Miyajima N.,
 RA Tabata S.;

us-09-724-406-16.rspt

Fri Jun 29 08:04:33 2001

"Structural analysis of Arabidopsis thaliana chromosome 5. IV.
 RT Sequence features of the regions of 1,456,315 bp covered by nineteen
 RT physically assigned pl and TAC clones.";
 RL DNA Res. 5:41-54(1998).
 DR EMBL; AB009049; BAB11275.1; -. SDBFCELF2213132 CRC64;
 SQ SEQUENCE 252 AA; 28680 MW; 5DBFCELF2213132 CRC64;

Query Match 66.7%; Score 36; DB 10; Length 252;
 Best Local Similarity 62.5%; Pred. No. 39;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QSNEDPWT 9
 DB 125 RSKDDPWT 132

RESULT 15

Q9URW7 PRELIMINARY; PRT; 549 AA.
 AC Q9URW7;
 DT 01-MAY-2000 (TREMELrel. 13, Created)
 DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
 DT 01-MAR-2001 (TREMELrel. 16, Last annotation update)
 DE PUTATIVE VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN.
 GN SPAP696.OIC.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomyces.
 OC NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972H-;
 RA McDougall R.C., Rajandream M.A., Barrell B.G., Brown S., Harris D.;
 RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AL133359; CAB62421.1; -.
 DR InterPro; IPR001683; -.
 DR Pfam; PF00787; PX; 1.
 DR SMART; SM00312; PX; 1.
 SQ SEQUENCE 549 AA; 60920 MW; F892A29B80380CD5 CRC64;

Query Match 66.7%; Score 36; DB 3; Length 549;
 Best Local Similarity 55.6%; Pred. No. 88;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QSNEDPWT 9
 DB 482 QKTNDQAWT 490

Search completed: June 28, 2001, 16:08:23
 Job time: 951 sec

GenCore version 4.5
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OM protein - protein search, using sw model
Run on: June 28, 2001, 16:14:36 ; Search time 362.28 Seconds
(without alignments)
20,918 Million cell updates/sec
Title: US-09-724-406-18
Perfect score: 674
Sequence: 1 EVKLVEGGGLVPGGSLRL.....NPHYAMDWGQGTSTVSS 125
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 412676 seqs, 60623988 residues
Total number of hits satisfying chosen parameters: 412676
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_0601.*
1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
1	585.5	86.9	124	18 AAW01594	Lead binding Mab 2
2	555.5	82.4	124	17 AAR90831	2B5 heavy chain va
3	553	82.0	140	13 AAR20790	Unprocessed variab
4	553	82.0	141	13 AAR30431	A5B7 antibody heav
5	553	82.0	250	17 AAW06177	Murine A5B7 Fd fr
6	553	82.0	473	18 AAW41415	Human B7.1-murine
7	553	82.0	643	20 AAW82739	Clone PNG4/A5B7VH-
8	553	82.0	647	20 AAW82747	Plasmid pUC19/muA5
9	546.5	81.1	122	16 AAR74942	Immunoglobulin hea
10	545.5	80.9	138	16 AAR74963	Anti-idiotypic anti
11	542.5	80.5	359	20 AAY29913	Human MCP-3 and mu

12	542.5	80.5	361	20 AAY29911	Human IP-10 and mu
13	542.5	80.5	374	20 AAY29916	Artificial synthe
14	521.5	77.4	141	17 AAR92757	Murine anti-human
15	520.5	77.2	392	16 AAR82835	scFv-PP. Syntheti
16	518.5	76.9	122	16 AAR74941	Immunoglobulin hea
17	518.5	76.9	146	16 AAR74962	Anti-idiotypic anti
18	516	76.6	119	20 AAY33425	Mouse antibody MAK
19	515.5	76.5	142	16 AAR92828	CI79Fv-PP variable
20	515	76.4	146	13 AAR22373	CDR-grafted, human
21	515	76.4	145	13 AAR22373	A5B7 gH-2 antibody
22	515	76.4	250	17 AAW06179	Humanised A5B57 Fd
23	513	76.1	119	11 AAR07316	VH domain of antib
24	513	76.1	119	17 AAW14484	Monoclonal antibod
25	513	76.1	119	17 AAR99873	Monoclonal antibod
26	513	76.1	119	21 AAY51368	Mouse monoclonal a
27	512.5	76.0	115	16 AAR82825	Variable heavy reg
28	505	74.9	151	4 AAR30252	Sequence of the le
29	505	74.9	249	13 AAR21262	pScFvN011 encoding
30	499	74.0	146	13 AAR20793	CDR-grafted, human
31	499	74.0	146	13 AAR26150	A5B7 gH-2 antibody
32	493.5	73.2	120	13 AAR27498	WNI 58-9 antibody
33	491.5	72.9	122	14 AAR38610	MCPC heavy chain.
34	491.5	72.9	122	19 AAW58487	Murine MCPC antibo
35	491.5	72.9	123	9 AAR80461	Sequence of the va
36	491.5	72.9	222	15 AAR53804	FAB heavy chain fo
37	491.5	72.9	277	14 AAR39336	scFv fragment enco
38	487.5	72.3	121	16 AAR68740	MAB MCP603 heavy
39	485.5	72.0	482	20 AAY06915	Amino acid sequenc
40	484.5	71.9	120	13 AAR27497	WNI 222-5 antibody
41	475.5	70.5	116	14 AAR38609	MCPC heavy chain.
42	475.5	70.5	141	17 AAR92764	Human/murine chima
43	473.5	70.3	141	17 AAR92766	Human/murine chima
44	471.5	70.0	141	17 AAR92765	Human/murine chima
45	467.5	69.4	141	17 AAR32763	Human/murine chima

ALIGNMENTS

RESULT	1
AAW01594	
ID	AAW01594 standard; Protein; 124 AA.
XX	
AC	AAW01594;
XX	
DT	22-AUG-1997 (first entry)
XX	
DE	Lead binding MAB 2E7 heavy chain variable region.
XX	
KW	Monoclonal antibody; Fd fragment; lead cation; perfume; cosmetic;
KW	pharmaceutical; health care; skin treatment; pesticide; herbicide;
KW	heavy metal.
XX	
OS	Mus musculus.
XX	
PN	WO9639518-A1.
XX	
PD	12-DEC-1996.
XX	
PF	05-JUN-1996; 96WO-US09258.
XX	
PR	10-OCT-1995; 95US-0541373.
XX	
PA	05-JUN-1995; 95US-0462798.
XX	
PI	(BION-) BIONEERASKA INC.
XX	
PI	Lopez O, Murray PJ, Wylie DE;
DR	WPI: 1997-043140/34.
DR	N-PSDB; AAT58268.
XX	
PT	DNA encoding heavy metal binding polypeptide sequences - used for
PT	detecting, removing, adding or neutralising heavy metals, such as

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Claim 8; Page 54-55; 106pp; English.

PS
XX
CC AAR90829-39 are monoclonal antibodies or a binding fragments produced by
CC using insect guts, partic. insect brush border membranes (BBMs), esp.
CC corn rootworm, as antigen; immunising a donor animal with the antigen;
CC isolating immunocompetent B cells from the immunised animal; fusing B
CC cells with a tumour cell line; isolating the fused cells, culturing them
CC and cloning positive hybrid cells; and screening the hybrid cells for
CC prodn. of the required MAbs. The MAbs bind to the gut of a target insect
CC but do not bind to mammalian BBMs. The DNA sequence can be operably
CC linked to a toxin moiety, esp. selected from e.g. Bacillus toxins,
CC pseudomonas exotoxin and phytoalexin, etc... The Abs are useful for
CC control of insect pests, e.g. Coleoptera, Diptera, Hymenoptera and
CC Lepidoptera. The pesticidal compsn. is pref. applied to a plant, e.g.
CC maize.

XX Sequence 124 AA;

Query Match 82.4%; Score 555.5; DB 17; Length 124;
Best Local Similarity 84.4%; Pred. No. 9.9e-42;
Matches 108; Conservative 5; Indels 7; Gaps 2;

QY 1 EVKLVEGGGLVOPGGSLRLSCATSGFTSDYIMNVRQPPGKALEWLGFRNKANGYTT 60
Db 1 qvqlqesggglvqpggsrlriscatsgfttdymwvrqppgkalewlgfirhkangytt 60
QY 61 EFSASVMGRFTISRDDSSQSLYLQMTLRAEDSATYICARDPPYGNPHY---AMDYWGQ 117
Db 61 eysasvkggrftisrdsqsllylqmtlraedsatyycardicg----ydvgalidywgq 116
QY 118 GTSVTVSS 125
Db 117 gtsvtvss 124

RESULT 3

AAR20790
ID AAR20790 standard; Protein: 140 AA.

XX
AC AAR20790;
DT 19-MAY-1992 (first entry)

XX Unprocessed variable region of heavy chain of A5B7 antibody.

XX murine monoclonal antibody; Mab; VH domain; humanised antibody; CEA;
XX complementarity determining region.

XX Mus musculus.

XX Key Location/Qualifiers

XX Cleavage-site 19..20 /note= "putative signal peptide cleavage site"

XX WO9201059-A.

XX 23-JAN-1992.

XX 05-JUL-1991; 91WO-GB01108.

XX 05-JUL-1991; 91WO-GB01108.

XX 05-JUL-1990; 90GB-0014932.

XX 21-DEC-1990; 90WO-GB02017.

XX (CELL-) CELLTech LTD.

XX Adair JR, Bodmer MW, Mountain A, Owens RJ;

XX WPI; 1992-056874/07.

XX N-PSDB; AAQ20984.

XX New CDR-grafted anti carcinoembryonic antigen antibodies - useful

PT

PT lead cations

XX Claim 12; Page 91; 125pp; English.

XX The present sequence represents the heavy chain variable region for
CC monoclonal antibody (Mab) 2E7, which immunoreacts with a lead cation.
CC The sequence was derived from RNA isolated from mouse hybridoma cells.
CC The protein can be used for binding heavy metals, such as lead cations.
CC It can be used for detecting, removing, adding or neutralising the
CC heavy metals in biological and inanimate systems. It can be used in
CC e.g. aqueous liquid systems, in biological or environmental systems or
CC in such compositions as perfumes, cosmetics, pharmaceuticals, health
CC care products, skin treatment products, pesticides, herbicides,
CC solvents used in the production of semi-conductor and integrated
CC circuit components and production materials for electronic components.
CC The products can provide for applications involving minute amounts of
CC specific heavy metals.

XX Sequence 124 AA;

Query Match 86.9%; Score 585.5; DB 18; Length 124;
Best Local Similarity 90.4%; Pred. No. 2.3e-44;
Matches 113; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 1 EVKLVEGGGLVOPGGSLRLSCATSGFTSDYIMNVRQPPGKALEWLGFRNKANGYTT 60
Db 1 evklvesggglvqpggsrlriscatsgfttdymwvrqppgkalewlgfirnkangytt 60
QY 61 EFSASVMGRFTISRDDSSQSLYLQMTLRAEDSATYICARDPPYGNPHYAMDYWGQTS 120
Db 61 eysasvkggrftisrdsqsllylqmtlraedsatyycard-lydydyamdywgqgts 119
QY 121 VTVSS 125
Db 120 vtvss 124

RESULT 2

AAR90831
ID AAR90831 standard; Protein: 124 AA.

XX
AC AAR90831;

XX 25-JUN-1996 (first entry)

XX 2B5 heavy chain variable region from pCIB4615.

XX delta endotoxin; Bacillus thuringiensis; western corn rootworm;
XX WCRW; maize; pesticide; brush border membrane vesicle; monoclonal;
XX antibody.

XX Insecta sp.

XX WO9600783-A1.

XX 11-JAN-1996.

XX 20-JUN-1995; 95WO-IB00497.

XX 28-JUN-1994; 94US-0267641.

XX (CIBA) CIBA GEIGY AG.

XX Carozzi NB, Koziel MG;

XX WPI; 1996-077494/08.

XX N-PSDB; AAT15727.

XX New monoclonal antibodies which bind insect gut proteins - used

PT partic. with toxin moieties for the control of insect pests, partic.

PT in plants

XX

PT in therapy and diagnosis of carcinoma

XX Example 1; Fig 1; 70pp; English.

CC The A5B7 MAB is a mouse MAB of the type IgG1-kappa raised against
CC CEA which had been denatured by heating to 85 degrees C for 35
CC minutes. The MAB has been extensively studied by Harwood et al.
CC (Br. J. Cancer, 54, 75-82, 1986). A cDNA library was prepared from
CC polyA RNA isolated from the A5B7 hybridoma cell line. A probe
CC complementary to mouse heavy chain constant region was used to
CC identify clone pBGI containing the complete leader, variable and
CC constant regions of the heavy chain. The amino acid sequence
CC predicted from the sequence encoding the unprocessed variable
CC region is given here.

XX Sequence 140 AA;

Query Match 82.0%; Score 553; DB 13; Length 140;
Best Local Similarity 86.4%; Pred. No. 1.9e-41;
Matches 108; Conservative 5; Mismatches 8; Indels 4; Gaps 2;

QY 1 EVKLVEGGGLVQPGGSLRLSCATSGFTSDYNNWVRQPPGKALEWLGFIKANGYTT 60

DB 20 EVKLVEGGGLVQPGGSLRLSCATSGFTSDYNNWVRQPPGKALEWLGFIKANGYTT 60
|||||

QY 61 EFSASVMGRFTISRDDSSQSLYLQMTLRAEDSATYCCARDPPYGNPHYVAMDYWGQGT 120

DB 80 EYSASVKGFRITSRDKSGSLYLQMTLRAEDSATYCCARDPPYGNPHYVAMDYWGQGT 120
|||||

QY 121 VTVSS 125

DB 136 ltvss 140

RESULT 4

AAAR30431
ID AAR30431 standard; Protein; 141 AA.

AC AAR30431;

DT 03-FEB-1993 (first entry)

DE A5B7 antibody heavy chain sequence.

XX humanised antibody; chimaeric; carcino-embryonic antigen; therapy;
KW diagnosis; carcinomas; CDR; IgG; human; murine; ss.
XX Chimaeric.

OS WO9201059-A.

PN 23-JAN-1992.

XX 05-JUL-1991; 91WO-GB01108.

XX 05-JUL-1991; 91WO-GB01108.

PR 05-JUL-1990; 90GB-0014932.

PR 21-DEC-1990; 90WO-GB02017.

XX (CELL-) CELTECH LTD.

PA Adair JR, Bodmer MW, Mountain A, Owens RJ;

PI WPI: 1992-284316/34.

DR N-PSDB; AAQ27351.

XX Humanised antibody molecules - comprising murine and human regions,
PT specific for carcino-embryonic antigen, useful for diagnosis and
PT therapy

XX Example 1; Figure 1; 71pp; English.

CC This sequence represents the A5B7 monoclonal antibody heavy chain.
CC It was decoded from the cDNA (AAQ27351). Sequence analysis confirmed
CC A5B7 to be an IgG1 K antibody.

XX Sequence 141 AA;

Query Match 82.0%; Score 553; DB 13; Length 141;
Best Local Similarity 86.4%; Pred. No. 1.9e-41;
Matches 108; Conservative 5; Mismatches 8; Indels 4; Gaps 2;

QY 1 EVKLVEGGGLVQPGGSLRLSCATSGFTSDYNNWVRQPPGKALEWLGFIKANGYTT 60

DB 20 EVKLVEGGGLVQPGGSLRLSCATSGFTSDYNNWVRQPPGKALEWLGFIKANGYTT 60
|||||

QY 61 EFSASVMGRFTISRDDSSQSLYLQMTLRAEDSATYCCARDPPYGNPHYVAMDYWGQGT 120

DB 80 EYSASVKGFRITSRDKSGSLYLQMTLRAEDSATYCCARDPPYGNPHYVAMDYWGQGT 120
|||||

QY 121 VTVSS 125

DB 136 ltvss 140

RESULT 5

AAW06177

ID AAW06177 standard; Protein; 250 AA.

AC AAW06177;

DT 17-FEB-1997 (first entry)

DE Murine A5B7 Fd fragment.

XX ribonuclease; human; bovine; pancreatic; anti-tumour therapy; ADEPT;
KW mustard-ribonuclease; antibody directed enzyme prodrug therapy;
KW anti-neoplastic; prodrug; reverse polarity; ion pair interaction;
KW reduced immunogenicity; non-selective triggering; primer;
KW polymerase chain reaction; PCR; HP-RNase; Fd; F(ab')₂.

OS Synthetic.

XX WO9620011-A1.

XX 04-JUL-1996.

XX 21-DEC-1995; 95WO-GB02991.

XX 16-AUG-1995; 95GB-0016810.

XX 23-DEC-1994; 94GB-0026192.

XX (ZENE) ZENECA LTD.

XX Blakey DC, Boyle FT, Davies DH, Eggelte HJ, Heaton DH;

XX Hennen JF, Hennequin LFA, Marsham PR, Rabin BR, Slater AM;

XX Tarragona-Fiol A, Taylorson CJ;

XX WPI: 1996-321650/32.

XX N-PSDB; AAT42507.

XX Two component system for anti-tumour therapy - comprising targeting
PT moiety linked to mutated enzyme which can transform an
PT anti-neoplastic prodrug

XX Example 6; Page 118-119; 182pp; English.

XX A two-component system for anti-tumour therapy comprises a targeting
CC moiety linked to a mutated enzyme which can transform an anti-neoplastic
CC prodrug. The system is based on antibody directed enzyme prodrug therapy
CC (ADEPT) using a non-naturally occurring mutant form of a host enzyme,
CC pref. human pancreatic ribonuclease (HP-RNase), (see AAT42478-83). The
CC targeting moiety can be an antibody, in partic. murine monoclonal
CC antibody A5B7 (which binds to human carcinoembryonic antigen). A5B7 is

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CC suitable for targeting colorectal carcinoma. Fragments, esp. F(ab')₂,
 CC of the antibody can be conjugated to HP-RNase. A5B7 Fd and L chain
 CC fragments were isolated by PCR using cDNA isolated from A5B7 hybridoma
 CC cells. The present sequence is that of the murine A5B7 Fd fragment.

XX SQ Sequence 250 AA;

Query Match 82.0%; Score 553; DB 17; Length 250;
 Best Local Similarity 86.4%; Pred. No. 3.4e-41;
 Matches 108; Conservative 5; Mismatches 8; Indels 4; Gaps 2;

QY 1 EVKLVSGLVQPGSLRLSCATSGFTESDYNNWVRQPPGKALEWLGFIIRNKANGYTT 60
 Db 20 EVKLVSGLVQPGSLRLSCATSGFTESDYNNWVRQPPGKALEWLGFIIRNKANGYTT 79
 QY 61 EFSASVMGRTISRDSSQSLYLQMTLRAEDSATYTCARDPPYGNPHYAMDYWGQGT 120
 Db 80 EFSASVMGRTISRDSSQSLYLQMTLRAEDSATYTCARDPPYGNPHYAMDYWGQGT 135
 QY 121 VIVSS 125
 Db 136 IIVSS 140

RESULT 6

AAW41415
 ID AAW41415 standard; Protein; 473 AA.

XX AC AAW41415;

XX DT 02-JUN-1998 (first entry)

XX DE Human B7.1-murine A5B7 F(ab')₂ fusion protein.

XX KW Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy;
 cancer diagnosis; complementarity determining region.

XX OS Chimeric - Homo sapiens.

XX OS Chimeric - Mus sp.

XX PN WO9742329-A1.

XX PD 13-NOV-1997.

XX PF 29-APR-1997; 97WO-GB01165.

XX PR 14-FEB-1997; 97GB-0003103.

XX PR 04-MAY-1996; 96GB-0009405.

XX PA (ZENE) ZENECA LTD.

XX PI Copley CG, Edge MD, Emery SC;

XX DR WPI: 1997-558987/51.

XX DR N-PSDB; AAV17340.

XX PT Anti-carcinoembryonic antigen antibody 806.077 Ab - used for

XX PT diagnosis and therapy of cancer

XX PS Reference Example 3; Page 190-193; 208pp; English.

XX CC This sequence is the human B7.1-murine A5B7 F(ab')₂ fusion protein
 CC (AB7), and is an example of the antibody of the invention. The antibody
 CC is an anti-CEA (carcinoembryonic antigen) antibody (preferably
 CC 806.077 Ab). Host cells or transgenic organisms transformed with DNA
 CC encoding the antibody, are used to make the antibody or conjugate. The
 CC conjugate is used in a medicament suitable for intravenous
 CC administration. The conjugate can be used for cancer therapy, selectively
 CC killing tumour cells. The antibody can be used for in vivo or in vitro
 CC diagnosis of cancer.

XX SQ Sequence 473 AA;

Query Match 82.0%; Score 553; DB 18; Length 473;
 Best Local Similarity 86.4%; Pred. No. 6.7e-41;
 Matches 108; Conservative 5; Mismatches 8; Indels 4; Gaps 2;

QY 1 EVKLVSGLVQPGSLRLSCATSGFTESDYNNWVRQPPGKALEWLGFIIRNKANGYTT 60
 Db 243 EVKLVSGLVQPGSLRLSCATSGFTESDYNNWVRQPPGKALEWLGFIIRNKANGYTT 302
 QY 61 EFSASVMGRTISRDSSQSLYLQMTLRAEDSATYTCARDPPYGNPHYAMDYWGQGT 120
 Db 303 EFSASVMGRTISRDSSQSLYLQMTLRAEDSATYTCARDPPYGNPHYAMDYWGQGT 358
 QY 121 VIVSS 125
 Db 359 IIVSS 363

RESULT 7

AAW82739
 ID AAW82739 standard; Protein; 643 AA.

XX AC AAW82739;

XX DT 10-MAY-1999 (first entry)

XX DE Clone pNG4/A5B7VH-IgG2CH1/CPG2 R6 protein.

XX KW Conjugate; cell targeting; cytotoxic drug; prodrug therapy system;
 prodrug-converting enzyme; cell surface antigen; treatment; cancer;
 inflammation; rheumatoid arthritis; antibody.

XX OS Synthetic.

XX PN WO9851787-A2.

XX PD 19-NOV-1998.

XX PF 05-MAY-1998; 98WO-GB01294.

XX PR 10-MAY-1997; 97GB-0009421.

XX PA (ZENE) ZENECA LTD.

XX PI Blakey DC, Emery SC;

XX DR WPI: 1999-059700/05.

XX DR N-PSDB; AAV72046.

XX PT New gene construct expressing conjugate of targeting agent and
 prodrug-converting enzyme - useful for, e.g. targeted production of
 cytotoxic drug in vivo, especially for treatment of cancer

XX PS Example 1e; Page 68-70; 100pp; English.

XX CC This sequence is used in a method for obtaining a novel gene construct
 CC (A) which expresses, in cells of a mammal, a conjugate (B) of a
 CC cell-targeting group (I) and a heterologous prodrug-converting enzyme
 CC (II), and (B) is directed to leave the cell for selective localisation at
 CC a cell surface antigen (Ag) recognised by (I). Delivery of (A) to a
 CC target site, then administration of (II) is used for targeted release of
 CC cytotoxic drug, specifically for treating cancer but also inflammation
 CC such as rheumatoid arthritis. In situ generation of the targeting
 CC antibody increases selectivity, reducing side effects at normal tissue.
 CC The method is applicable to any antibody-directed enzyme prodrug therapy
 CC system.

XX SQ Sequence 643 AA;

Query Match 82.0%; Score 553; DB 20; Length 643;
 Best Local Similarity 86.4%; Pred. No. 9.3e-41;

Matches 108; Conservative 5; Mismatches 8; Indels 4; Gaps 2;

QY 1 EVKLVEGGGLVQPGSLRLSCATSGFTFSDYYMNMVROPVPGKALEWLGFIKNGKANGYTT 60
 |||||
 Db 20 EVKLVEGGGLVQPGSLRLSCATSGFTFSDYYMNMVROPVPGKALEWLGFIKNGKANGYTT 79
 |||||
 QY 61 EFSASVMGRFTISRDSSQSLYLQMTLRAEDSATYTCARDPPYGNPHYYAMDYWGQGT 120
 |||||
 Db 80 EYSASVGRFTISRDKSQSLYLQMTLRAEDSATYTCARDPPYGNPHYYAMDYWGQGT 135
 |||||
 QY 121 VTVSS 125
 |||||
 Db 136 ltvss 140

RESULT 8

AAW82747
 ID AAW82747 standard; Protein; 647 AA.

XX AC AAW82747;

DT 10-MAY-1999 (first entry)

DE Plasmid pUC19/muA5B7-RC/CPG2(R6) protein.

XX Conjugate; cell targeting; cytotoxic drug; plasmid; fusion protein;
 KW prodrug-converting enzyme; cell surface antigen; treatment; cancer;
 KW inflammation; rheumatoid arthritis; antibody; prodrug therapy system.

XX Synthetic.

OS Mus sp.

XX FH Key Location/Qualifiers

FT Peptide 1..19

FT Protein /label= signal_peptide

FT /note= "murine Fd linker"

XX WO9851787-A2.

XX 19-NOV-1998.

XX 05-MAY-1998; 98WO-GB01294.

XX 10-MAY-1997; 97GB-0009421.

XX (ZENE) ZENECA LTD.

XX Blakey DC, Emery SC;

XX WPI: 1999-050700/05.

XX N-PSDB; AAV72082.

PT New gene construct expressing conjugate of targeting agent and
 PT prodrug-converting enzyme - useful for, e.g. targeted production of
 PT cytotoxic drug in vivo, especially for treatment of cancer

PS Example 22; Page 97-98; 100pp; English.

XX This sequence is a used in a method for obtaining a novel gene construct
 CC (A) which expresses, in cells of a mammal, a conjugate (B) of a
 CC cell-targeting group (I) and a heterologous prodrug-converting enzyme
 CC (II), and (B) is directed to leave the cell for selective localisation
 CC at a cell surface antigen (Ag) recognised by (I). Delivery of (A) to a
 CC target site, then administration of (III) is used for targeted release of
 CC cytotoxic drug, specifically for treating cancer but also inflammation
 CC such as rheumatoid arthritis. In situ generation of the targeting
 CC antibody increases selectivity, reducing side effects at normal tissue.
 CC The method is applicable to any antibody-directed enzyme prodrug therapy
 CC system.

XX Sequence 647 AA;

Query Match 82.08; Score 553; DB 20; Length 647;
 Best Local Similarity 86.4%; Pred. No. 9.3e-41;
 Matches 108; Conservative 5; Mismatches 8; Indels 4; Gaps 2;

QY 1 EVKLVEGGGLVQPGSLRLSCATSGFTFSDYYMNMVROPVPGKALEWLGFIKNGKANGYTT 60
 |||||
 Db 20 EVKLVEGGGLVQPGSLRLSCATSGFTFSDYYMNMVROPVPGKALEWLGFIKNGKANGYTT 79
 |||||
 QY 61 EFSASVMGRFTISRDSSQSLYLQMTLRAEDSATYTCARDPPYGNPHYYAMDYWGQGT 120
 |||||
 Db 80 EYSASVGRFTISRDKSQSLYLQMTLRAEDSATYTCARDPPYGNPHYYAMDYWGQGT 135
 |||||
 QY 121 VTVSS 125
 |||||
 Db 136 ltvss 140

RESULT 9

AAW74942
 ID AAW74942 standard; peptide; 122 AA.

XX AC AAW74942;

DT 19-JAN-1996 (first entry)

XX Immunoglobulin heavy chain of anti-idiotypic antibody against human
 DE anticancer antibody.

XX KW Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin;
 KW complementarity determining region.

XX OS Mus sp.

XX FH Key Location/Qualifiers

FT Region 31..35

FT /label= CDR1

FT Region 50..68

FT /label= CDR2

FT Region 101..111

FT /label= CDR3

XX JP07101999-A.

XX 18-APR-1995.

XX 06-OCT-1993; 93JP-0272950.

XX 06-OCT-1993; 93JP-0272950.

XX (HAGI/) HAGIWARA Y.

XX WPI: 1995-182987/24.

XX Novel anti-idiotypic antibody against an human anticancer monoclonal
 PT antibody - and DNA sequences encoding the antibody, useful in
 PT pharmacology, medicine and biochemical fields.

PS Claim 4; Page 2; 28pp; Japanese.

XX AAW74940-R74943 are possible heavy chains of a new anti-idiotypic
 CC antibody against a human anticancer monoclonal antibody. This antibody
 CC contains in its heavy chain 3 complementarity determining regions CDR1
 CC (AAW74929-R74931) CDR2 (AAW74932-R74935) and CDR3 (AAW74936-R74939),
 CC this is also true of the light chain which has its own CDR1
 CC (AAW74944-R74946 and AAW85774), CDR2 (AAW74947-R74949) and CDR3
 CC (AAW74950-R74954). The antibody and DNA encoding it are useful in
 CC pharmacological, medical and biochemical fields.

XX Sequence 122 AA;

Query Match 81.1%; Score 546.5; DB 16; Length 122;

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us-09-724-406-18.rag

Best Local Similarity 85.6%; Pred. No. 6e-41;
Matches 107; Conservative 5; Mismatches 10; Indels 3; Gaps 1;
QY 1 EVKLVEGGGLVOPGGSLRLSCATSGFTSDYIMNWVRPPGKALEWLGFIIRNKANGYTT 60
Db 1 EVKLVEGGGLVOPGGSLRLSCATSGFTSDYIMNWVRPPGKALEWLGFIIRNKANGYTT 60
QY 61 EFSASVMGRFTISRDDQSILYLQMNLTLEADSATYICARDPPYGNPHYAMDYWGQGT 120
Db 61 EFSASVMGRFTISRDDQSILYLQMNLTLEADSATYICARDPPYGNPHYAMDYWGQGT 120
QY 121 VTVSS 125
Db 128 VTVSS 132

RESULT 10
AAR74963
ID AAR74963 standard; Protein; 138 AA.
AC AAR74963;
DT 02-FEB-1996 (first entry)
XX Anti-idiotype antibody Idio27 clone 27GA5.
DE Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin;
KW complementarity determining region.
XX Mus sp.
FH Key Location/Qualifiers
FT Peptide 1..10
FT /label= signal_peptide
PN JP07101999-A.
XX 18-APR-1995.
XX 06-OCT-1993; 93JP-0272950.
XX 06-OCT-1993; 93JP-0272950.
XX (HAGI/) HAGIWARA Y.
XX WPI; 1995-182987/24.
DR N-PSDB; AAQ90428.
XX Novel anti-idiotype antibody against an human anticancer monoclonal
PT antibody - and DNA sequences encoding the antibody, useful in
PT pharmacology, medicine and biochemical fields.
XX Example 5; Page 16; 28pp; Japanese.

PS AAR74960-R74969 are clones of the anti-idiotype antibodies Idio3.
CC Idio17, Idio20, Idio27 and Idio33 against a human anticancer monoclonal
CC antibody. These antibodies and DNA encoding them are useful in
CC pharmacological, medical and biochemical fields of research.
XX Sequence 138 AA;
Query Match 80.9%; Score 545.5; DB 16; Length 138;
Best Local Similarity 85.6%; Pred. No. 8.3e-41;
Matches 107; Conservative 5; Mismatches 10; Indels 3; Gaps 1;
QY 1 EVKLVEGGGLVOPGGSLRLSCATSGFTSDYIMNWVRPPGKALEWLGFIIRNKANGYTT 60
Db 11 EVKLVEGGGLVOPGGSLRLSCATSGFTSDYIMNWVRPPGKALEWLGFIIRNKANGYTT 70
QY 61 EFSASVMGRFTISRDDQSILYLQMNLTLEADSATYICARDPPYGNPHYAMDYWGQGT 120
Db 71 EFSASVMGRFTISRDDQSILYLQMNLTLEADSATYICARDPPYGNPHYAMDYWGQGT 127

QY 121 VTVSS 125
Db 128 VTVSS 132
RESULT 11
AAY29913
ID AAY29913 standard; Protein; 359 AA.
AC AAY29913;
XX 17-NOV-1999 (first entry)
XX Human MCP-3 and murine scFv38 fusion protein.
DE Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;
KW immune response; HIV; infection.
XX Homo sapiens.
OS Mus sp.
OS Synthetic.
XX WO9946392-A1.
XX 16-SEP-1999.
XX 12-MAR-1999; 99WO-US05345.
XX 12-MAR-1998; 98US-0077745.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX Kwak LW, Biragyn A;
XX WPI; 1999-551418/46.
XX New fusion polypeptides comprising a chemokine and a tumour antigen or
PT HIV antigen, used for treating cancers or treating or preventing HIV
PT infection -
XX Disclosure; Page 118-119; 142pp; English.

PS The present invention describes fusion proteins comprising a chemokine
CC and a tumour antigen or HIV antigen. Specifically claimed fusion proteins
CC comprise: (1) human monocyte chemotactic protein-3 (MCP-3) and human
CC Muc-1; (2) human interferon-induced protein 10 (IP-10) and human Muc-1;
CC (3) human macrophage-derived chemokine (MDC) and human MCP-3 and
CC SDF-1 and human Muc-1; (5) human IP-10 and HIV gp120; (6) human MCP-3 and
CC HIV gp120; (7) human MDC and HIV gp120; and (8) human SDF-1 and HIV
CC gp120. The fusion proteins, and nucleotide sequences encoding them, can
CC be used for producing an immune response, e.g. an effector T cell immune
CC response. They can also be used for treating cancer or treating or
CC preventing HIV infection. The fusion proteins and/or nucleotide sequences
CC can be used in in vitro diagnostic assays, as well as in screening assays
CC for identifying unknown tumour antigen epitopes and fine mapping of
CC tumour antigen epitopes. The present sequence represents a fusion protein
CC from the present invention.
XX Sequence 359 AA;
Query Match 80.5%; Score 542.5; DB 20; Length 359;
Best Local Similarity 82.5%; Pred. No. 4.2e-40;
Matches 104; Conservative 7; Mismatches 14; Indels 1; Gaps 1;
QY 1 EVKLVEGGGLVOPGGSLRLSCATSGFTSDYIMNWVRPPGKALEWLGFIIRNKANGYTT 60
Db 90 EVKLVEGGGLVOPGGSLRLSCATSGFTSDYIMNWVRPPGKALEWLGFIIRNKANGYTT 149
QY 61 EFSASVMGRFTISRDDQSILYLQMNLTLEADSATYICARDPPYGNPHYAMDYWGQGT 119
Db 150 EFSASVMGRFTISRDDQSILYLQMNLTLEADSATYICARDPPYGNPHYAMDYWGQGT 209

QY 120 SVTVSS 125
Db 210 tltvss 215

RESULT 12

AAAY29911
ID AAY29911 standard; Protein; 361 AA.

XX AC AAY29911;

XX DT 17-NOV-1999 (first entry)

XX Human IP-10 and murine scFv38 fusion protein.

XX Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;
XX Immune response; HIV; infection.

XX Homo sapiens.

XX Mus sp.

XX OS Synthetic.

XX PN WO9946392-A1.

XX PD 16-SEP-1999.

XX PF 12-MAR-1999; 99WO-US05345.

XX PR 12-MAR-1998; 98US-0077745.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Kwak LW, Biragyn A;

XX DR WPI; 1999-551418/46.

XX New fusion polypeptides comprising a chemokine and a tumour antigen or
PT HIV antigen, used for treating cancers or treating or preventing HIV
PT infection

XX PS Disclosure; Page 115-116; 142pp; English.

XX The present invention describes fusion proteins comprising a chemokine
CC and a tumour antigen or HIV antigen. Specifically claimed fusion proteins
CC comprise: (1) human monocyte chemoattractant protein-3 (MCP-3) and human
CC Muc-1; (2) human interferon-induced protein 10 (IP-10) and human
CC Muc-1; (3) human macrophage-derived chemokine (MDC) and human Muc-1;
CC SDF-1 and human Muc-1; (5) human IP-10 and human Muc-1; (4) human
CC HIV gp120; (7) human MDC and HIV gp120; and (8) human MCP-3 and
CC gp120. The fusion proteins, and nucleotide sequences encoding them, can
CC be used for producing an immune response, e.g. an effector T cell immune
CC response. They can also be used for treating cancer or treating or
CC preventing HIV infection. The fusion proteins and/or nucleotide sequences
CC can be used in in vitro diagnostic assays, as well as in screening assays
CC for identifying unknown tumour antigen epitopes and fine mapping of
CC tumour antigen epitopes. The present sequence represents a fusion protein
CC from the present invention.

XX SQ Sequence 361 AA;

Query Match 80.5%; Score 542.5; DB 20; Length 361;
Best Local Similarity 82.5%; Pred. No. 4.2e-40;
Matches 104; Conservative 7; Mismatches 14; Indels 1; Gaps 1;

Qy 1 EVKLVEGGGLVQPGGSLRLSCATSGFTFSDYVMNVRPPGKALEWLGFIKNGKGYTT 60

Db 92 EVKLVEGGGLVQPGGSLRLSCATSGFTFSDYVMNVRPPGKALEWLGFIKNGKGYTT 151

Qy 61 EFSASVNGRTFISRDSSQSLYLQMTLRAEDSATYICARDPPYPGNPHYYA-MDYWGQCT 119

Db 152 EYSASVKGRTFISRDSSQSLYLQMTLRAEDSATYICARDPPYPGNPHYYA-MDYWGQCT 211

QY 120 SVTVSS 125
Db 212 tltvss 217

RESULT 13

AAAY29916
ID AAY29916 standard; Protein; 374 AA.

XX AC AAY29916;

XX DT 17-NOV-1999 (first entry)

XX Artificial synthetic construct protein SEQ ID NO:15.

XX Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;
XX Immune response; HIV; infection.

XX OS Synthetic.

XX PN WO9946392-A1.

XX PD 16-SEP-1999.

XX PF 12-MAR-1999; 99WO-US05345.

XX PR 12-MAR-1998; 98US-0077745.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Kwak LW, Biragyn A;

XX DR WPI; 1999-551418/46.

XX New fusion polypeptides comprising a chemokine and a tumour antigen or
PT HIV antigen, used for treating cancers or treating or preventing HIV
PT infection

XX PS Disclosure; Page 117-118; 142pp; English.

XX The present invention describes fusion proteins comprising a chemokine
CC and a tumour antigen or HIV antigen. Specifically claimed fusion
CC proteins comprise: (1) human monocyte chemoattractant protein-3 (MCP-3) and
CC human Muc-1; (2) human interferon-induced protein 10 (IP-10) and human
CC Muc-1; (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4)
CC human SDF-1 and human Muc-1; (5) human IP-10 and human Muc-1; (6) human
CC MCP-3 and HIV gp120; (7) human MDC and HIV gp120; and (8) human SDF-1 and
CC HIV gp120. The fusion proteins, and nucleotide sequences encoding them,
CC can be used for producing an immune response, e.g. an effector T cell
CC immune response. They can also be used for treating cancer or treating
CC preventing HIV infection. The fusion proteins and/or nucleotide
CC sequences can be used in in vitro diagnostic assays, as well as in
CC screening assays for identifying unknown tumour antigen epitopes and fine
CC mapping of tumour antigen epitopes. AAY29916 and AA221156 to AA221168 are
CC sequences given in the SEQ ID LISTING in the present invention but which
CC are not mentioned further within the specification.

XX SQ Sequence 374 AA;

Query Match 80.5%; Score 542.5; DB 20; Length 374;
Best Local Similarity 82.5%; Pred. No. 4.4e-40;
Matches 104; Conservative 7; Mismatches 14; Indels 1; Gaps 1;

Qy 1 EVKLVEGGGLVQPGGSLRLSCATSGFTFSDYVMNVRPPGKALEWLGFIKNGKGYTT 60

Db 215 EVKLVEGGGLVQPGGSLRLSCATSGFTFSDYVMNVRPPGKALEWLGFIKNGKGYTT 274

Qy 61 EFSASVNGRTFISRDSSQSLYLQMTLRAEDSATYICARDPPYPGNPHYYA-MDYWGQCT 119

Db 275 EYSASVKGRTFISRDSSQSLYLQMTLRAEDSATYICARDPPYPGNPHYYA-MDYWGQCT 334

QY 120 SVTVSS 125
Db 335 tltvss 340

RESULT 14
AAR92757
ID AAR92757 standard; Protein; 141 AA.
XX AC
XX AC AAR92757;
XX DT
XX DE
XX DE Murine anti-human IL-8 monoclonal Ab variable heavy chain.
XX KW pUC-WS4-VH; variable; heavy chain; WS4; hybridoma; monoclonal;
KW antibody; MAb; BALB/c mouse; spleen cell; human; interleukin-8;
KW IL-8; myeloma P3X63-Ag8.653 cell; CDR; framework; chimeric
KW complementarity determining region; chimeric; murine;
KW inflammation; disease; mediated; low antigenicity.
XX OS Mus musculus.

XX FH Key Location/Qualifiers
FT Peptide 1..19
FT Peptide /label= sig_peptide
FT Peptide 20..141
FT Peptide /label= mat_peptide
FT Region 50..54
FT /note= "complementarity determining region 1"
FT Region 69..87
FT /note= "complementarity determining region 2"
FT Region 120..130
FT /note= "complementarity determining region 3"
XX FH WO9602576-A1.
XX PD 01-FEB-1996.
XX PF 12-JUL-1995; 95WO-JP01396.
XX PR 14-DEC-1994; 94JP-0310785.
XX PR 13-JUL-1994; 94JP-0161481.
XX PR 24-NOV-1994; 94JP-0289951.
XX PA (CHUS) CHUGAI SEIYAKU KK.
XX PA Matsumoto Y, Matsushima K, Sato K, Tsuchiya M, Yamada Y;
PI Yamazaki T;
XX WPI; 1996-105864/11.
XX N-PSDB; AAT16904.
XX Reconstituted human antibody recognising human interleukin-8
PT containing mouse anti-IL8 antibody variable region sequences, has
PT low antigenicity in humans
XX Claim 4; Pages 72-73; 125pp; Japanese.

XX The present sequence, encoded by pUC-WS4-VH, is the variable heavy
XX chain from a WS4 hybridoma monoclonal antibody (MAb). The hybridoma
XX was constructed by fusing BALB/c mouse spleen cells, immunised with
XX human IL-8, with mouse myeloma P3X63-Ag8.653 cells. Complementarity
XX determining region (CDR) DNA from pUC-WS4-VH and its light chain
XX equivalent pUC-WS4-VL, was used together with human framework
XX region DNA to construct chimeric H and L region, V region DNA. The
XX DNA was then inserted into a HEF vector along with human C-kappa
XX and C-gamma-1, C region DNA to produce a vector capable of
XX expressing a human/murine chimeric MAb. The MAb can be used for
XX the treatment of inflammatory diseases mediated by IL-8, and as the
XX major part of the MAb comes from a human Ab, and only the CDR
XX regions are of murine origin, the MAb has the advantage of having
XX low antigenicity to the human body when used therapeutically.

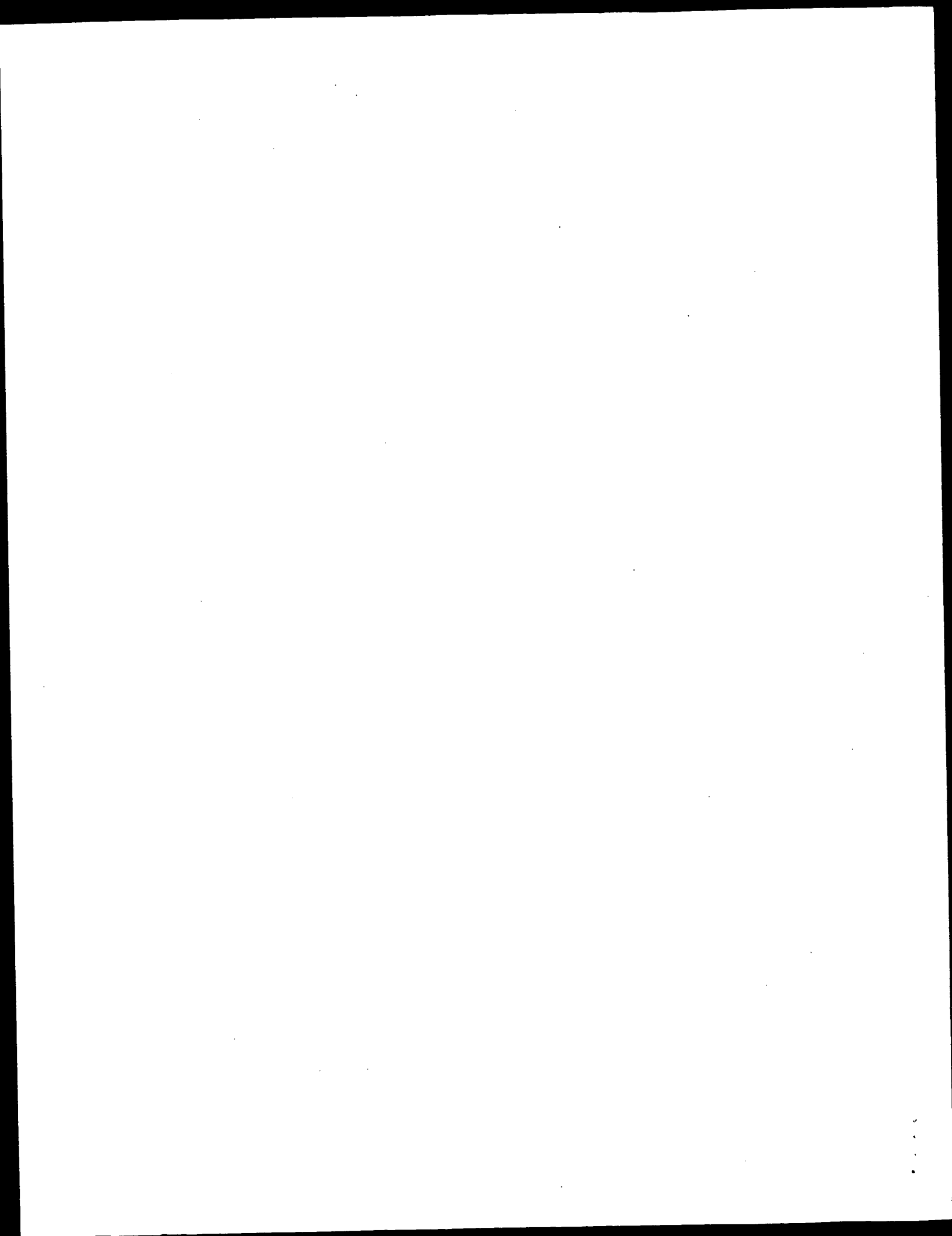
XX SQ Sequence 141 AA;
Query Match 77.4%; Score 521.5; DB 17; Length 141;
Best Local Similarity 80.2%; Pred. No. 1.1e-38;
Matches 101; Conservative 8; Mismatches 12; Indels 5; Gaps 2;
QY 1 EVKLIVSGGLVOPGSLRSLSCATSGFTSDYMMVWVROPKALEWLGFIKRNKANGYTT 60
Db 20 evklivesggliqpgdrlrlscvtsqftsfdyylswvrppgkalewglrnkangytr 79
QY 61 EFSASVMGRETISRDSQSILYLQMTLRAEDSATYVCARDPPYGNPHY-YAMDIWGGGT 119
Db 80 eysasvkgfrtisrdsqslilylqmntlrgedsatyyccare----nyrydvelaywgggt 135
QY 120 SVTVSS 125
Db 136 ltvtsa 141

RESULT 15
AAR82835
ID AAR82835 standard; Protein; 392 AA.
XX AC
XX AC AAR82835;
XX DT 09-MAY-1996 (first entry)
XX DE scFv-PP.
XX KW Antibody; human; influenza type A virus; H1N1; H2N2; H3N2; HA; diagnosis;
KW haemagglutinin; variable heavy chain; therapy.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Protein 23..144
FT Protein /note= "variable heavy chain"
FT Protein 164..263
FT Protein /note= "variable light chain"
FT Domain 273..330
FT Domain /note= "Fc binding domain-like structure"
FT Domain 331..388
FT /note= "Fc binding domain-like structure"
XX PN EP675199-A2.
XX PD 04-OCT-1995.
XX PF 14-MAR-1995; 95EP-0301664.
XX PR 30-MAR-1994; 94JP-0082693.
XX PA (TAKI) TAKARA SHUZO CO LTD.
XX PI Atsushi O, Hirofumi Y, Ikunoshin K, Takashi T, Yoshinobu O;
XX WPI; 1995-338286/44.
XX N-PSDB; AAT04180.
XX Gene encoding variable region of anti-human influenza A type virus
PT antibody - useful for prodn. of artificial antibodies
XX Example 4; Page 36-38; 42pp; English.
XX This sequence represents the scFv-PP fusion polypeptide. This sequence
XX is an anti-human influenza A type virus antibody. The antibody
XX recognises the stem region of the haemagglutinin (HA) molecule of the
XX H1N1 and H2N2 subtypes of human influenza A type virus, and shows
XX neutralisation activity against these two subtypes. The antibody shows
XX no recognition of the H3N2 subtype. Artificial antibodies (such as this)
XX and polypeptides are useful in the diagnosis and treatment of human

CC influenza. As the antibodies recognise the stem region of the HA
 CC molecule, the influenza virus will be recognised even if the HA molecule
 CC changes. This provides an advantage over current vaccines, as the virus
 CC periodically alters it's HA molecule.
 XX
 SQ Sequence 392 AA;

Query Match 77.2%; Score 520.5; DB 16; Length 392;
 Best Local Similarity 80.0%; Pred. No. 3.9e-38;
 Matches 100; Conservative 9; Mismatches 13; Indels 3; Gaps 1;
 Qy 1 EVKLVEGGGLVQGGSLRLSCATSGFTFSDYMNWVROPKGALEWLGFIKANGYTT 60
 Db :||| ||||| ||||| ||||| ||||| :||| ||||| ||||| ||||| |||||
 23 qvqlqesggglvqpggslrlscgtsqftltdymtwrqpkaalewigfirdrangytt 82
 Qy 61 EFSASVMGRETISRDSQSILYLQMTLRAEDSATYYICARDPPYGNPHYYAMDYWGQGT 120
 Db :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 83 eysasvkgftrsrdsqstivylqmntlrvedsatyyicarpky---fpyandywgqgts 139
 Qy 121 VTVSS 125
 Db :|||
 140 vlvss 144

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OM protein - protein search, using sw model

Run on: June 28, 2001, 16:01:14 ; Search time 138.34 Seconds
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Listing first 45 summaries

Database : Issued patents 22.2

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query %			DB	ID	Description
	Score	Match	Length			
1	585.5	86.9	124	4	US-08-767-128-38	Sequence 38, Appl
2	555.5	82.4	124	1	US-08-442-542-6	Sequence 6, Appl
3	555.5	82.4	124	3	US-08-765-469-6	Sequence 6, Appl
4	553	82.0	140	2	US-08-445-287-4	Sequence 4, Appl
5	521.5	77.4	141	2	US-08-765-783A-29	Sequence 29, Appl
6	521.5	77.4	141	3	US-08-921-100-29	Sequence 29, Appl
7	521.5	77.4	141	3	US-08-880-142-29	Sequence 29, Appl
8	521.5	77.4	141	3	US-08-902-201-29	Sequence 29, Appl
9	517.5	76.8	116	1	US-08-401-908-1	Sequence 1, Appl
10	515	76.4	146	2	US-08-449-287-12	Sequence 12, Appl
11	513	76.1	119	1	US-08-459-310-2	Sequence 2, Appl
12	513	76.1	119	2	US-08-308-494A-9	Sequence 9, Appl
13	513	76.1	119	4	US-03-280-028-2	Sequence 2, Appl
14	499	74.0	146	2	US-08-449-287-10	Sequence 10, Appl
15	498.5	74.0	120	2	US-08-647-144-4	Sequence 4, Appl
16	491.5	72.9	122	1	US-08-107-669D-6	Sequence 6, Appl
17	491.5	72.9	122	1	US-08-472-788A-6	Sequence 6, Appl
18	491.5	72.9	122	2	US-08-477-531B-6	Sequence 6, Appl
19	491.5	72.9	122	2	US-08-082-842A-6	Sequence 6, Appl
20	491.5	72.9	277	2	US-08-256-790-2	Sequence 2, Appl
21	487.5	72.3	121	1	US-08-077-252B-2	Sequence 2, Appl
22	487.5	72.3	121	4	US-09-002-753A-2	Sequence 2, Appl
23	487.5	72.3	121	5	PCT-US94-06687-2	Sequence 2, Appl
24	484.5	71.9	141	2	US-08-647-144-2	Sequence 2, Appl
25	475.5	70.5	141	3	US-08-765-783A-55	Sequence 55, Appl
26	475.5	70.5	141	3	US-08-921-100-55	Sequence 55, Appl
27	475.5	70.5	141	3	US-08-880-142-55	Sequence 55, Appl

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SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-767-128-38

Query Match      86.9%; Score 585.5; DB 4; Length 124;
Best Local Similarity 90.4%; Pred. No. 3e-51; Indels 1; Gaps 1;
Matches 113; Conservative 5; Mismatches 6;

QY 1 EVKLVEGGGLVQPGGSLRLSCATSGFTSDYMNVRQPPGKALEWLGFIIRNKANGYTT 60
Db 1 EVKLVEGGGLVQPGGSLRLSCATSGFTSDYMNVRQPPGKALEWLGFIIRNKANGYTT 60
QY 61 EFSASVMGRFTISRDSQSILYLQMTLRAEDSATYTCARDPPYGNPHYYAMDYWGQTS 120
Db 61 EFSASVMGRFTISRDSQSILYLQMTLRAEDSATYTCARD-YYDYDYAMDYWGQTS 119
QY 121 VTVSS 125
Db 120 VTVSS 124

RESULT 2
US-08-442-542-6
; Sequence 6, Application US/08442542
; Patent No. 5686600
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine B.
; APPLICANT: Kozziel, Michael G.
; TITLE OF INVENTION: Antibodies which Bind to Insect Gut
; TITLE OF INVENTION: Proteins and their Use
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/442.542
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/267,641
; FILING DATE: 28-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: CGC 1750
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8615
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-442-542-6

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Query Match      82.4%; Score 555.5; DB 1; Length 124;
Best Local Similarity 84.4%; Pred. No. 2.8e-48; Indels 7; Gaps 2;
Matches 108; Conservative 8; Mismatches 5;

QY 1 EVKLVEGGGLVQPGGSLRLSCATSGFTSDYMNVRQPPGKALEWLGFIIRNKANGYTT 60
Db 1 QVOLQESGGGLVQPGGSLRLSCATSGFTSDYMNVRQPPGKALEWLGFIIRNKANGYTT 60
QY 61 EFSASVMGRFTISRDSQSILYLQMTLRAEDSATYTCARDPPYGNPHYY---ANDYWGQ 117
Db 61 EFSASVMGRFTISRDSQSILYLQMTLRAEDSATYTCARDICYG----YDVGALDIWGQ 116
QY 118 GTSVTSS 125
Db 117 GTSVTSS 124

RESULT 3
US-08-765-469-6
; Sequence 6, Application US/08765469
; Patent No. 6069301
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine B.
; APPLICANT: Kozziel, Michael G.
; TITLE OF INVENTION: Antibodies which Bind to Insect Gut
; TITLE OF INVENTION: Proteins and their Use
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/765,469
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/267,641
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: CGC 1750
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8615
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-765-469-6

Query Match      82.4%; Score 555.5; DB 3; Length 124;
Best Local Similarity 84.4%; Pred. No. 2.8e-48; Indels 7; Gaps 2;
Matches 108; Conservative 8; Mismatches 5;

QY 1 EVKLVEGGGLVQPGGSLRLSCATSGFTSDYMNVRQPPGKALEWLGFIIRNKANGYTT 60
Db 1 QVOLQESGGGLVQPGGSLRLSCATSGFTSDYMNVRQPPGKALEWLGFIIRNKANGYTT 60
QY 61 EFSASVMGRFTISRDSQSILYLQMTLRAEDSATYTCARDPPYGNPHYY---ANDYWGQ 117
Db 61 EFSASVMGRFTISRDSQSILYLQMTLRAEDSATYTCARDPPYGNPHYY---ANDYWGQ 117

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Db 61 EYSASVKGRTISRDSQSLYLQMTLRAEDSATYTCARDICYG-----YDVGALDYWGQ 116
QY 118 GTSVTVSS 125
Db 117 GTSVTVSS 124

RESULT 4
US-08-449-287-4
; Sequence 4, Application US/08449287
; Patent No. 5877293
; GENERAL INFORMATION:
; APPLICANT: ADAIR, John Robert
; APPLICANT: BOWMER, Mark William
; APPLICANT: MOUNTAIN, Andrew
; APPLICANT: OWENS, Raymond John
; TITLE OF INVENTION: CDR Grafted Anti-CEA Antibodies and
; TITLE OF INVENTION: Their Production
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449, 287
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/154,389
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT GB91/01108
; FILING DATE: 05-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9014932.9
; FILING DATE: 05-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT GB90/02017
; FILING DATE: 21-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 40283/110 CARA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-449-287-4

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Query Match 82.0%; Score 553; DB 2; Length 140;
Best Local Similarity 86.4%; Pred. No. 5.7e-48;
Matches 108; Conservative 5; Mismatches 8; Indels 4; Gaps 2;

QY 1 EVKLVSGLVPGGSLRLSCATSGFTSDYNNVWVQPPGKALEWLGFIIRNKANGYTT 60
Db 20 EVKLVSGLVPGGSLRLSCATSGFTSDYNNVWVQPPGKALEWLGFIIRNKANGYTT 79
QY 61 EFSASVWGRTISRDSQSLYLQMTLRAEDSATYTCARDPPYGNPNHYANDYWGQTS 120

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Db 80 EYSASVKGRTISRDSQSLYLQMTLRAEDSATYTCARD--RGLRFF--DYWGQYTT 135
QY 121 VTVSS 125
Db 136 LTVSS 140

RESULT 5
US-08-765-783A-29
; Sequence 29, Application US/08765783A
; Patent No. 5994524
; GENERAL INFORMATION:
; APPLICANT: Matsushima, Kouji
; APPLICANT: Matsumoto, Yoshihiro
; APPLICANT: Yamada, Yoshiki
; APPLICANT: Sato, Koh
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yanazaki, Tatsumi
; TITLE OF INVENTION: Reshaped Human Antibody to
; TITLE OF INVENTION: Interleukin-8
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,783A
; FILING DATE: 07-MAR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 35029-20001.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX:
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 141 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Signal Sequence
; LOCATION: 1...19
; OTHER INFORMATION:
; US-08-765-783A-29

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Query Match 77.4%; Score 521.5; DB 2; Length 141;
Best Local Similarity 80.2%; Pred. No. 7.7e-45;
Matches 101; Conservative 8; Mismatches 12; Indels 5; Gaps 2;

QY 1 EVKLVSGLVPGGSLRLSCATSGFTSDYNNVWVQPPGKALEWLGFIIRNKANGYTT 60
Db 20 EVKLVSGLVPGGSLRLSCATSGFTSDYNNVWVQPPGKALEWLGFIIRNKANGYTT 79
QY 61 EFSASVWGRTISRDSQSLYLQMTLRAEDSATYTCARDPPYGNPNHY-YANDYWGQCT 119

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Db 80 EYSASVKGRTISRDSQSILYLQMTLRGDSATYYCARE-----NYRYDVELAYWGQGT 135

QY 120 SVTVSS 125
Db 136 LVTUSA 141

RESULT 6
US-08-921-100-29
; Sequence 29, Application US/08921100
; Patent No. 6024956
; GENERAL INFORMATION:
; APPLICANT: MATSUSHIMA, KOUJI
; APPLICANT: MATSUMOTO, YOSHIHIRO
; APPLICANT: YAMADA, YOSHIKI
; APPLICANT: SATO, KOH
; APPLICANT: TSUCHIYA, MASSAYUKI
; APPLICANT: YAMAZAKI, TATUMI
; TITLE OF INVENTION: HUMANIZED ANTI-IL8 ANTIBODY
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. NW, Suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/921,100
; FILING DATE: 29-AUG-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/437,323
; FILING DATE: 09-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 15580-0001.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 141 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-921-100-29

Query Match 77.4%; Score 521.5; DB 3; Length 141;
Best Local Similarity 80.2%; Pred. No. 7.7e-45;
Matches 101; Conservative 8; Mismatches 12; Indels 5; Gaps 2;

QY 1 EVKLVEGGGLVQPGGSLRLSCATSGFTSDYIMNVRQPPGKALEWLGFIIRNKANGYTT 60
Db 20 EVKLVEGGGLVQPGGSLRLSCVTSFTSDYILSVNRQPPGKALEWGLIRNKANGYTR 79
QY 61 EFSASVMGRFTISRDSQSILYLQMTLRGDSATYYCARE-----NYRYDVELAYWGQGT 119
Db 80 EYSASVKGRTISRDSQSILYLQMTLRGDSATYYCARE-----NYRYDVELAYWGQGT 135
QY 120 SVTVSS 125
Db 136 LVTUSA 141

RESULT 7
US-08-880-142-29
; Sequence 29, Application US/08880142
; Patent No. 6048972
; GENERAL INFORMATION:
; APPLICANT: MATSUSHIMA, KOUJI
; APPLICANT: MATSUMOTO, YOSHIHIRO
; APPLICANT: YAMADA, YOSHIKI
; APPLICANT: SATO, KOH
; APPLICANT: TSUCHIYA, MASSAYUKI
; APPLICANT: YAMAZAKI, TATUMI
; TITLE OF INVENTION: HUMANIZED ANTI-IL8 ANTIBODY
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. NW, Suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/880,142
; FILING DATE: 20-JUN-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/345,145
; FILING DATE: 28-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 15580-0001.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 141 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-880-142-29

Query Match 77.4%; Score 521.5; DB 3; Length 141;
Best Local Similarity 80.2%; Pred. No. 7.7e-45;
Matches 101; Conservative 8; Mismatches 12; Indels 5; Gaps 2;

QY 1 EVKLVEGGGLVQPGGSLRLSCATSGFTSDYIMNVRQPPGKALEWLGFIIRNKANGYTT 60
Db 20 EVKLVEGGGLVQPGGSLRLSCVTSFTSDYILSVNRQPPGKALEWGLIRNKANGYTR 79
QY 61 EFSASVMGRFTISRDSQSILYLQMTLRGDSATYYCARE-----NYRYDVELAYWGQGT 119
Db 80 EYSASVKGRTISRDSQSILYLQMTLRGDSATYYCARE-----NYRYDVELAYWGQGT 135
QY 120 SVTVSS 125
Db 136 LVTUSA 141

RESULT 8
US-08-902-201-29
; Sequence 29, Application US/08902201
; Patent No. 6068840
; GENERAL INFORMATION:
; APPLICANT: MATSUSHIMA, KOUJI

APPLICANT: MATSUMOTO, YOSHIHIRO
 APPLICANT: YAMADA, YOSHIKI
 APPLICANT: SATO, KOH
 APPLICANT: TSUCHIYA, MASSAUKI
 APPLICANT: YAMAZAKI, TATUMI
 TITLE OF INVENTION: HUMANIZED ANTI-IL8 ANTIBODY
 NUMBER OF SEQUENCES: 77
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOERSTER
 STREET: 2000 Pennsylvania Ave. NW, Suite 5500
 City: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20006-1888
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/902,201
 FILING DATE: 29-JUL-1997
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/437,328
 FILING DATE: 09-MAY-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: MURASHIGE, KATE H.
 REGISTRATION NUMBER: 29,959
 REFERENCE/DOCKET NUMBER: 15580-0001.01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 887-1500
 TELEFAX: (202) 887-0763
 TELEX: 90-4030
 INFORMATION FOR SEQ ID NO: 29:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 141 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-902-201-29

Query Match	77.4%	Score 521.5;	DB 3;	Length 141;
Best Local Similarity	80.2%;	Pred. NO. 7.7e-45;		
Matches 101;	Conservative	8;	Mismatches 12;	Indels 5;
				Gaps
QY	1	EYKLVESGGIVQPGGSLRLSCATSGFTTSDYIYMNWVRPPGKALEWLGFTFRNKANGYTT	60	
Db	20	EYKLVESGGIIQPGDSLRLSCVTSCTGFTTSDYIYLSWVRPPGKALEWGLIRNKANGYTR	79	
QY	61	EFSASVMGRTISRDDSQSLIYLQMTNLRASDATTYCARDPPYGNPHY-YAMDYWGQGT	119	
Db	80	EFSASVMGRTISRDDSQSLIYLQMTNLRAGEDSATYTCARE----	135	
QY	120	SVTVSS	125	
Db	136	LVTGSA	141	

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RESULT          9
US-08-401-908-1
; Sequence 1, Application US/08401908
; Patent No. 5684:46
; GENERAL INFORMATION:
; APPLICANT: Yoshinobu OKUNO et al.
; TITLE OF INVENTION: A DNA WHICH CODES FOR THE VARIABLE REGION OF
; TITLE OF INVENTION: ANTIBODY
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
;

```

STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/401,908
FILING DATE: March 10, 1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 116
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-401-908-1

Query Match	76.8%	Score 517.5;	DB 1;	Length 116;
Best Local Similarity	83.2%	Prod No. 1544		

	QY	Db	QY	Db
1	EVLKVESGGGLVQPGGSLRLSCATSGFTSYDMNVVRQPPGKALSWLGFIIRNKANGYTT	60	1	EVLKVESGGGLVQPGGSLRLSCGTSGFTLTDYVTWVRQPPGKALSWLGFIIRNRGTTTT
2			2	
3			3	
4			4	
5			5	
6			6	
7			7	
8			8	
9			9	
10			10	
11			11	
12			12	
13			13	
14			14	
15			15	
16			16	
17			17	
18			18	
19			19	
20			20	
21			21	
22			22	
23			23	
24			24	
25			25	
26			26	
27			27	
28			28	
29			29	
30			30	
31			31	
32			32	
33			33	
34			34	
35			35	
36			36	
37			37	
38			38	
39			39	
40			40	
41			41	
42			42	
43			43	
44			44	
45			45	
46			46	
47			47	
48			48	
49			49	
50			50	
51	EFSSAYMGRTISRDDQSIIYLQWNLTLRADSDATYCCARDPPYGPHHYAMDYWGQT	119	61	EYSASYKGRFTISRDNDSQSIIVLQWNLTLRVEDSATYCARKPGY---PFYANDYWGQT
52			62	
53			63	
54			64	
55			65	
56			66	
57			67	
58			68	
59			69	
60			70	
61			71	
62			72	
63			73	
64			74	
65			75	
66			76	
67			77	
68			78	
69			79	
70			80	
71			81	
72			82	
73			83	
74			84	
75			85	
76			86	
77			87	
78			88	
79			89	
80			90	
81			91	
82			92	
83			93	
84			94	
85			95	
86			96	
87			97	
88			98	
89			99	
90			100	

```

1  RESULT 10
2  US-08-449-287-12
3  ; Sequence 12, Application US/08449287
4  ; Patent No. 5877293
5  ;
6  ; GENERAL INFORMATION:
7  ;
8  ; APPLICANT: ADAIR, John Robert
9  ; APPLICANT: BODMER, Mark William
10 ; APPLICANT: MOUNTAIN, Andrew
11 ; APPLICANT: OWENS, Raymond John
12 ;
13 ; TITLE OF INVENTION: CDR Grafted Anti-CEA Antibodies and
14 ; TITLE OF INVENTION: Their Production
15 ;
16 ; NUMBER OF SEQUENCES: 27
17 ;
18 ; CORRESPONDENCE ADDRESS:
19 ;
20 ; ADDRESSEE: Foley & Lardner
21 ; STREET: 3000 K Street, N.W., Suite 500
22 ; CITY: Washington, D.C.
23 ; COUNTRY: USA
24 ;
25 ; ZIP: 20007-5109
26 ;
27 ; COMPUTER READABLE FORM:
28 ;
29 ; MEDIUM TYPE: Floppy disk
30 ; COMPUTER: IBM PC compatible
31 ; OPERATING SYSTEM: PC-DOS/MS-DOS
32 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
33 ;
34 ; CURRENT APPLICATION DATA:
35 ;
36 ; APPLICATION NUMBER: US/08/449,287
37 ; FILING DATE:
38 ; CLASSIFICATION:

```

us-09-724-406-18.ra

Fri Jun 29 08:04:34 2001

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/154,389
FILING DATE: 03-AUG-1993
APPLICATION NUMBER: DE P 422 58 53.7
FILING DATE: 05-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Wadler, Linda A.
REGISTRATION NUMBER: 33,218
REFERENCE/DOCKET NUMBER: 02481.1317-00000
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-459-310-2

Query Match 76.4%; Score 515; DB 2; Length 146;
Best Local Similarity 80.8%; Pred. No. 3.5e-44;
Matches 101; Conservative 7; Mismatches 13; Indels 4; Gaps 2;

QY 1 EVKLIVSGGGLVQPGGSLRLSCATSGFTSDYIMNVRQPPGKALEWLGFTIRNKANGYTT 60
DB 20 EVQLLESGGGLVQPGGSLRLSCATSGFTSDYIMNVRQPPGKALEWLGFTIRNKANGYTT 79
QY 61 EFSASVNGRFTISRDSSQSLYLQMTNLAEDSATYVCARDPPYGNPHYAMDYWGQGT 120
DB 80 EYSASVNGRFTISRDSSQSLYLQMTNLAEDSATYVCARDK--GIRYF--DVMGQGT 135
QY 121 VTVSS 125
DB 136 VTVSS 140

RESULT 11
US-08-459-310-2
Sequence 2, Application US/08459310
Patent No. 5645817
GENERAL INFORMATION:
APPLICANT: Seemann, Gerhard
TITLE OF INVENTION: Granulocyte-Binding Antibody Constructs,
THEIR PREPARATION AND USE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garret &
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,310
FILING DATE:
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/100,963
FILING DATE: 03-AUG-1993
APPLICATION NUMBER: DE P 422 58 53.7
FILING DATE: 05-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Wadler, Linda A.
REGISTRATION NUMBER: 33,218
REFERENCE/DOCKET NUMBER: 02481.1317-00000
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-459-310-2

Query Match 76.1%; Score 513; DB 1; Length 119;
Best Local Similarity 82.4%; Pred. No. 4.4e-44;
Matches 103; Conservative 9; Mismatches 9; Indels 6; Gaps 3;

QY 1 EVKLIVSGGGLVQPGGSLRLSCATSGFTSDYIMNVRQPPGKALEWLGFTIRNKANGYTT 60
DB 1 QVQLQESGGGLVQPGGSLRLSCATSG--FSDYIMNVRQPPGKALEWLGFTIRNKANGYTT 58
QY 61 EFSASVNGRFTISRDSSQSLYLQMTNLAEDSATYVCARDPPYGNPHYAMDYWGQGT 120
DB 59 EYSASVNGRFTISRDSSQSLYLQMTNLAEDSATYVCARDK--GIRYF--DVMGQGT 114
QY 121 VTVSS 125
DB 115 VTVSS 119

RESULT 12
US-08-308-494A-9
Sequence 9, Application US/08308494A
Patent No. 5959083
GENERAL INFORMATION:
APPLICANT: Bosslet, Klaus
TITLE OF INVENTION: Tetraivalent Bispecific Receptors, The
PREPARATION AND USE THEREOF
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garret &
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,494A
FILING DATE: 21-SEP-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/891,739
FILING DATE: 01-JUN-1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4118120.4
FILING DATE: 03-JUN-1991
ATTORNEY/AGENT INFORMATION:

NAME: Kulik, David J.
REGISTRATION NUMBER: 36,576
REFERENCE/DOCKET NUMBER: 05552-1186-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-308-494A-9

Query Match 76.1%; Score 513; DB 2; Length 119;
Best Local Similarity 82.4%; Pred. No. 4.4e-44;
Matches 103; Conservative 7; Mismatches 9; Indels 6; Gaps 3;
QY 1 EVKLVEGGGLVQPGGSLRLSCATSGFTSDYYMNNVROPKGALEWLGFIKNGKNGYTT 60
DB 1 QVQLQESGGGLVQPGGSLRLSCATSG--FSDYYMNNVROPKGALEWLGFIKNGKNGHTT 58
QY 61 EFSASVNGRTTISRDSQSILYLQMTLRAEDSATYICARDPPYGNPHYAMDYWGQGT 120
DB 59 EYSASVNGRTTISRDSQSILYLQMTLRAEDSATYICARDK--GIRWYF--DVWGQGT 114
QY 121 VTVSS 125
DB 115 VTVSS 119

RESULT 13
US-09-280-028-2
Sequence 2, Application US/09280028
Patent No. 6241961
GENERAL INFORMATION:
APPLICANT: BENES, IVAN FRIEDRICH
APPLICANT: BOSSLET, KLAUS
TITLE OF INVENTION: RADIOIMMUNO CONJUGATES FOR USE IN HUMAN THERAPY AND
FILE REFERENCE: BENES
CURRENT APPLICATION NUMBER: US/09/280,028
CURRENT FILING DATE: 1999-03-26
EARLIER APPLICATION NUMBER: 199 11 329.7
EARLIER FILING DATE: 1999-03-15
EARLIER APPLICATION NUMBER: 198 13 687.0
EARLIER FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 119
TYPE: PRT
ORGANISM: Mus musculus
US-09-280-028-2

Query Match 76.1%; Score 513; DB 4; Length 119;
Best Local Similarity 82.4%; Pred. No. 4.4e-44;
Matches 103; Conservative 7; Mismatches 9; Indels 6; Gaps 3;
QY 1 EVKLVEGGGLVQPGGSLRLSCATSGFTSDYYMNNVROPKGALEWLGFIKNGKNGYTT 60
DB 1 QVQLQESGGGLVQPGGSLRLSCATSG--FSDYYMNNVROPKGALEWLGFIKNGKNGHTT 58
QY 61 EFSASVNGRTTISRDSQSILYLQMTLRAEDSATYICARDPPYGNPHYAMDYWGQGT 120
DB 59 EYSASVNGRTTISRDSQSILYLQMTLRAEDSATYICARDK--GIRWYF--DVWGQGT 114
QY 121 VTVSS 125
DB 115 VTVSS 119

RESULT 14
US-08-449-287-10
Sequence 10, Application US/08449287
Patent No. 5877293
GENERAL INFORMATION:
APPLICANT: ADAIR, John Robert
APPLICANT: BODMER, Mark William
APPLICANT: MOUNTAIN, Andrew
APPLICANT: OWENS, Raymond John
TITLE OF INVENTION: CDR Grafted Anti-CEA Antibodies and
TITLE OF INVENTION: Their Production
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,287
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/154,389
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT GB91/01108
FILING DATE: 05-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9014932.9
FILING DATE: 05-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT GB90/02017
FILING DATE: 21-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 40283/110 CARA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-449-287-10

Query Match 74.08; Score 499; DB 2; Length 146;
Best Local Similarity 79.2%; Pred. No. 1.4e-42;
Matches 99; Conservative 7; Mismatches 15; Indels 4; Gaps 2;
QY 1 EVKLVEGGGLVQPGGSLRLSCATSGFTSDYYMNNVROPKGALEWLGFIKNGKNGYTT 60
DB 20 EVQLLEGGGLVQPGGSLRLSCATSGFTFDYYMNNVROPKGALEWLGFIKNGKNGYTT 79
QY 61 EFSASVNGRTTISRDSQSILYLQMTLRAEDSATYICARDPPYGNPHYAMDYWGQGT 120
DB 80 EYSASVNGRTTISRDSKSTLYLQMNGLQAQVSAIYYCTRD--RGLRFYF--DYWGQGT 135
QY 121 VTVSS 125
DB 136 VTVSS 140

Search completed: June 28, 2001, 16:01:14
Job time: 522 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2001, 15:58:44 ; Search time 234.85 Seconds
(without alignments)
40.544 Million cell updates/sec

Title: US-09-724-406-18
Perfect score: 674
Sequence: 1 EVKLVEGGGLVQPGSLRL.....NPHYAMDYWGQTSVTVSS 125

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	580	86.1	119	2 D30540	Ig heavy chain V r
2	574	85.2	123	2 S32186	Ig heavy chain V r
3	550.5	81.7	118	2 E30540	Ig heavy chain V r
4	542.5	80.5	145	2 S03844	Ig heavy chain V r
5	537.5	79.7	126	2 S16280	Ig heavy chain pre
6	530	78.6	124	2 PT0388	Ig heavy chain (38
7	528	78.3	122	1 AVMSX2	Ig heavy chain V r
8	522	77.4	117	1 AVMS47	Ig heavy chain V r
9	520.5	77.2	114	2 PH1027	Ig heavy chain V r
10	519.5	77.1	121	2 PT0391	Ig heavy chain V r
11	517.5	76.8	122	2 S20642	Ig heavy chain V r
12	513.5	76.2	124	2 H30539	Ig heavy chain V r
13	512	76.0	120	2 PT0393	Ig heavy chain V r
14	512	76.0	124	2 G30540	Ig heavy chain V r
15	510.5	75.7	125	2 G30539	Ig heavy chain V r
16	510	75.7	122	2 PT0392	Ig heavy chain V r
17	510	75.7	123	2 PT0354	Ig heavy chain V r
18	509.5	75.6	118	2 PT0355	Ig heavy chain V r
19	509.5	75.6	123	2 PT0386	Ig heavy chain V r
20	509	75.5	123	1 AVMSH6	Ig heavy chain V r
21	508.5	75.4	124	2 E30539	Ig heavy chain V r
22	508.5	75.4	124	2 F30539	Ig heavy chain V r
23	508	75.4	124	2 PT0389	Ig heavy chain V r
24	507.5	75.3	121	2 E30502	Ig heavy chain V r
25	507.5	75.3	123	2 PT0384	Ig heavy chain V r
26	505.5	75.0	124	2 A30539	Ig heavy chain V r
27	505	74.9	123	1 AVMS75	Ig heavy chain V r
28	504	74.8	119	2 S24517	Ig heavy chain V r
29	503	74.6	123	2 B30540	Ig heavy chain V r

30	503	74.6	123	2 I30538	Ig heavy chain V r
31	502	74.5	125	2 PT0353	Ig heavy chain V r
32	499.5	74.1	124	1 AVMS51	Ig heavy chain V r
33	497.5	73.8	123	2 PT0383	Ig heavy chain V r
34	497	73.7	123	1 AVMS14	Ig heavy chain V r
35	496.5	73.7	115	2 S20706	Ig heavy chain V r
36	496.5	73.7	123	2 PT0387	Ig heavy chain V r
37	496	73.6	140	2 S32805	Ig heavy chain V r
38	495.5	73.5	123	2 PT0385	Ig heavy chain V r
39	495.5	73.5	124	2 A30515	Ig heavy chain V r
40	495	73.4	123	1 AVMSH7	Ig heavy chain V r
41	495	73.4	144	1 AVMS67	Ig heavy chain V r
42	493	73.1	123	2 B30566	Ig heavy chain pre
43	492	73.0	119	2 S24520	Ig heavy chain V r
44	492	73.0	121	2 PT0352	Ig heavy chain V r
45	491.5	72.9	122	1 AVMS63	Ig heavy chain V r

ALIGNMENTS

RESULT 1

D30540
Ig heavy chain V region (174.3F4) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 10-Feb-1989 #sequence_revision 10-Feb-1989 #text_change 16-Aug-1996
C:Accession: D30540
R:Claflin, J.L.; Berry, J.

J. Immunol. 141, 4012-4019, 1988

A:Title: Genetics of the phosphocholine-specific antibody response to Streptococcus p

A:Reference number: A30534; MUID:89035545

A:Accession: D30540

A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual

A:Molecule type: mRNA

A:Residues: 1-119 <CL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-100/Domain: immunoglobulin homology <IM>

Query Match 86.1%; Score 580; DB 2; Length 119;
Best Local Similarity 89.6%; Pred. No. 2.2e-45;
Matches 112; Conservative 4; Mismatches 3; Indels 6; Gaps 1;

QY 1 EVKLVEGGGLVQPGSLRLSCATSGFTSDYMNWVRQPPGKALEWLGFRNKANGYTT 60

Db 1 EVKLVEGGGLVQPGSLRLSCATSGFTSDYMNWVRQPPGKALEWLGFRNKANGYTT 60

QY 61 EFSASVMGRFTISRDDQSILYLQMTLRADTSATYTCARDPPYGNPHYAMDYWGQTS 120

Db 61 EYSASVKGRRFTSRDNSQSILYLQMTLRADTSATYTCARDPPYGNPHYAMDYWGQTS 114

QY 121 VTVSS 125

Db 115 VTVSS 119

RESULT 2

S32186

Ig heavy chain V region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 23-Jul-1999

C:Accession: S32186

R:Izui, S.

submitted to the EMBL Data Library, February 1993

A:Reference number: S32185

A:Accession: S32186

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-123 <I>ZU>

A:Cross-references: EMBL:X70093; NID:g288249; PIDN:CAA49698.1; PID:g288250

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Matches	102;	Conservative	8;	Mismatches	11;	Indels	4;	Gaps	
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Query Match 77.2%; Score 520.5; DB 2; Length 114;

Ddb 1 EVKLVESGGGLVQPGNSLSLSCAAGFTTDTYMMNVVRQPPGKALEWLALIRNKANGYTT 60

Qy 61 EFSASVMGRFTISRDDSQSILYLQMNTLRAEDSATYYCARDPPYGPNPHYAMDYWGQGST 120
::: |: |||||||:||||||| ||||||||| | |||||||||
Ddb 61 EYTSLSKGRTFISRONSNILYLQMNLRADSAIYYCTRK---AASRGAMDYWGQGST 117

Qy 121 VTVSS 125
|||||

Ddb 118 VTVSS 122

RESULT 12

H30539

Ig heavy chain V region (252.5E10) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 10-Feb-1989 #sequence_revision 10-Feb-1989 #text_change 16-Aug-1996

C:Accession: H30539

R:Claflin, J.L.; Berry, J.

J. Immunol. 141, 4012-4019, 1988

A:Title: Genetics of the phosphocholine-specific antibody response to Streptococcus p

A:Reference number: A30534; MUID:89035545

A:Accession: H30539

A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual

A:Molecule type: mRNA

A:Residues: 1-124 <CLA>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-100/Domain: immunoglobulin homology <IMM>

Query Match 76.2%; Score 513.5; DB 2; Length 124;
Best Local Similarity 78.4%; Pred. No. 2.1e-39;
Matches 98; Conservative 9; Mismatches 17; Indels 1; Gaps 1;

Qy 1 EVKLVESGGGLVOPGGSLRLSCATSGFTSFSDYYMNVVRQPPGKALEWLGFI RNKANGYTT 60
||||| ||||||| ||||||| ||||||| ||||||| |||: ||||||| |||

Ddb 1 EVKLVESGGGLVOPGGSLRLSCATSGFTSFDFMEWVRQPPGKRLEWIAASRNKANDIT 60

Qy 61 EFSASVMGRFTISRDDSQSILYLQMNTLRAEDSATYYCARDPPYGPNPHYAMDYWGQGST 120
|:||||| ||| :||| ||||||| ||||||| ||||||| |||: ||| |||:

Ddb 61 EYSASVAGRFTIVSRDTSQSILYLQMNLRADTFAIYYCARD-VYGSYYVFYDVWGAGTT 119

Qy 121 VTVSS 125
|||||

Ddb 120 VTVSS 124

RESULT 13

PT0393

Ig heavy chain V region (SI07/VH11 group 6-26) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C:Accession: PT0393

R:Behar, S.M.; Lustgarten, D.L.; Corbet, S.; Shariff, M.D.

J. Exp. Med. 173, 731-741, 1991

A:Title: Characterization of somatically mutated SI07 VH11-encoded anti-DNA autoantib

A:Reference number: PT0376; MUID:91147903

A:Accession: PT0393

A:Molecule type: DNA

A:Residues: 1-120 <BEH>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-100/Domain: immunoglobulin homology <IMM>

Query Match 76.0%; Score 512; DB 2; Length 120;
Best Local Similarity 78.4%; Pred. No. 2.8e-39;
Matches 98; Conservative 7; Mismatches 14; Indels 6; Gaps 1;

Qy 1 EVKLVESGGGLVOPGGSLRLSCATSGFTSFSDYYMNVVRQPPGKALEWLGFI RNKANGYTT 60
t- 1 EVKLVESGGGLVOPGGSLRLSCATSGFTSFSDYYMNVVRQPPGKALEWLGFI RNKANGYTT 60

us-09-724-406-18.rpr

Fri Jun 29 08:04:35 2001

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 28, 2001, 15:54:37 ; Search time 105.36 Seconds
(without alignments)
40.641 Million cell updates/sec

Title: US-09-724-406-18
Perfect score: 674
Sequence: 1 EVKLVESGGLVQPGSLRL.....NPHYAMDYWGQTSVTSS 125

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	522	77.4	117	1	HV17_MOUSE
2	509	75.5	123	1	HV22_MOUSE
3	507	75.2	123	1	HV18_MOUSE
4	505	74.9	123	1	HV19_MOUSE
5	497	73.7	123	1	HV25_MOUSE
6	495	73.4	123	1	HV23_MOUSE
7	495	73.4	144	1	HV26_MOUSE
8	491.5	72.9	122	1	HV20_MOUSE
9	490.5	72.8	122	1	HV21_MOUSE
10	485	72.0	123	1	HV24_MOUSE
11	431	63.9	142	1	HV01_RAT
12	424.5	63.0	122	1	HV36_HUMAN
13	411	61.0	125	1	HV32_MOUSE
14	409.5	60.8	136	1	HV16_MOUSE
15	406	60.2	113	1	HV30_MOUSE
16	401.5	59.6	111	1	HV35_MOUSE
17	401	59.5	113	1	HV27_MOUSE
18	399	59.2	113	1	HV31_MOUSE
19	397	58.9	115	1	HV33_MOUSE
20	395	58.6	113	1	HV28_MOUSE
21	393	58.3	113	1	HV29_MOUSE
22	392	58.2	117	1	HV42_MOUSE
23	391	58.0	121	1	HV3J_HUMAN
24	384	57.0	115	1	HV3F_HUMAN
25	381	56.5	115	1	HV3D_HUMAN
26	380	56.4	120	1	HV3E_HUMAN
27	377.5	56.0	119	1	HV3N_HUMAN
28	377	55.9	113	1	HV34_MOUSE
29	375.5	55.7	114	1	HV3B_HUMAN
30	375.5	55.7	119	1	HV3M_HUMAN
31	375.5	55.7	122	1	HV3A_HUMAN
32	374.5	55.6	119	1	HV40_MOUSE
33	374.5	55.6	126	1	HV3K_HUMAN

34	372.5	55.3	119	1	HV37_MOUSE
35	370.5	55.0	122	1	HV3H_HUMAN
36	369.5	54.8	119	1	HV38_MOUSE
37	366.5	54.4	116	1	HV3T_HUMAN
38	362.5	53.8	116	1	HV05_CARAU
39	357	53.0	117	1	HV3C_HUMAN
40	357	53.0	118	1	HV39_MOUSE
41	355	52.7	117	1	HV41_MOUSE
42	355	52.7	119	1	HV3I_HUMAN
43	351.5	52.2	117	1	HV3O_HUMAN
44	348.5	51.7	114	1	HV01_CANFA
45	348.5	51.7	119	1	HV3P_HUMAN

ALIGNMENTS

RESULT 1					
HV17_MOUSE					
ID	HV17_MOUSE	STANDARD;	PRT;	117 AA.	
AC	P01786;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	IG HEAVY CHAIN V REGION MOPC 47A.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE.				
RA	MEDLINE=80049769; PubMed=115869;				
RA	Robinson E.A., Appella E.;				
RT	"Amino acid sequence of a mouse myeloma immunoglobulin heavy chain				
RT	(MOPC 47 A) with a 100-residue deletion.";				
RL	J. Biol. Chem. 254:11418-11430(1979).				
CC	-I- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA				
CC	PROTEIN THAT CONTAINS ONE LIGHT AND ONE HEAVY CHAIN PER MOLECULE,				
CC	LINKED BY A DISULFIDE BOND. IN CONTRAST, NORMAL MOUSE IGA				
CC	MOLECULES CONTAIN TWO LIGHT AND TWO HEAVY CHAINS AND LACK A				
CC	LIGHT-HEAVY CHAIN DISULFIDE BOND.				
PIR:	A02069; AIMS47.				
HSSP:	P01789; 2MCP.				
InterPro:	IPR003006; .				
Prfam:	PF00047; Ig; 1.				
KW	Immunoglobulin V region.				
FT	NON_TER 117 117				
SQ	SEQUENCE 117 AA; 12975 MW; 0C74BE8BB154BDF4 CRC64;				
Query Match 77.4%; Score 522; DB 1; Length 117;					
Best Local Similarity 80.0%; Pred. No. 1.7e-46;					
Matches 100; Conservative 9; Mismatches 8; Indels 8; Gaps 2;					
QY	1	EVKLVESGGLVQPGSLRLSCATSGFTSDYIMNVRQPPGKALEWLGFRNKANGYTT	60		
Db	1	EVKLVESGGLVQPGSLRLSCATSGFTSDYIMNVRQPPGKALEWLGFRNKANGYTT	60		
QY 61 EFSASVMGRFTISRDDSSILYLQMTLRAEDSATYTCARDPPYGNPHYAMDYWGQTS 120					
Db	61	EYSA-VKGRFTISRDBSGLYLQMTLRAEDSATYTCARDPPYGNPHYAMDYWGQTS 112			
QY	121	VTVSS 125			
Db	113	VTVSS 117			
RESULT 2					
HV22_MOUSE					
ID	HV22_MOUSE	STANDARD;	PRT;	123 AA.	
AC	P01791;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				

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15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION HPCM6.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RN SEQUENCE.
RP MEDLINE=81197602; PubMed=7231520;
RX Gearhart P.J., Johnson N.D., Douglas R., Hood L.;
RA "IgG antibodies to phosphorylcholine exhibit more diversity than
RT their IgM counterparts.";
RL Nature 291:29-34(1981).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BINDS PHOSPHORYLCHOLINE.
DR PIR: A02070; AVMS15.
DR HSSP: P01789; 2MCP.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region; Hybridoma.
FT NON_TER 123 123
SQ SEQUENCE 123 AA; 13895 MW; 81361892ECBF7000 CRC64;

Query Match 75.5%; Score 509; DB 1; Length 123;
Best Local Similarity 79.2%; Pred. No. 3.8e-45;
Matches 99; Conservative 7; Mismatches 17; Indels 2; Gaps 2;

QY 1 EVKLVEGGGLVQPGGSLRLSCATSGFTSFDDYMEWRQPPGKRLWIAAASRNKANDYTT 60
DB 1 EVKLVEGGGLVQPGGSLRLSCATSGFTSFDDYMEWRQPPGKRLWIAAASRNKANDYTT 60

QY 61 EFSASVNGRFTISRDSQSILYLQNTLRAEDSATYICARDPPYGNPHYYAMDYWGQGTS 120
DB 61 EFSASVNGRFTISRDSQSILYLQNTLRAEDSATYICARDPPYGNPHYYAMDYWGQGTS 120

QY 121 VTVSS 125
DB 121 VTVSS 125

QY 119 VTVSS 123
DB 119 VTVSS 123

RESULT 3
HV19_MOUSE
ID HV19_MOUSE STANDARD; PRT; 123 AA.
AC P01788;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE IG HEAVY CHAIN V REGION H8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN SEQUENCE.
RP Barstad P.;
RA Thesis (1975), California Institute of Technology / Pasadena, U.S.A.
RL -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BINDS PHOSPHORYLCHOLINE.
DR PIR: A02070; AVMS15.
DR HSSP: P01789; 2MCP.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region.
FT NON_TER 123 123
SQ SEQUENCE 123 AA; 13805 MW; 9D581401912F7000 CRC64;

Query Match 75.2%; Score 507; DB 1; Length 123;
Best Local Similarity 78.4%; Pred. No. 6.1e-45;
Matches 98; Conservative 9; Mismatches 16; Indels 2; Gaps 2;

QY 1 EVKLVEGGGLVQPGGSLRLSCATSGFTSFDDYMNWVRQPPGKALEWLGFI RNKANGYTT 60
DB 1 EVKLVEGGGLVQPGGSLRLSCATSGFTSFDDYMNWVRQPPGKALEWLGFI RNKANGYTT 60

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1 EVKLVEGGGLVQPGGSLRLSCATSGFTSFDDYMEWRQPPGKRLWIAAASRNKANDYTT 60
61 EFSASVNGRFTISRDSQSILYLQNTLRAEDSATYICARDPPYGNPHYYAMDYWGQGTS 120
61 EFSASVNGRFTISRDSQSILYLQNTLRAEDSATYICARDPPYGNPHYYAMDYWGQGTS 120
121 VTVSS 125
119 VTVSS 123

RESULT 4
HV18_MOUSE
ID HV18_MOUSE STANDARD; PRT; 123 AA.
AC P01787;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE IG HEAVY CHAIN V REGION TEPC 15/S107/HPCM1/HPCM2/HPCM3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN SEQUENCE (TEPC 15).
RP MEDLINE=76222762; PubMed=819932;
RA Rudikoff S., Potter M.;
RT "Size differences among immunoglobulin heavy chains from
RT phosphorylcholine-binding proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 73:2109-2112(1976).
RN [2]
RN SEQUENCE FROM N.A. (H107).
RX MEDLINE=80199926; PubMed=6769593;
RA Early P., Huang H., Davis M., Calame K., Hood L.;
RT "An immunoglobulin heavy chain variable region gene is generated from
RT three segments of DNA: VH, D and JH.";
RL Cell 19:981-992(1980).
RN [3]
RN SEQUENCE (S107).
RX MEDLINE=76110488; PubMed=813561;
RA Rudikoff S., Barstad P., Potter M., Hood L.;
RL Unpublished results, cited by:
RL Hood L., Campbell J.H., Elgin S.C.R.;
RN Annu. Rev. Genet. 9:305-353(1975).
RN [4]
RN SEQUENCE (HPCM1; HPCM2 AND HPCM3).
RX MEDLINE=81197602; PubMed=7231520;
RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.;
RT "IgG antibodies to phosphorylcholine exhibit more diversity than
RT their IgM counterparts.";
RL Nature 291:29-34(1981).
CC -1- MISCELLANEOUS: ALL THOSE SEQUENCE APPEARS TO BE IDENTICAL.
CC -1- MISCELLANEOUS: THESE CHAINS WERE ISOLATED FROM MYELOMA AND
CC HYBRIDOMA PROTEINS THAT BIND PHOSPHORYLCHOLINE.
DR PIR: A02070; AVMS15.
DR HSSP: P01789; 2MCP.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region; Hybridoma.
FT NON_TER 123 123
SQ SEQUENCE 123 AA; 13777 MW; 9D58086DE12F7000 CRC64;

Query Match 74.9%; Score 505; DB 1; Length 123;
Best Local Similarity 78.4%; Pred. No. 9.7e-45;
Matches 98; Conservative 9; Mismatches 16; Indels 2; Gaps 2;

QY 1 EVKLVEGGGLVQPGGSLRLSCATSGFTSFDDYMNWVRQPPGKALEWLGFI RNKANGYTT 60
DB 1 EVKLVEGGGLVQPGGSLRLSCATSGFTSFDDYMNWVRQPPGKALEWLGFI RNKANGYTT 60
61 EFSASVNGRFTISRDSQSILYLQNTLRAEDSATYICARDPPYGNPHYYAMDYWGQGTS 120

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Db 61 EYSASVKGREIVSRDTSQSLYLQNMALRAEDTAIYYCARD--YGGSSYWF-FDWMGAGTT 118
 QY 121 VTSS 125
 Db 119 VTSS 123

RESULT 5
 HV25_MOUSE
 ID HV25_MOUSE STANDARD; PRT; 123 AA.
 AC P01794;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION HPG14.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=81197602; PubMed=7231520;
 RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.;
 RT "IgG antibodies to phosphorylcholine exhibit more diversity than
 their IgM counterparts.";
 RL Nature 291:29-34(1981).
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
 BINDS PHOSPHORYLCHOLINE.
 DR PIR; A02070; AVMS75.
 DR HSSP; P01789; 2MCP.
 DR InterPro; IPR003006; -.
 DR Pfam; PF00047; ig; 1.
 KW Immunoglobulin V region; Hybridoma.
 FT NON_TER 123 123
 SQ SEQUENCE 123 AA; 13807 MW; A7584FB098B7785D CRC64;

Query Match 73.7%; Score 497; DB 1; Length 123;
 Best Local Similarity 76.8%; Pred. No. 6.3e-44;
 Matches 96; Conservative 9; Mismatches 18; Indels 2; Gaps 1;

QY 1 EVKLVEGGGLVQPGGSLRLSCATSGFTSFYNNWVRQPPGKALEWLGFIIRNKANGYTT 60
 Db 1 EVKLVEGGGLVQPGGSLRLSCATSGFTSFYNNWVRQPPGKALEWLGFIIRNKANGYTT 60
 QY 61 EFSASVMGRFTISRDSQSLYLQNMALRAEDSATIYYCARDPPYGNPHIYAMDYWGQGTS 120
 Db 61 EYSASVKGREIVSRDTSQSLYLQNMALRAEDTAIYYCARD--YGGSSYWF-FDWMGAGTT 118
 QY 121 VTSS 125
 Db 119 VTSS 123

RESULT 6
 HV23_MOUSE
 ID HV23_MOUSE STANDARD; PRT; 123 AA.
 AC P01792;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION HPG8.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=81197602; PubMed=7231520;
 RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.;
 RT "IgG antibodies to phosphorylcholine exhibit more diversity than
 their IgM counterparts.";

RL Nature 291:29-34(1981).
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
 BINDS PHOSPHORYLCHOLINE.
 DR PIR; A02070; AVMS75.
 DR HSSP; P01789; 2MCP.
 DR InterPro; IPR003006; -.
 DR Pfam; PF00047; ig; 1.
 KW Immunoglobulin V region; Hybridoma.
 FT NON_TER 123 123
 SQ SEQUENCE 123 AA; 13879 MW; 4559D3106CAF7D8D CRC64;

Query Match 73.4%; Score 495; DB 1; Length 123;
 Best Local Similarity 76.8%; Pred. No. 1e-43;
 Matches 96; Conservative 7; Mismatches 20; Indels 2; Gaps 1;
 QY 1 EVKLVEGGGLVQPGGSLRLSCATSGFTSFYNNWVRQPPGKALEWLGFIIRNKANGYTT 60
 Db 1 EVKLVEGGGLVQPGGSLRLSCATSGFTSFYNNWVRQPPGKALEWLGFIIRNKANGYTT 60
 QY 61 EFSASVMGRFTISRDSQSLYLQNMALRAEDSATIYYCARDPPYGNPHIYAMDYWGQGTS 120
 Db 61 EYSASVKGREIVSRDTSQSLYLQNMALRAEDTAIYYCARD--YGGSSYWF-FDWMGAGTT 118
 QY 121 VTSS 125
 Db 119 VTSS 123

RESULT 7
 HV26_MOUSE
 ID HV26_MOUSE STANDARD; PRT; 144 AA.
 AC P01795;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION M167 PRECURSOR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93358330; PubMed=6101208;
 RA Kim S., Davis M., Sinn E., Patten P., Hood L.;
 RT "Antibody diversity: somatic hypermutation of rearranged VH genes.";
 RL Cell 27:573-581(1981).
 RN [2]
 RP SEQUENCE OF 20-142
 RX MEDLINE=76222762; PubMed=819932;
 RA Rudikoff S., Potter M.;
 RT "Size differences among immunoglobulin heavy chains from
 phosphorylcholine-binding proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 73:2109-2112(1976).
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN
 THAT BINDS PHOSPHORYLCHOLINE.

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 EMBL; J00516; AAC18867.1; -.
 DR PIR; A02071; AVMS67.
 DR HSSP; P01789; 2MCP.
 DR InterPro; IPR003006; -.
 DR Pfam; PF00047; ig; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 CHAIN 20 144 IG HEAVY CHAIN V REGION M167.

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FT CONFLICT 125 125 N -> D (IN REF. 2).
FT NON_TER 144 144
SQ SEQUENCE 144 AA; 16219 MW; BECB4A2C956CF769 CRC64;

Query Match 73.4%; Score 495; DB 1; Length 144;
Best Local Similarity 73.6%; Pred. No. 1.2e-43;
Matches 92; Conservative 12; Mismatches 21; Indels 0; Gaps 0;

QY 1 EVKLVEGGGLVQPGGSLRLSCATSGFTSDYYMNMVROPQPGKALEWLGFI RNKANGYTT 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 20 EVKVVESGGGLVQPGGSLRLSCATSGFTSDYYMNMVROPQPGKALEWLGFI RNKANGYTT 79
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 EFSASVMGRFTISRDDQSILYLQMNLTLRADTSATYYCARDPPYGNPHYAMDYWGQGT 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 80 EYSASVKGRFIVSRDTSQSVLYLQMNALRAEDTATYYCTRDADYGSYFGYFDVWGAGTT 139
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 VTVSS 125
   |||||
DB 140 VTVSS 144
   |||||

RESULT 8
HV20_MOUSE STANDARD; PRT; 122 AA.
AC P01789;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION M603.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80199926; PubMed=6769593;
RA Early P., Huang H., Davis M., Calame K., Hood L.;
RT "An immunoglobulin heavy chain variable region gene is generated from
RL three segments of DNA: VH, D and JH."
RN [2]
RP SEQUENCE OF 1-120.
RX MEDLINE=75017346; PubMed=4213527;
RA Rudikoff S., Potter M.;
RT "Variable region sequence of the heavy chain from a phosphorylcholine
RL binding myeloma protein."
RN [3]
RP Biochemistry 13:4033-4038(1974).
RX X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF FAB FRAGMENT.
RP MEDLINE=75065510; PubMed=4530984;
RA Segal D.M., Padlan E.A., Cohen G.H., Rudikoff S., Potter M.,
RA Davies D.R.;
RT "The three-dimensional structure of a phosphorylcholine-binding mouse
RL immunoglobulin Fab and the nature of the antigen binding site."
RN [4]
RP Proc. Natl. Acad. Sci. U.S.A. 71:4298-4302(1974).
CC -1- MISCELLANEOUS; THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS PHOSPHORYLCHOLINE.
CC PIR; A02070; AVMS75.
DR HSSP; P01789; 2MCP.
DR InterPro; IPR003006; -.
DR PDB; 1MCP; 15-JUL-92.
DR PDB; 2MCP; 15-JUL-92.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; ig; 1.
DR Immunoglobulin V region; 3D-structure.
KW SITE 33 33 H-BOND WITH THE PHOSPHATE GROUP OF PHOS-
FT SITE 33 33 PHORYLCHOLINE.
FT SITE 52 52 H-BOND WITH THE PHOSPHATE GROUP OF PHOS-
FT SITE 52 52 PHORYLCHOLINE.
FT STRAND 3 7
FT STRAND 11 12
FT TURN 14 15
FT STRAND 17 25
FT STRAND 29 31
FT HELIX 29 31

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FT STRAND 33 39
FT TURN 41 42
FT STRAND 46 50
FT TURN 54 55
FT STRAND 61 61
FT TURN 64 66
FT STRAND 67 67
FT TURN 68 69
FT STRAND 70 75
FT TURN 76 79
FT STRAND 80 86
FT HELIX 90 92
FT STRAND 94 103
FT STRAND 107 112
FT STRAND 116 120
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13626 MW; BA2C864438B64F0F CRC64;

Query Match 72.9%; Score 491.5; DB 1; Length 122;
Best Local Similarity 76.8%; Pred. No. 2.3e-43;
Matches 96; Conservative 9; Mismatches 17; Indels 3; Gaps 2;

QY 1 EVKLVEGGGLVQPGGSLRLSCATSGFTSDYYMNMVROPQPGKALEWLGFI RNKANGYTT 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 EVKLVEGGGLVQPGGSLRLSCATSGFTSDYYMNMVROPQPGKALEWLGFI RNKANGYTT 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 EFSASVMGRFTISRDDQSILYLQMNLTLRADTSATYYCARDPPYGNPHYAMDYWGQGT 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 EYSASVKGRFIVSRDTSQSVLYLQMNALRAEDTATYYCARN-YVGSTWYF--DVWGAGTT 117
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 VTVSS 125
   |||||
DB 118 VTVSS 122
   |||||

RESULT 9
HV21_MOUSE STANDARD; PRT; 122 AA.
AC P01790;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION M511.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81054880; PubMed=6776528;
RA Robinson E.A., Appella E.;
RT "Complete amino acid sequence of a mouse immunoglobulin alpha chain
RL (MOPC 511).";
CC -1- MISCELLANEOUS; THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS PHOSPHORYLCHOLINE.
CC PIR; A02070; AVMS75.
DR HSSP; P01789; 2MCP.
DR InterPro; IPR003006; -.
DR PDB; PF00047; ig; 1.
DR Immunoglobulin V region.
KW NON_TER 122 122
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13652 MW; 9F4837731EA50207 CRC64;

Query Match 72.8%; Score 490.5; DB 1; Length 122;
Best Local Similarity 76.8%; Pred. No. 2.9e-43;
Matches 96; Conservative 9; Mismatches 17; Indels 3; Gaps 2;

QY 1 EVKLVEGGGLVQPGGSLRLSCATSGFTSDYYMNMVROPQPGKALEWLGFI RNKANGYTT 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 EVKLVEGGGLVQPGGSLRLSCATSGFTSDYYMNMVROPQPGKALEWLGFI RNKANGYTT 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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RESULT	11
ID	HV01_RAT
HWID	P01805;
TAC	STANDARD; PRT; 142 AA.
DT	21-JUL-1986 (Rel. 01, Created)
OT	21-JUL-1986 (Rel. 01, Last sequence update)
DE	15-JUL-1999 (Rel. 38, Last annotation update)
JC	IG HEAVY CHAIN V REGION IR2 PRECURSOR.
SC	Rattus norvegicus (Rat).
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
NCBI_TaxID=10116;	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
[1]	
SEQUENCE FROM N.A.	
MDLINE=83064537; PubMed=6292865;	
Hellman L., Pettersson U., Engstroem A., Karlsson T., Bennich H.;	

	Query Match	63.08;	Score 424.5;	DB 1;	Length 122;
Best Local Similarity	65.9%;	Mismatches 21;			
Matches	83;	Conservative 17;	Indels 5;	Gaps 3;	
QY	1	EYKLVESGGGLVQPGGSLRLS	CAPTSGFTSDYNNMVVRPPGKALEWLFIRNKANGYTT	60	
	:				
Db	1	QVELVESGGGVZPGRSLRSL	CAASGFTSFNYAHMVVRPPGKLEWAVI	58	
	:				
QY	61	EFASVWGRFTISRDSSQSI	LYLQMTNLRADSATTCYARDPP	119	
	:				

protein.";
Biochemistry 16:1170-1175(1977).
ISOLATED FROM A MYELOMA PROTEIN THAT

protein.";
Biochemistry 16:1170-1175(1977).
ISOLATED FROM A MYELOMA PROTEIN THAT

```

CC BINDS INULIN.
DR PIR: A90400: AVMSB7.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; 1g; 1.
KW Immunoglobulin V region.
FT DISULFID 22 98
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12675 MW; 76658C16C779845E CRC64;

Query Match      60.2%; Score 406; DB 1; Length 113;
Best Local Similarity 63.4%; Pred. No. 1e-34;
Matches 78; Conservative 13; Mismatches 22; Indels 10; Gaps 1;

QY 1 EVKLVESGGGLVQPGGSLRLSCLATSGGTFSDYNNWVVRQPPGKALEWLGFI RNKANGYTT 60
DB 1 EVKLEESGGGLVQPGGSKLSCVAGSGETFSNYWNNWVRQSPKGLWVAEIRL KSHNYAT 60
QY 61 EFSASVMGRFTISRDDQSILYLQNMNLRADTSATYICARDPPYGNPHYYAMDYWGQTS 120
DB 61 HYAESVKGRFTISRDDSKSSVYLQNMNLRADETAIYYCST-----GFAYWGQGT 110
QY 121 VTV 123
DB 111 VTV 113

```

Search completed: June 28, 2001, 15:54:37
Job time: 125 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 28, 2001, 16:08:23 ; Search time 411.58 Seconds
(without alignments)
40.182 Million cell updates/sec

Title: US-09-724-406-18
Perfect score: 674

Sequence: 1 EVKLVESGGGLVQPGGSLRL.....NPHYAMDYWGQGTSTVTVSS 125

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

```
Maximum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 su
```

Database : SPTREMBL 16.*

SP_RMBL_16:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_unclassified:*
13: sp_vertebrate:*
14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		Length	DB	ID	Description
		Query Match					
1	415	61.6		113	4	Q9UL90	Q9ul90 homo sapien
2	400.5	59.4		118	4	Q9UL91	Q9ul91 homo sapien
3	388.5	59.1		112	4	Q9HCC1	Q9heci1 homo sapien
4	386.5	58.8		118	4	Q9UL72	Q9ul72 homo sapien
5	396.5	58.8		147	4	Q9Y509	Q9y509 homo sapien
6	395	58.6		131	4	Q9UL88	Q9ul88 homo sapien
7	389	57.7		121	4	Q9UL71	Q9ul71 homo sapien
8	380	56.4		116	4	Q9UL93	Q9ul93 homo sapien
9	374.5	55.6		122	4	Q9UL84	Q9ul84 homo sapien
10	358	53.1		117	11	Q9QXE9	Q9qx9 mus musculus
11	357.5	53.0		298	11	Q9QYF0	Q9qyf0 mus musculus
12	338	50.1		119	5	Q9GY22	Q9gy22 schistosoma
13	337	50.0		95	4	Q9ULB6	Q9ulb6 homo sapien
14	336.5	49.9		124	4	Q9UL92	Q9ul92 homo sapien
15	334	49.6		117	11	Q9QXF0	Q9qxf0 mus musculus
16	331.5	49.2		437	11	Q9RLA4	Q9rla4 mus musculus
17	322.5	47.8		124	6	Q9N0W4	Q9n0w4 oryctolagus
18	322	47.8		125	4	Q9UL95	Q9ul95 homo sapien
19	319.5	47.4		124	6	Q9N0W6	Q9n0w6 oryctolagus

ALIGNMENTS

[illegible]

Query Match	59.4%	Score 400.5;	DB 4;	Length 118;
Best Local Similarity	65.3%	Pred. No. 1.9e-35;		
Mismatch	91.	Conservative	12.	Mismatches 24.
				Indels 7;
				Gaps 2;

RESULT	3	
Q9HCC1		
ID	Q9HCC1	PRELIMINARY; PRT; 112 AA.
AC	Q9HCC1;	
DT	01-MAR-2001	(TREMBLrel. 16, Created)
DT	01-MAR-2001	(TREMBLrel. 16, Last sequence update)
DT	01-MAR-2001	(TREMBLrel. 16, Last annotation update)
DE	DE SINGLE CHAIN FV FRAGMENT (FRAGMENT).	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.	
OX	NCBI_Taxid=9606;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RP	Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;	
RT	"An antibody fragment2A3 specific for native lysozyme :isolation from a	
RT	bacterial library and characterization."	

Query Match	59.1%	Score 398.5;	DB 4;	Length 112;
Best Local Similarity	64.5%	Pred. No. 2.9e-35;		
Best "..."	16.0%	Mismatches 18.		
			Indels 9;	Gaps 2;

RESULT	4
Q9UL72	
ID	PRELIMINARY; PRT; 118 AA.
AC	Q9UL72;
DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE	MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS	Homo sapiens (Human)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.

RX	MEDLINE=98277139; PubMed=9614934;	
RA	Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,	
RA	Young D.C.;	
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal	
RT	fetus.";	
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).	
CC	-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX	
	DOMAIN:	
CC	EMBL; AF035042; AAD56278.1; -.	
DR	HSP; P01772; 2F84.	
DR	InterPro; IPR003006; -.	
DR	InterPro; IPR003596; -.	
DR	Pfam; PF00047; ig; 1.	
DR	SMART; SM00406; igv; 1.	
FT	NON_TER	1
FT	NON_TER	118
FT	SEQUENCE	118 AA; 12872 MW; B4D1A5944B2D5CCA CRC64;
SO		

Query Match	58.8%;	Score 396.5;	DB 4;	Length 118;
Best Local Similarity	65.6%;	Pred. No. 5e-35;		
Matches 82;	Conservative 13;	Mismatches 23;	Indels 7;	Gaps 3;

Qy	1	EYKLVESGGGLVQGGSLRLSCATSGFTSDYNNKVVQPPCKALEWLGIIRNKANGYIT	60
Db	1	EVOLVESGGGLVQGGSLRLSCAASGFTSYNNKVVQPPCKGLESVSYTSGGSSY	58
Qy	61	EPSASVWGKRTISRDSQSILYLQMTLRAEDSAYIYCAPPYGNPHYAYMDYWGQGT	120
Db	59	-YADSYWGKRTISRDSKNTLYLQMSLRAEDTAFIYCARD-REFE--FLFYWGQGT	113
Qy	121	VTVSS	125
Db	114	VTVSS	118

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RESULT 5
Q9Y509 ID Q9Y509 PRELIMINARY; PRT; 147 AA.
AC Q9Y509;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DE VH3 PROTEIN (FRAGMENT).
GN VH3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96071149; PubMed=7475288;
RA Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
RA Lichtenstein A.K., Berenson J.R.;
RT "A CD10-positive subset of malignant cells is identified in multiple
RT myeloma using PCR with patient-specific immunoglobulin gene primers.";
RL Leukemia 9:1948-1953(1995).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; S80860; RAD14339.1; -.
DR HSSP; P01772; 2FBA.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT SEQUENCE -47 AA; 15768 MW; 8489FCAA7BC925C CRC64;
SQ

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Query Match 58.8%; Score 396.5; DB 4; Length 147;
Best Local Similarity 62.5%; Pred. No. 6.6e-35;
Matches 80; Conservative 17; Mismatches 26; Indels 5; Gaps 3;

QY 1 EVKLVEGGGLVQPGGSLRLSCATSGFTSDYVMNWVRQPPGKALEWLGFIIRNKANGYTT 60
Db 1 QVHLVESGGGVQPGGSLRLSCATSGFTSDYVMNWVRQPPGKALEWLGFIIRNKANGYTT 58
QY 61 EFSASVNGRTTISRDSQSILYLQMTLRAEDSATYICARDPPYGNP--HYVA-MDYWGO 117
Db 59 YVAGSVKGRFTISRDNKNTLYLQMTSLRVEDTAVYICAKDGNFYDSVGYVYAGIDYWGQ 118
QY 118 GTSVTYSS 125
Db 119 GTLVTVSS 126

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RESULT 6
Q9UL88 ID Q9UL88 PRELIMINARY; PRT; 131 AA.
AC Q9UL88;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.

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```

DR EMBL; AF035026; AAD56262.1; -.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 131
FT SEQUENCE 131 AA; 14142 MW; 96E7D668E375DEAO CRC64;
SQ

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```

Query Match 58.6%; Score 395; DB 4; Length 131;
Best Local Similarity 58.8%; Pred. No. 8.3e-35;
Matches 77; Conservative 20; Mismatches 28; Indels 6; Gaps 1;

QY 1 EVKLVEGGGLVQPGGSLRLSCATSGFTSDYVMNWVRQPPGKALEWLGFIIRNKANGYTT 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSKAMSWVRQAPGKLEWVGRIKSKTDGGTT 60
QY 61 EFSASVNGRTTISRDSQSILYLQMTLRAEDSATYICARDPPY-----GNPHYVAMDY 114
Db 61 DYAAPVGRFTISRDSKNTLYLRMNSLKTEDTAVYYCTGITMIIVITSSKRTSFEY 120
QY 115 WGQTSVTYSS 125
Db 121 WGQGLTVTVSS 131

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```

RESULT 7
Q9UL71 ID Q9UL71 PRELIMINARY; PRT; 121 AA.
AC Q9UL71;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035043; AAD56279.1; -.
DR HSSP; P01772; 2FBA.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 121
FT SEQUENCE 121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;
SQ

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Query Match 57.7%; Score 389; DB 4; Length 121;
Best Local Similarity 63.2%; Pred. No. 3.3e-34;
Matches 79; Conservative 14; Mismatches 28; Indels 4; Gaps 2;

QY 1 EVKLVEGGGLVQPGGSLRLSCATSGFTSDYVMNWVRQPPGKALEWLGFIIRNKANGYTT 60
Db 1 EVQLVESGGGVQPGGSLRLFCAASGFTFDGYAMHWVRQAPGKLEWVSLI--SGDGGST 58
QY 61 EFSASVNGRTTISRDSQSILYLQMTLRAEDSATYICARDPPYGNPHYVAMDYWGQTS 120
Db 59 YVAGSVKGRFTISRDNKNTLYLQMTSLRVEDTAVYICAKGV--TTIYDRFDINGQGT 116
QY 121 VTVSS 125

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CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.

CC EMBL: AF035030; AAD56266.1; -.
DR HSP: P01772; 2FB4.
DR InterPro: IPR003006; -.
DR InterPro: IPR003596; -.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13579 MW; 36054D41366545B8 CRC64;

Query Match 55.6%; Score 374.5; DB 4; Length 122;
Best Local Similarity 62.4%; Pred. No. 1.2e-32;
Matches 78; Conservative 16; Mismatches 28; Indels 3; Gaps 2;

QY 1 EVKLVEGGGLVQPGSLRLSCATSGFTSDYNNVVRQPPGKALEWLGFIIRKANGYTT 60
Db 1 EVKLVEGGGLVQPGSLRLSCATSGFTSDYNNVVRQPPGKALEWLGFIIRKANGYTT 58

QY 61 EFSASVMGRFTISRDDSSQSLYLQMTLRAEDSATYTCARDPPYGNPHYAMDYWGQTS 120
Db 59 FYADSVKGRFTIFRDNKNNMQLMNSLRADTAVYICAKD-ERGLVGTYPDYWGQTL 117

QY 121 VTSS 125
Db 118 VTSS 122

RESULT 10
Q9QXE9 PRELIMINARY; PRT; 117 AA.

ID Q9QXE9
AC Q9QXE9
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Clemens A., Rademakers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ25174; CAB65237.1; -.
DR InterPro: IPR003006; -.
DR InterPro: IPR003596; -.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 13000 MW; CDDE2AF84D49734 CRC64;

Query Match 53.1%; Score 358; DB 11; Length 117;
Best Local Similarity 56.0%; Pred. No. 6.6e-31;
Matches 70; Conservative 20; Mismatches 27; Indels 8; Gaps 3;

QY 1 EVKLVEGGGLVQPGSLRLSCATSGFTSDYNNVVRQPPGKALEWLGFIIRKANGYTT 60
Db 1 EVKLVEGGGLVQPGSLRLSCATSGFTSDYNNVVRQPPGKALEWLGFIIRKANGYTT 58

QY 61 EFSASVMGRFTISRDDSSQSLYLQMTLRAEDSATYTCARDPPYGNPHYAMDYWGQTS 120
Db 59 SYNQKFKATITVDKSSSTAYMQLNSLTSDSAVYICARD-----RYIANDIWGQTS 112

QY 121 VTSS 125
Db 113 VTSS 117

Db 117 VTSS 121

RESULT 8
Q9UL93 PRELIMINARY; PRT; 116 AA.

AC Q9UL93
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.

DR EMBL: AF035021; AAD56257.1; -.
DR InterPro: IPR003006; -.
DR InterPro: IPR003596; -.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12434 MW; 0DA0348154DD6061 CRC64;

Query Match 56.4%; Score 380; DB 4; Length 116;
Best Local Similarity 62.9%; Pred. No. 2.9e-33;
Matches 78; Conservative 13; Mismatches 25; Indels 8; Gaps 2;

QY 2 VKLVEGGGLVQPGSLRLSCATSGFTSDYNNVVRQPPGKALEWLGFIIRKANGYTT 61
Db 1 VQLVESGGGVQPGSLRLSCATSGFTSSYAMHWVRQAPGKLEWVAVI--SYDGSNKY 58

QY 62 FASVSMGRFTISRDDSSQSLYLQMTLRAEDSATYTCARDPPYGNPHYAMDYWGQTSV 121
Db 59 YADSVKGRFTISRDNKNTLYLQMTLRAEDTAVYICAGGGGLG-----LGYWGQGLV 112

QY 122 TVSS 125
Db 113 TVSS 116

RESULT 9
Q9UL84 PRELIMINARY; PRT; 122 AA.

AC Q9UL84
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).


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RESULT 11
Q9QYF0
ID Q9QYF0 PRELIMINARY; PRT; 298 AA.
AC Q9QYF0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE CN 8 SCFV.
GN CN 8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=SPLEEN;
RA Shinohara N., Demura T., Fukuda H.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=SPLEEN;
RA Shinohara N., Demura T., Fukuda H.;
RL "Isolation of a novel type of vascular cell wall-specific monoclonal
antibody recognizing a cell polarity using a phage display subtraction
method.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB036341; BAA88633.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGv; 1.
SQ SEQUENCE 298 AA; 31867 MW; E0F9688A17004317 CRC64;

Query Match 53.0%; Score 357.5; DB 11; Length 298;
Best Local Similarity 56.0%; Pred. No. 2.3e-30;
Matches 70; Conservative 23; Mismatches 25; Indels 7; Gaps 2;

QY 1 EVKLVEGGGLVQPGGSLRLSCATSGFTSDYYMNVVRQPPGKALEWLGFI RNKANGYTT 60
Db 40 QVQLQSGGGLVQPGGSLRLSCAASGFSRYMWSVVRQAPGKGLEWIGENIPDSS--TI 97
QY 61 EFSASVGMGRTISRDSQSILYLQMTLRAEDSATYTCARDPPYGNPHYYAMDYWGQGTS 120
Db 98 NTPSLKDKFIISRDNAKNTLYLQMSKVRSEDALYYCARASYIGH-----SAYWGQGT 152
QY 121 VTSS 125
Db 153 VTSS 157

RESULT 12
Q9GYZ2
ID Q9GYZ2 PRELIMINARY; PRT; 119 AA.
AC Q9GYZ2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE MONOCLONAL ANTI-IDIOTYPIC ANTIBODY NP30 HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
OC Trematoda; Digenea; Strigeldida; Schistosomatidae; Schistosomatidae;
OC Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RA Song X.T., Feng Z.Q., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the heavy chain
variable region gene of monoclonal anti-idiotypic antibody NP30 of
Schistosoma japonicum.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

```

```

DR EMBL; AF282622; AAG01452.1; -.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13567 MW; BA893873FD5FA6AB CRC64;

Query Match 50.1%; Score 338; DB 5; Length 119;
Best Local Similarity 52.8%; Pred. No. 9.3e-29;
Matches 66; Conservative 22; Mismatches 31; Indels 6; Gaps 4;

QY 1 EVKLVEGGGLVQPGGSLRLSCATSGFTSDYYMNVVRQPPGKALEWLGFI RNKANGYTT 60
Db 1 QVQLVESGAERKPGASVRVSCASGYFTFTGYMNVVRQAPGKGLEWIGYI-NPSRGY-T 58
QY 61 EFSASVGMGRTISRDSQSILYLQMTLRAEDSATYTCARDPPYGNPHYYAMDYWGQGTS 120
Db 59 NYNOKFKDRVTMTDKSFSTAYMDLRLSLRSLRADSANVYCAR---YYDDH-YCLDYWGQGT 114
QY 121 VTSS 125
Db 115 VTSS 119

RESULT 13
Q9ULB6
ID Q9ULB6 PRELIMINARY; PRT; 95 AA.
AC Q9ULB6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE IMMUNOGLOBULIN HEAVY CHAIN (FRAGMENT).
GN VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tange Y., Kayano H.;
RT "Human VH gene sequence.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
CC EMBL; AB035268; BAA87067.1; -.
DR HSSP; P01772; 2FH4.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; -Gv; 1.
FT NON_TER 1
FT NON_TER 95
SQ SEQUENCE 95 AA; 10527 MW; 90A8C6D16D22574A CRC64;

Query Match 50.0%; Score 337; DB 4; Length 95;
Best Local Similarity 68.0%; Pred. No. 9e-29;
Matches 66; Conservative 12; Mismatches 17; Indels 2; Gaps 1;

QY 2 VKLVEGGGLVQPGGSLRLSCATSGFTSDYYMNVVRQPPGKALEWLGFI RNKANGYTT 61
Db 1 VQLVESGGGLVQPGGSLRLSCAASGFTSSYMWVVRQAPGKGLEWANI--KDGSEKY 58
QY 62 FSAASVGMGRTISRDSQSILYLQMTLRAEDSATYTC 98
Db 59 YDVSVKGRFTISRDNKSNKSLQLQMSLRADETAYTC 95

RESULT 14
Q9UL92
ID Q9UL92 PRELIMINARY; PRT; 124 AA.
AC Q9UL92;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

```

```
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: AF035022; AAD56258.1; -.
DR InterPro: IPR003006; -.
DR InterPro: IPR003596; -.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IG; 1.
FT NON_TER 1
FT NON_TER 124
SQ SEQUENCE 124 AA; 13580 MW; 1BAAACBD96ACD2A2 CRC64;
```

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Query Match 49.9%; Score 336.5; DB 4; Length 124;
Best Local Similarity 50.8%; Pred. No. 1.4e-28;
Matches 64; Conservative 26; Mismatches 33; Indels 3; Gaps 2;

QY 1 EVKLVEGGGLVQPGGSLRLSCATSGFTFSYDMNVRQPPGKALEWLGFI RNKANGYTT 60
DB 1 EVQLQSGPELVKPGASVKMSCKASSYFTDYIMKWKVQSHGKSLIEWIGDI-NPNNG-GT 58

QY 61 EFSASVMGRFTISRDDQSILYLQMNLTLRADTSATYYCARDPPYGNPHYYA-MDYWGQGT 119
DB 59 SYAQKFGQGRVTMTDTSITVYMELSLRSEDYAVYCARGLYVWVPAAFSFRDYWGQGT 118

QY 120 SVTVSS 125
DB 119 LTVSS 124
```

```
RESULT 15
Q9QXF0 Q9QXF0 PRELIMINARY; PRT; 117 AA.
AC Q9QXF0;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAY-2001 (Tremblrel. 16, Last annotation update)
DE IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Clemens A., Rademakers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ225171; CAB65236.1; -.
DR InterPro: IPR003006; -.
DR InterPro: IPR003596; -.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IG; 1.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 13060 MW; D816AD0858A47E4C CRC64;
```

```
Query Match 49.6%; Score 334; DB 11; Length 117;
Best Local Similarity 52.8%; Pred. No. 2.4e-28;
Matches 66; Conservative 23; Mismatches 28; Indels 8; Gaps 4;
```

```
QY 1 EVKLVEGGGLVQPGGSLRLSCATSGFTFSYDMNVRQPPGKALEWLGFI RNKANGYTT 60
DB 1 EVQLQSGPELVKPGASVKMSCKASSYFTDYIMKWKVQSHGKSLIEWIGDI-NPNNG-GT 58

QY 61 EFSASVMGRFTISRDDQSILYLQMNLTLRADTSATYYCARDPPYGNPHYYA-MDYWGQGT 120
DB 59 SYAQKFGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDKY----YF--DYWGQGT 112

QY 121 VTVSS 125
DB 113 LTVSS 117
```

Search completed: June 28, 2001, 16:08:23
Job time: 951 sec

0

0

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2001, 16:14:36 ; Search time 362.28 Seconds
(without alignments)
0.837 Million cell updates/sec

Title: US-09-724-406-20
Perfect score: 31
Sequence: 1 DYYMN 5

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues
Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_0601.*
1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.*
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9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.*
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19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	31	100.0	5	16	AA1980
2	31	100.0	5	20	AA1981
3	31	100.0	5	21	AA1982
4	31	100.0	111	20	AA1983
5	31	100.0	119	11	AA1984
6	31	100.0	119	15	AA1985
7	31	100.0	119	11	AA1986
8	31	100.0	119	17	AA1987
9	31	100.0	119	20	AA1988
10	31	100.0	119	21	AA1989
11	31	100.0	122	16	AA1990

12	31	100.0	122	16	AA1991
13	31	100.0	138	16	AA1992
14	31	100.0	140	13	AA1993
15	31	100.0	141	13	AA1994
16	31	100.0	146	13	AA1995
17	31	100.0	146	13	AA1996
18	31	100.0	146	13	AA1997
19	31	100.0	146	13	AA1998
20	31	100.0	146	13	AA1999
21	31	100.0	146	16	AA2000
22	31	100.0	250	17	AA2001
23	31	100.0	250	17	AA2002
24	31	100.0	473	18	AA2003
25	31	100.0	643	20	AA2004
26	28	90.3	647	20	AA2005
27	28	90.3	100	18	AA2006
28	28	90.3	234	21	AA2007
29	28	90.3	248	21	AA2008
30	28	90.3	253	21	AA2009
31	28	90.3	317	21	AA2010
32	28	90.3	327	21	AA2011
33	28	90.3	344	21	AA2012
34	28	90.3	414	18	AA2013
35	28	90.3	416	18	AA2014
36	28	90.3	499	16	AA2015
37	28	90.3	499	16	AA2016
38	28	90.3	511	21	AA2017
39	28	90.3	567	16	AA2018
40	28	90.3	703	16	AA2019
41	28	90.3	708	16	AA2020
42	28	90.3	736	20	AA2021
43	28	90.3	736	21	AA2022
44	28	90.3	753	16	AA2023
45	28	90.3	753	16	AA2024

ALIGNMENTS

RESULT 1
AA1993
ID AA1993 standard; peptide; 5 AA.
AC AA1993;
DT 19-JAN-1996 (first entry)
XX H-CDR-1 of anti-idiotypic antibody against human anticancer antibody.
DE Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin;
KW complementarity determining region.
XX Mus sp.
XX JP07101999-A.
XX 18-APR-1995.
XX 06-OCT-1993; 93JP-0272950.
XX 06-OCT-1993; 95JP-0272950.
XX (HAGI/) HAGIWARA Y.
XX WPI; 1995-182987/24.
XX Novel anti-idiotypic antibody against a human anticancer monoclonal
PT antibody - and DNA sequences encoding the antibody, useful in
PT pharmacology, medicine and biochemical fields.
XX Claim 1; Page 2; 28pp; Japanese.
XX A new anti-idiotypic antibody against a human anticancer monoclonal

Immunoglobulin hea
Anti-idiotypic anti
Unprocessed variab
A5B7 antibody heav
CDR-grafted, human
CDR-grafted, human
A5B7 gH-2 antibody
Anti-idiotypic anti
Humanised A5B57 Fd
Murine A5B57 Fd fr
Human B7.1-murine
Clone pG4/A5B7VH-
Plasmid pUC19/muA5
H. pylori cell env
Zea mays protein f
Zea mays protein f
Zea mays protein f
Zea mays protein f
Zea mays protein f
H. pylori ORF 02ae
H. pylori ORF 07ce
Rat cell cycle pro
Human cell cycle p
Human cancer assoc
Bovine foetal hear
Human placental en
Bovine foetal hear
Human PRO403 prote
Human PRO403 prote
Endothelin convert
Human endothelin c
Bovine endothelin

De

Query Match 100.0%; Score 31; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5
 |||||
 Db 1 dyymn 5

RESULT 4
 AAW89172
 ID AAW89172 standard; peptide; 111 AA.
 AC AAW89172;
 XX
 DT 25-MAR-1999 (first entry)
 XX
 DE Anti-p53 monoclonal antibody 248 variable heavy chain sequence.
 XX
 DE Anti-p53; monoclonal antibody 240; immunogen; anti-tumour; immunity;
 KW Immune response; tumour associated antigen; metastatic cancer.
 KW
 XX

OS Mus sp.
 OS Synthetic.
 XX
 PN WO9856416-A.
 XX
 PD 17-DEC-1998.

XX
 PF 09-JUN-1998; 98WO-IL00266.
 XX
 PR 09-JUN-1997; 97IL-0121041.
 XX
 PA (YEDA) YEDA RES & DEV CO LTD.

XX PI Cohen IR, Erez-Alon N, Herkel J, Rotter V, Ruiz PJ;
 PI Wolkowicz R;
 DR WPI: 1999-070296/06.

PT Use of a monoclonal antibody to a tumour-associated antigen - to
 PT induce anti-tumour immunity or elicit an increased immune response
 PT to the antigen

XX PS Example 3; Fig 3; 47pp; English.

XX CC The present invention describes the use of an immunogen (A) to induce
 CC anti-tumour immunity; to elicit an increased immune response to tumour
 CC associated antigen (TAA) and/or to induce an immune response to mutant
 CC or wild-type forms of TAA in mammals. (A) is: (i) a monoclonal antibody
 CC (Mab) to TAA, or its fragment; (ii) a peptide based on a CDR
 CC (complementarity determining region) on the heavy or light chain of Mab
 CC (able to elicit antibodies to TAA); or (iii) a DNA that encodes the
 CC variable (V) region of Mab, in a gene delivery vehicle. The present
 CC sequence represents the variable heavy chain sequence from anti-p53 Mab
 CC 248. Also described is a method for generating sequence-specific,
 CC anti-DNA antibodies (Ab) by immunising a mammal with a Mab directed to a
 CC domain containing a DNA-binding site of a DNA-binding protein. (A) is
 CC used to treat a wide variety of primary and metastatic cancers,
 CC particularly those where p53 is involved. Ab are used for diagnosis (e.g
 CC to determine critical sequences in animal or plant breeding); to
 CC identify bacteria and other parasites; to determine parentage; in
 CC forensic science; to isolate specific genes for DNA vaccination; in
 CC sequencing and cloning; also possibly for activation of selected
 CC therapeutic genes in plants, animals and humans. (A) induce an effective
 CC anti-tumour response without causing harm to the patient. The method
 CC uses (A) to generate anti-TAA by exploiting the anti-idiotypic network.

XX SQ Sequence 111 AA;

Query Match 100.0%; Score 31; DB 20; Length 111;
 Best Local Similarity 100.0%; Pred. No. 23;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYYMN 5
 |||||
 Db 28 dyymn 32

RESULT 5
 AAR07316
 ID AAR07316 standard; protein; 119 AA.
 XX
 AC AAR07316;
 XX
 DT 22-JAN-1991 (first entry)
 XX
 DE VH domain of antibody A against tumour-associated antigens.
 XX
 DE Tumour-associated antigen; murine monoclonal antibody A;
 KW granulocyte compartment; carcinoma; colon; pancreas; lung; mammary;
 KW diagnosis.
 KW
 XX

OS Mus musculus.
 XX
 PN EP388914-A.
 XX
 PD 26-SEP-1990.

XX PF 21-MAR-1990; 90EP-0105322.
 XX
 PR 24-MAR-1989; 89DE-3909799.
 XX
 PA (BEHW) BEHRINGWERKE AG.

XX PI Bosslet K, Seemann G, Sedlacek HH;
 XX WPI: 1990-291873/39.
 DR N-PSDB; AAQ06212.

XX PT Monoclonal antibodies to tumour associated antigens - used for
 PT diagnosis of malignant tumours etc.

XX PS Disclosure; Page 11; 18pp; German.

XX CC Antibody A is produced as described in EP-141079 and binds to cells
 CC of the granulocyte compartment and to colonic, pancreatic and
 CC certain pulmonary and mammary carcinomas. They are useful in tumour
 CC diagnosis and therapy.
 CC See also AAQ06213 for VK of Mab A, AAQ07314-15 for Mab B, and
 CC AAQ06227-30 for Mab C and D.

XX SQ Sequence 119 AA;

Query Match 100.0%; Score 31; DB 11; Length 119;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5
 |||||
 Db 29 dyymn 33

RESULT 6
 AAR47221
 ID AAR47221 standard; Protein; 119 AA.
 XX
 AC AAR47221;

XX DT 04-AUG-1994 (first entry)
 XX
 DE Antibody heavy chain used in construction of humanised antibody.

XX KW Antibody; light chain; heavy chain; monoclonal; humanised;

Fri Jun 29 08:04:42 2001

us-09-724-406-20.rag

KW diagnosis; detection; therapy; inflammation; tumour; metastasis;
 KW lymphoma; carcinoma.

OS Chimeric: Mus musculus.
 OS Chimeric: Homo sapiens.

XX DB4225853-A.
 XX 10-FEB-1994.

XX 05-AUG-1992; 92DE-4225853.

XX 05-AUG-1992; 92DE-4225853.

XX (BEHW). BEHRINGWERKE AG.

XX Bosslet K, Seemann G;

XX WPI; 1994-049745/07.

XX N-PSDB; AAQ56145.

XX Humanised antibody chains - derived from mouse monoclonal antibody
 PT and humanised antibodies useful for diagnosis or therapy of
 PT inflammations and tumours

XX Claim 2; Page 10; 12pp; German.

XX This antibody heavy chain is derived from the mouse monoclonal
 CC antibody BW 250/183. After mutagenesis of the coding sequence,
 CC the resulting protein sequence was used in the construction of a
 CC humanised antibody directed against nonspecific crossreacting
 CC antigen NCA 95 and carcinoembryonic antigen (CEA). The antibody
 CC may be used for diagnosis and/or therapy of inflammations and
 CC tumours which metastasise to bone marrow, especially lymphomas and
 CC mammary, prostatic and small cell carcinomas.

XX Sequence 119 AA;

Query Match 100.0%; Score 31; DB 15; Length 119;

Best Local Similarity 100.0%; Pred. NO. 25;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5

|||||

Db 29 dyyrn 33

RESULT 7

AAW14484

ID AAW14484 standard; Protein; 119 AA.

XX AAW14484;

XX 28-JAN-1997 (first entry)

XX Monoclonal antibody A VH.

XX heavy; light chain; monoclonal antibody; antigen 3; marker; melanoma;
 KW permanent human tumour cell line; tumour-associated antigen; epitope;
 KW gastrointestinal tumour; pancreatic carcinoma; diagnostic; therapeutic;
 KW antigen 11; Vibrio cholera; neuraminidase-resistant; ganglioside GD2.

XX Synthetic.

XX EP727436-A1.

XX 21-AUG-1996.

XX 21-MAR-1990; 90EP-0105322.

XX 24-MAR-1989; 89DE-3909799.

(BEHW) BEHRINGWERKE AG.

XX Auerbach B, Bosslet K, Sedlacek H, Seemann G;

XX WPI; 1996-372836/38.

XX N-PSDB; AAT63501.

XX Monoclonal antibody to tumour-associated antigen - useful as
 PT gastrointestinal tumour marker

XX Claim 1; Page 11; 19pp; German.

XX AAW14484-85 are the heavy and light chains (respectively) of monoclonal
 CC antibody (Mab) A. Mab A recognises antigen 3 of a permanent human tumour
 CC cell line. This tumour-associated antigenic epitope occurs at high
 CC concn. in the serum of patients with gastrointestinal tumours, e.g.
 CC pancreatic carcinoma, and is thus useful as a tumour marker for
 CC diagnostic or therapeutic purposes. Mabs B, C and D (see AAW14486-91) are
 CC mentioned in the specification, but are not part of the claims. Mab B
 CC recognises antigen 11 of permanent human tumour cell line. Mab C also
 CC recognises an epitope of a tumour-associated antigen occurring at high
 CC concn. in the serum of patients with gastrointestinal tumours. Mab D
 CC recognises a Vibrio cholera neuraminidase-resistant epitope of
 CC ganglioside GD2, from a human melanoma cell line.

XX Sequence 119 AA;

Query Match 100.0%; Score 31; DB 17; Length 119;

Best Local Similarity 100.0%; Pred. NO. 25;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5

|||||

Db 29 dyyrn 33

RESULT 8

AAW99873

ID AAW99873 standard; Protein; 119 AA.

XX AAW99873;

XX 28-JAN-1997 (first entry)

XX Monoclonal antibody A VH.

XX Monoclonal antibody; Mab; epitope; tumour-associated antigen;
 KW marker; antigen.

XX Synthetic.

XX EP727435-A1.

XX 21-AUG-1996.

XX 21-MAR-1990; 90EP-0105322.

XX 24-MAR-1989; 89DE-3909799.

XX (BEHW) BEHRINGWERKE AG.

XX Auerbach B, Bosslet K, Sedlacek H, Seemann G;

XX WPI; 1996-372835/38.

XX N-PSDB; AAT36661.

XX Monoclonal antibody to tumour-associated antigen - useful as
 PT gastrointestinal tumour marker

XX Disclosure; Page 11; 19pp; German.

XX Mab C (AAT36659-T36660) is a monoclonal antibody that recognises an

CC epitope of a tumour-associated antigen occurring at high concn. in
 CC the serum of patients with gastrointestinal tumours, e.g. pancreatic
 CC carcinoma, and is thus useful as a tumour marker for diagnostic or
 CC therapeutic purposes.
 CC MABs A, B and D are mentioned in the specification, but are not
 CC part of the claims.
 CC MAB A (AAT36661-T36662) recognises antigen 3 of permanent human
 CC tumour cell line.
 CC MAB B (AAT36663-T36664) recognises antigen 11 of permanent human
 CC tumour cell line.
 CC MAB D (AAT36665-T36666) recognises a Vibrio cholera neuraminidase-
 CC resistant epitope of ganglioside GD2, from a human melanoma cell
 CC line.
 CC
 SQ Sequence 119 AA;

Query Match 100.0%; Score 31; DB 17; Length 119;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYYMN 5
 |||||
 Db 29 dyyrn 33

RESULT 9
 AAY33425
 ID AAY33425 standard; Protein; 119 AA.
 AC AAY33425;
 XX
 XX 13-DEC-1999 (first entry)
 DT
 DE Mouse antibody MAK heavy chain VH region protein fragment.
 DE
 KW Murine; antibody; MAK; heavy chain; VH region; alpha emitter; therapy;
 KW beta emitter; radioimmunoconjugate; hematopoietic disease; solid tumor;
 KW metastasis; inflammatory disease; chemotherapy; irradiation.
 XX
 OS Mus sp.
 XX
 PN DE19813687-A1.
 XX
 PD 30-SEP-1999.
 XX
 PF 27-MAR-1998; 98DE-1013687.
 XX
 PR 27-MAR-1998; 98DE-1013687.
 XX
 PA (BENE/) BENES I F.
 PA (BOSS/) BOSSLET K.
 XX
 PI Benes IF, Bosslet K, Maecke HR;
 XX
 PS WPI; 1999-541798/46.
 DR N-PSDB; AA223369.
 XX
 PT New radioimmunoconjugate, useful for treating hematopoietic diseases,
 PT solid tumors and their metastases and inflammatory diseases -
 XX
 PS Example 1; Page 6-7; 12pp; German.

This invention describes a novel radioimmunoconjugate comprising an alpha
 or beta emitter other than iodine, coupled to an antibody without using a
 complexing agent. The conjugate is especially useful for therapy of
 hematopoietic diseases, as well as solid tumors and their metastases and
 inflammatory diseases, optionally in combination with chemotherapy.
 preferably as a substitute for high-dose chemotherapy and/or total
 body irradiation. The conjugate is more stable than prior art directly
 coupled conjugates and does not elicit an immune response to a
 complexing agent. This sequence represents a fragment of the murine MAK
 antibody heavy chain VH region which is used in the method of the

CC invention.
 XX Sequence 119 AA;
 SQ

Query Match 100.0%; Score 31; DB 20; Length 119;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYYMN 5
 |||||
 Db 29 dyyrn 33

RESULT 10
 AAY51368
 ID AAY51368 standard; Protein; 119 AA.
 AC AAY51368;
 XX
 XX 27-APR-2000 (first entry)
 DT
 DE Mouse monoclonal antibody VH chain protein fragment.
 DE
 KW Variable region; heavy chain; monoclonal antibody; VH region; murine;
 KW radioimmunoconjugate; anticancer; cytostatic; antineoplastic; tumor;
 KW chemotherapy; radiotherapy; treatment; hematopoietic disease; carcinoma;
 KW metastasis; inflammatory disease; leukemia; pemphigus; bone marrow.
 XX
 OS Mus sp.
 XX
 PN EP972528-A2.
 XX
 PD 19-JAN-2000.
 XX
 PF 25-MAR-1999; 99EP-0106013.
 XX
 PR 27-MAR-1998; 98DE-1013687.
 PR 15-MAR-1999; 99DE-1011329.
 XX
 PA (BENE/) BENES I F.
 PA (BOSS/) BOSSLET K.
 XX
 PI Benes IF, Bosslet K;
 XX
 DR WPI; 2000-138524/13.
 DR N-PSDB; AA288540.
 XX
 PT Radioimmunoconjugates useful for treating hematopoietic diseases, solid
 PT tumors, tumor metastases and inflammatory diseases comprise an alpha or
 PT beta emitter coupled to an antibody -
 XX
 PS Example 1; Page 11-12; 18pp; German.

This invention describes novel radioimmunoconjugates (I), in which an
 alpha or beta emitter (II and III) is stably coupled to an antibody (IV)
 without using a complexing agent, provided that the radioisotope is not
 iodine. The conjugate of the invention have anticancer, cytostatic and
 antineoplastic activity. (I) are useful, either alone or in combination
 with chemotherapy or radiotherapy, for treating hematopoietic diseases,
 solid tumors, tumor metastases and inflammatory diseases, especially
 malignant hematopoietic diseases such as acute and chronic myeloid
 leukemias, malignant pemphigus (optionally in combination with bone
 marrow transplantation), or preferably bone marrow metastases. (I) are
 particularly useful for treating carcinomas of the prostate, lung,
 pancreas, stomach, liver, colon, rectum, kidney, testicle, ovary, muscle,
 bone, bladder, throat, nose and ear, lymphomas, bone marrow depletion
 prior to transplantation, or for treating diseases in which bone marrow
 conditioning is carried out. (I) may be used in combination with known
 ligands specific for lymphocyte antigens such as CD19, CD20, CD22, HLA2
 and HLA DR 10beta. (I) elicit no immune response to complexing agents.
 This sequence represents the variable region heavy chain fragment of a
 mouse monoclonal antibody which is used to illustrate the method of the

CC invention.
XX Sequence 119 AA;
SQ

Query Match 100.0%; Score 31; DB 21; Length 119;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYYMN 5
Db 29 dyyrn 33

RESULT 11
AAR74941
ID AAR74941 standard; peptide; 122 AA.

XX AC AAR74941;

XX DT 19-JAN-1996 (first entry)

XX DE Immunoglobulin heavy chain of anti-idiotypic antibody against human
XX DE anticancer antibody.

XX KW Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin;
XX KW complementarity determining region.

XX OS Mus sp.

XX FH Key Location/Qualifiers
XX FT Region 31..35
XX FT /label= CDR1
XX FT Region 50..68
XX FT /label= CDR2
XX FT Region 101..111
XX FT /label= CDR3

XX PN JP07101999-A.

XX PD 18-APR-1995.

XX PF 06-OCT-1993; 93JP-0272950.

XX PR 06-OCT-1993; 93JP-0272950.

XX PA (HAGI/) HAGIWARA Y.

XX PX WPI; 1995-182987/24.

XX Novel anti-idiotypic antibody against a human anticancer monoclonal
XX antibody - and DNA sequences encoding the antibody, useful in
XX pharmacology, medicine and biochemical fields.

XX PS Claim 3; Page 2; 28pp; Japanese.

XX CC AAR74940-R74943 are possible heavy chains of a new anti-idiotypic
XX antibody against a human anticancer monoclonal antibody. This antibody
XX contains in its heavy chain 3 complementarity determining regions CDR1
XX (AAR74929-R74931) CDR2 (AAR74932-R74935) and CDR3 (AAR74936-R74939),
XX this is also true of the light chain which has its own CDR1
XX (AAR74944-R74946 and AAR85774), CDR2 (AAR74947-R74949) and CDR3
XX (AAR74950-R74954). The antibody and DNA encoding it are useful in
XX pharmacological, medical and biochemical fields.

XX SQ Sequence 122 AA;

Query Match 100.0%; Score 31; DB 16; Length 122;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYYMN 5

Db 31 dyyrn 35

RESULT 12

AAR74942
ID AAR74942 standard; peptide; 122 AA.

XX AC AAR74942;

XX DT 19-JAN-1996 (first entry)

XX DE Immunoglobulin heavy chain of anti-idiotypic antibody against human
XX DE anticancer antibody.

XX KW Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin;
XX KW complementarity determining region.

XX OS Mus sp.

XX FH Key Location/Qualifiers
XX FT Region 31..35
XX FT /label= CDR1
XX FT Region 50..68
XX FT /label= CDR2
XX FT Region 101..111
XX FT /label= CDR3

XX PN JP07101999-A.

XX PD 18-APR-1995.

XX PF 06-OCT-1993; 93JP-0272950.

XX PR 06-OCT-1993; 93JP-0272950.

XX PA (HAGI/) HAGIWARA Y.

XX PX WPI; 1995-182987/24.

XX Novel anti-idiotypic antibody against a human anticancer monoclonal
XX antibody - and DNA sequences encoding the antibody, useful in
XX pharmacology, medicine and biochemical fields.

XX PS Claim 4; Page 2; 28pp; Japanese.

XX CC AAR74940-R74943 are possible heavy chains of a new anti-idiotypic
XX antibody against a human anticancer monoclonal antibody. This antibody
XX contains in its heavy chain 3 complementarity determining regions CDR1
XX (AAR74929-R74931) CDR2 (AAR74932-R74935) and CDR3 (AAR74936-R74939),
XX this is also true of the light chain which has its own CDR1
XX (AAR74944-R74946 and AAR85774), CDR2 (AAR74947-R74949) and CDR3
XX (AAR74950-R74954). The antibody and DNA encoding it are useful in
XX pharmacological, medical and biochemical fields.

XX SQ Sequence 122 AA;

Query Match 100.0%; Score 31; DB 16; Length 122;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYYMN 5

Db 31 dyyrn 35

RESULT 13

AAR74963
ID AAR74963 standard; Protein; 138 AA.

XX AC AAR74963;

Qy 1 DYYMN 5

DT 02-FEB-1995 (first entry)
 XX Anti-idiotypic antibody Idio27 clone 27GA5.
 DE Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin;
 KW complementarity determining region.
 XX Mus sp.

XX Key Location/Qualifiers
 FH Peptide 1..10
 FT /label= signal_peptide

XX JP07101999-A.
 XX 18-APR-1995.
 XX 06-OCT-1993; 93JP-0272950.
 XX 06-OCT-1993; 93JP-0272950.
 XX (HAGI/) HAGIWARA Y.
 XX WPI: 1995-182987/24.
 XX N-PSDB; AAQ90428.

Novel anti-idiotypic antibody against an human anticancer monoclonal antibody - and DNA sequences encoding the antibody, useful in pharmacology, medicine and biochemical fields.

Example 5; Page 16; 28pp; Japanese.

CC AAR74960-R74969 are clones of the anti-idiotypic antibodies Idio3,
 CC Idio17, Idio20, Idio27 and Idio33 against a human anticancer monoclonal
 CC antibody. These antibodies and DNA encoding them are useful in
 CC pharmacological, medical and biochemical fields of research.

XX Sequence 138 AA;

Query Match 100.0%; Score 31; DB 16; Length 138;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5
 Db 41 dyymin 45

RESULT 14
 AAR20790
 ID AAR20790 standard; Protein; 140 AA.
 AC AAR20790;
 XX 19-MAY-1992 (first entry)
 DE Unprocessed variable region of heavy chain of A5B7 antibody.
 XX murine monoclonal antibody; MAb; VH domain; humanised antibody; CEA;
 KW complementarity determining region.
 XX Mus musculus.

XX Key Location/Qualifiers
 FH Cleavage-site 19..20
 FT /note= "putative signal peptide cleavage site"

XX WO9201059-A.
 XX 23-JAN-1992.
 XX 05-JUL-1991; 91WO-GB01108.

XX 05-JUL-1991; 91WO-GB01108.
 PR 05-JUL-1990; 90GB-0014932.
 PR 21-DEC-1990; 90WO-GB02017.
 XX (CELL-) CELLTech LTD.
 XX Adair JR, Bodmer MW, Mountain A, Owens RJ;
 XX WPI: 1992-056874/07.
 DR N-PSDB; AAQ20984.
 XX New CDR-grafted anti carcinoembryonic antigen antibodies - useful
 PT in therapy and diagnosis of carcinoma
 XX Example 1; Fig 1; 70pp; English.

CC The A5B7 MAB is a mouse MAB of the type IgG1-kappa raised against
 CC CEA which had been denatured by heating to 85 degrees C for 35
 CC minutes. The MAB has been extensively studied by Harwood et al.
 CC (Br. J. Cancer, 54, 75-82, 1986). A cDNA library was prepared from
 CC polyA RNA isolated from the A5B7 hybridoma cell line. A probe
 CC complementary to mouse heavy chain constant region was used to
 CC identify clone PBG1 containing the complete leader, variable and
 CC constant regions of the heavy chain. The amino acid sequence
 CC predicted from the sequence encoding the unprocessed variable
 CC region is given here.

XX Sequence 140 AA;

Query Match 100.0%; Score 31; DB 13; Length 140;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5
 Db 50 dyymin 54

RESULT 15
 AAR30431
 ID AAR30431 standard; Protein; 141 AA.

AC AAR30431;

XX 03-FEB-1993 (first entry)

XX A5B7 antibody heavy chain sequence.

XX humanised antibody; chimaeric; carcino-embryonic antigen; therapy;
 KW diagnosis; carcinomas; CDR; IgG; human; murine; ss.

XX Chimaeric.

XX WO9201059-A.

XX 23-JAN-1992.

XX 05-JUL-1991; 91WO-GB01108.

XX 05-JUL-1991; 91WO-GB01108.

PR 05-JUL-1990; 90GB-0014932.

XX 21-DEC-1990; 90WO-GB02017.

XX (CELL-) CELLTech LTD.

XX Adair JR, Bodmer MW, Mountain A, Owens RJ;

XX WPI: 1992-284316/34.

XX N-PSDB; AAQ27351.

XX Humanised antibody molecules - comprising murine and human regions,
 PT

PT specific for carcino-embryonic antigen, useful for diagnosis and
therapy
XX
PS
XX Example 1; Figure 1; 71pp; English.
XX
CC This sequence represents the A5B7 monoclonal antibody heavy chain.
CC It was decoded from the cDNA (AAQ27351). Sequence analysis confirmed
CC A5B7 to be an IgG1 K antibody.
XX
SQ Sequence 141 AA;

Query Match 100.0%; Score 31; DB 13; Length 141;
Best Local Similarity 100.0%; Pred. NO. 30;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DYYMN 5
| | | | |
Db 50 dyymn 54

Search completed: June 28, 2001, 16:14:37
Job time: 1325 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2001, 16:01:14 ; Search time 138.34 Seconds
(without alignments)
0.728 Million cell updates/sec

Title: US-09-724-406-20
Perfect score: 31
Sequence: 1 DYMN 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	5	1	US-08-318-970B-2
2	31	100.0	5	4	US-09-280-028-6
3	31	100.0	119	1	US-08-459-310-2
4	31	100.0	119	1	US-08-459-310-12
5	31	100.0	119	2	US-08-308-494A-9
6	31	100.0	119	4	US-09-280-028-2
7	31	100.0	128	1	US-08-202-047-21
8	31	100.0	128	3	US-08-964-690-21
9	31	100.0	140	2	US-08-449-287-4
10	31	100.0	146	2	US-08-449-287-10
11	31	100.0	146	2	US-08-449-287-12
12	28	90.3	30	3	US-08-433-522A-22
13	28	90.3	30	3	US-09-135-166-22
14	28	90.3	31	3	US-08-433-522A-23
15	28	90.3	31	3	US-09-135-166-23
16	28	90.3	499	5	PCT-US95-01806-2
17	28	90.3	499	5	PCT-US95-01806-4
18	28	90.3	567	3	US-08-646-273-19
19	28	90.3	703	3	US-08-646-273-25
20	28	90.3	703	3	US-08-646-273-23
21	28	90.3	753	3	US-08-646-273-36
22	28	90.3	754	3	US-08-646-273-30
23	28	90.3	758	1	US-08-289-112-2
24	28	90.3	772	1	US-08-258-639A-2
25	28	90.3	772	2	US-08-900-931-2
26	28	90.3	772	5	PCT-US95-07391A-2
27	28	90.3	787	1	US-08-574-763-2

28	28	90.3	792	3	US-08-433-522A-8	Sequence 8, Appli
29	28	90.3	792	3	US-09-135-166-8	Sequence 8, Appli
30	28	90.3	793	3	US-08-433-522A-10	Sequence 10, Appli
31	28	90.3	793	3	US-09-135-166-10	Sequence 10, Appli
32	28	90.3	797	3	US-08-433-522A-2	Sequence 2, Appli
33	28	90.3	797	3	US-08-433-522A-4	Sequence 2, Appli
34	28	90.3	797	3	US-08-433-522A-6	Sequence 4, Appli
35	28	90.3	797	3	US-09-135-166-2	Sequence 2, Appli
36	28	90.3	797	3	US-09-135-166-4	Sequence 2, Appli
37	28	90.3	797	3	US-09-135-166-6	Sequence 2, Appli
38	27	87.1	138	3	US-08-603-024-2	Sequence 2, Appli
39	27	87.1	139	1	US-08-253-877C-8	Sequence 19, Appli
40	27	87.1	139	1	US-08-253-877C-19	Sequence 19, Appli
41	27	87.1	139	2	US-08-452-164A-8	Sequence 19, Appli
42	27	87.1	139	2	US-08-452-164A-19	Sequence 18, Appli
43	27	87.1	139	3	US-08-603-024-18	Sequence 7, Appli
44	27	87.1	246	1	US-08-257-341-7	Sequence 4, Appli
45	27	87.1	252	1	US-08-461-838-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-318-970B-2
; Sequence 2, Application US/08318970B
; Patent No. 5589573
; GENERAL INFORMATION:
; APPLICANT: Hideaki HAGIWARA, et al.
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF ANTI-IDIOTYPIC ANTIBODIES AGAINST ANTI-CANCER HUMAN MONOCLONAL ANTIBODY
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Office of Sherman and Shalloway
; STREET: 413 N. Washington Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: Dell System 210; Intel 80 285 Microprocessor
; OPERATING SYSTEM: MS DOS 3.3
; SOFTWARE: Word Perfect, Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,970B
; FILING DATE: October 6, 1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Richard A. Steinberg
; REGISTRATION NUMBER: 26,588
; REFERENCE/DOCKET NUMBER: S-2371
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 549-2282
; TELEFAX: (703) 836-0106
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: H-CDRI-2
; OTHER INFORMATION: hypervariable region
US-08-318-970B-2

Query Match 100.0%; Score 31; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYMN 5

Fri Jun 29 08:04:43 2001

us-09-724-406-20.ra1

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Db 1 DXYMN 5
|||||
REFERENCE/DOCKET NUMBER: 02481.1317-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-459-310-2

Query Match 100.0%; Score 31; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXYMN 5
|||||
Db 29 DXYMN 33
|||||

RESULT 4
US-08-459-310-12
; Sequence 12, Application US/08459310
; Patent No. 5645817
; GENERAL INFORMATION:
; APPLICANT: Seemann, Gerhard
; APPLICANT: Bosslet, Klaus
; TITLE OF INVENTION: Granulocyte-Binding Antibody Constructs,
; TITLE OF INVENTION: Their Preparation and Use
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,310
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/100,963
; FILING DATE: 03-AUG-1993
; APPLICATION NUMBER: DE P 422 58 53.7
; FILING DATE: 05-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Wadler, Linda A.
; REGISTRATION NUMBER: 33,218
; REFERENCE/DOCKET NUMBER: 02481.1317-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-459-310-12

Query Match 100.0%; Score 31; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09-280-028-6
; Sequence 6, Application US/09280028
; Patent No. 6241961
; GENERAL INFORMATION:
; APPLICANT: BENES, IVAN FRIEDRICH
; APPLICANT: BOSSLET, KLAUS
; TITLE OF INVENTION: RADIOIMMUNO CONJUGATES FOR USE IN HUMAN THERAPY AND
; TITLE OF INVENTION: METHOD FOR THEIR PREPARATION
; FILE REFERENCE: BENES
; CURRENT APPLICATION NUMBER: US/09/280,028
; CURRENT FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 199 11 329.7
; EARLIER FILING DATE: 1999-03-15
; EARLIER APPLICATION NUMBER: 198 13 687.0
; EARLIER FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-280-028-6

Query Match 100.0%; Score 31; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXYMN 5
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Db 1 DXYMN 5
|||||

RESULT 3
US-08-459-310-2
; Sequence 2, Application US/08459310
; Patent No. 5645817
; GENERAL INFORMATION:
; APPLICANT: Seemann, Gerhard
; APPLICANT: Bosslet, Klaus
; TITLE OF INVENTION: Granulocyte-Binding Antibody Constructs,
; TITLE OF INVENTION: Their Preparation and Use
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,310
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/100,963
; FILING DATE: 03-AUG-1993
; APPLICATION NUMBER: DE P 422 58 53.7
; FILING DATE: 05-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Wadler, Linda A.
; REGISTRATION NUMBER: 33,218
```

QY 1 DYMN 5
Db 29 DYMN 33

RESULT 5
US-08-308-494A-9
; Sequence 9, Application US/08308494A
; Patent No. 595083
; GENERAL INFORMATION:
; APPLICANT: Bosslet, Klaus
; APPLICANT: Seeman, Gerhard
; TITLE OF INVENTION: Tetraivalent Bispecific Receptors, The
; TITLE OF INVENTION: Preparation and Use thereof
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/308,494A
; FILING DATE: 21-SEP-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/891,739
; FILING DATE: 01-JUN-1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P4118120.4
; FILING DATE: 03-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Kulik, David J.
; REGISTRATION NUMBER: 36,576
; REFERENCE/DOCKET NUMBER: 05552-1186-02000
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-308-494A-9

Query Match 100.0%; Score 31; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYMN 5
Db 29 DYMN 33

RESULT 6
US-09-280-028-2
; Sequence 2, Application US/09280028
; Patent No. 6241961
; GENERAL INFORMATION:
; APPLICANT: BENES, IVAN FRIEDRICH
; APPLICANT: BOSSLET, KLAUS

; TITLE OF INVENTION: RADIOIMMUNO CONJUGATES FOR USE IN HUMAN THERAPY AND
; FILE REFERENCE: BENES
; CURRENT APPLICATION NUMBER: US/09/280,028
; CURRENT FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 199 11 329.7
; EARLIER FILING DATE: 1999-03-15
; EARLIER APPLICATION NUMBER: 198 13 687.0
; EARLIER FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-280-028-2

Query Match 100.0%; Score 31; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYMN 5
Db 29 DYMN 33

RESULT 7
US-08-202-047-21
; Sequence 21, Application US/08202047
; Patent No. 5800815
; GENERAL INFORMATION:
; APPLICANT: CHESNUT, Robert W.
; APPLICANT: POLLEY, Margaret J.
; APPLICANT: PAULSON, James C.
; APPLICANT: JONES, S. Tarran
; APPLICANT: SALDANHA, Jose W.
; APPLICANT: BENDIG, Mary M.
; TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,047
; FILING DATE: 25-FEB-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14137-77
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1...28

OTHER INFORMATION: /label= MOUSE_IIA
US-08-202-047-21

Query Match 100.0%; Score 31; DB 1; Length 128;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYYMN 5
|
|
|
|
Db 31 DYYMN 35

RESULT 8
US-08-964-690-21
; Sequence 21, Application US/08964690
; Patent No. 6033667
; GENERAL INFORMATION:
; APPLICANT: CHESNUT, Robert W.
; APPLICANT: POLLEY, Margaret J.
; APPLICANT: PAULSON, James C.
; APPLICANT: JONES, S. Tarran
; APPLICANT: SALDANHA, Jose W.
; APPLICANT: BENDIG, Mary M.
; TITLE OF INVENTION: Antibodies to p-selectin and Their Uses
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/964,690
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,047
; FILING DATE: 25-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14137-77
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..128
; OTHER INFORMATION: /label= MOUSE_IIA
US-08-964-690-21

Query Match 100.0%; Score 31; DB 3; Length 128;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYYMN 5
|
|
|
|
Db 31 DYYMN 35

RESULT 9
US-08-449-287-4
; Sequence 4, Application US/08449287
; Patent No. 5877293
; GENERAL INFORMATION:
; APPLICANT: ADAIR, John Robert
; APPLICANT: BODMER, Mark William
; APPLICANT: MOUNTAIN, Andrew
; APPLICANT: OWENS, Raymond John
; TITLE OF INVENTION: CDR Grafted Anti-CEA Antibodies and
; TITLE OF INVENTION: Their Production
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,287
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/154,389
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT GB91/01108
; FILING DATE: 05-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9014932.9
; FILING DATE: 05-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT GB90/02017
; FILING DATE: 21-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 40283/110 CARA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-449-287-4

Query Match 100.0%; Score 31; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYYMN 5
|
|
|
|
Db 50 DYYMN 54

RESULT 10
US-08-449-287-10
; Sequence 10, Application US/08449287
; Patent No. 5877293
; GENERAL INFORMATION:
; APPLICANT: ADAIR, John Robert

APPLICANT: BODMER, Mark William
APPLICANT: MOUNTAIN, Andrew
APPLICANT: OWENS, Raymond John
TITLE OF INVENTION: CDR Grafted Anti-CEA Antibodies and
THEIR PRODUCTION
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,287
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/154,389
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT GB91/01108
FILING DATE: 05-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9014932.9
FILING DATE: 05-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT GB90/02017
FILING DATE: 21-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 40283/110 CARA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-449-287-10

Query Match 100.0%; Score 31; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5
Db 50 DYYMN 54

RESULT 11
US-08-449-287-12
Sequence 12, Application US/08449287
Patent No. 5877293
GENERAL INFORMATION:
APPLICANT: ADAIR, John Robert
APPLICANT: BODMER, Mark William
APPLICANT: MOUNTAIN, Andrew
APPLICANT: OWENS, Raymond John
TITLE OF INVENTION: CDR Grafted Anti-CEA Antibodies and
THEIR PRODUCTION
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,287
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/154,389
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT GB91/01108
FILING DATE: 05-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9014932.9
FILING DATE: 05-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT GB90/02017
FILING DATE: 21-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 40283/110 CARA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-449-287-12

Query Match 100.0%; Score 31; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5
Db 50 DYYMN 54

RESULT 12
US-08-433-522A-22
Sequence 22, Application US/08433522A
Patent No. 6013514
GENERAL INFORMATION:
APPLICANT: CHONG, Pele
APPLICANT: THOMAS, Wayne
APPLICANT: YANG, Yan Ping
APPLICANT: LOOSMORE, Sheena
APPLICANT: SIA, Dwo Yuan Charles
APPLICANT: KLEIN, Michel
TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6TH Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,522A
; FILING DATE: 12-SEP-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-434 MIS:jb
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-433-522A-22

Query Match 90.3%; Score 28; DB 3; Length 30;
Best Local Similarity 80.0%; Pred. No. 15;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5
| | | : |
DB 26 DYYLN 30

RESULT 13
US-09-135-166-22
; Sequence 22, Application US/09135166
; Patent No. 6083743
; GENERAL INFORMATION:
; APPLICANT: CHONG, Pele
; APPLICANT: THOMAS, Wayne
; APPLICANT: YANG, Yan Ping
; APPLICANT: LOOSMORE, Sheena
; APPLICANT: SIA, Dwo Yuan Charles
; APPLICANT: KLEIN, Michel
; TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6TH Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 12-SEP-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-829 MIS:jb
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 22:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-135-166-22

Query Match 90.3%; Score 28; DB 3; Length 30;
Best Local Similarity 80.0%; Pred. No. 15;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5
| | | : |
DB 26 DYYLN 30

RESULT 14
US-08-433-522A-23
; Sequence 23, Application US/08433522A
; Patent No. 6013514
; GENERAL INFORMATION:
; APPLICANT: CHONG, Pele
; APPLICANT: THOMAS, Wayne
; APPLICANT: YANG, Yan Ping
; APPLICANT: LOOSMORE, Sheena
; APPLICANT: SIA, Dwo Yuan Charles
; APPLICANT: KLEIN, Michel
; TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6TH Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,522A
; FILING DATE: 12-SEP-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-434 MIS:jb
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-433-522A-23

Query Match 90.3%; Score 28; DB 3; Length 31;
Best Local Similarity 80.0%; Pred. No. 15;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5
| | | : |
DB 6 DYYLN 10

RESULT 15
US-09-135-166-23

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; Sequence 23, Application US/09135166
; Patent No. 6083743
; GENERAL INFORMATION:
; APPLICANT: CHONG, Pele
; APPLICANT: THOMAS, Wayne
; APPLICANT: YANG, Yan Ping
; APPLICANT: LOOSMORE, Sheena
; APPLICANT: SIA, Dwo Yuan Charles
; APPLICANT: KLEIN, Michel
; TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6TH Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/135,166
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/433,522
; FILING DATE: 12-SEP-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-829 MIS:jb
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-135-166-23

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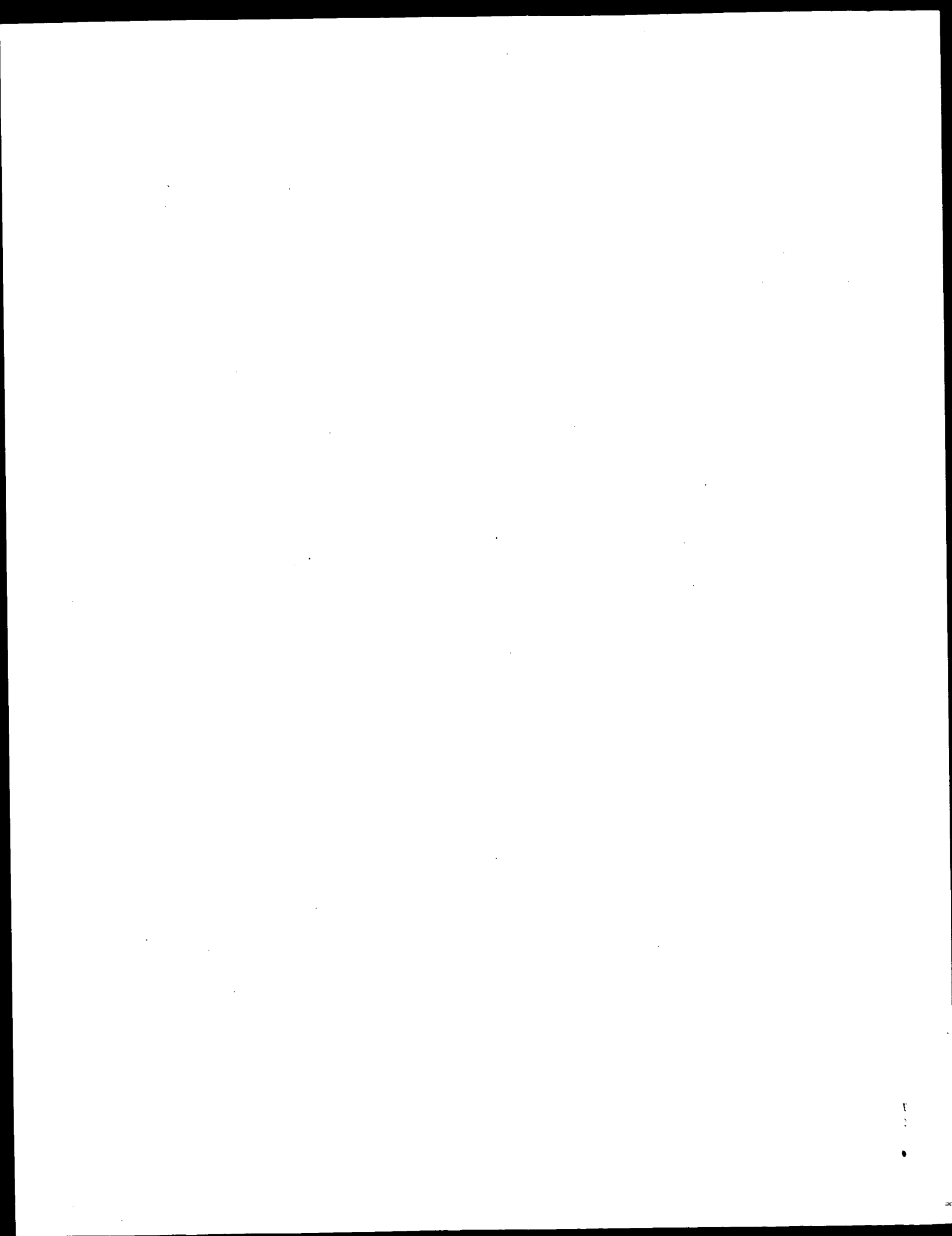
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Best Local Similarity 80.0%; Pred.No.15;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYYMN 5
DB      6 DYYLN 10

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Search completed: June 28, 2001, 16:01:14
Job time: 522 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run On: June 28, 2001, 15:58:44 ; Search time 234.85 Seconds
(without alignments)
1.622 Million cell updates/sec

Title: US-09-724-406-20

Perfect score: 31

Sequence: 1 DRYM 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR68:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	34	2 S46469	Ig heavy chain V r
2	31	100.0	71	2 PH1167	Ig heavy chain V r
3	31	100.0	109	2 PH0973	Ig heavy chain V r
4	31	100.0	112	2 S09957	Ig heavy chain V-D
5	31	100.0	113	2 PH0974	Ig heavy chain V r
6	31	100.0	114	2 PH1027	Ig heavy chain V r
7	31	100.0	118	1 MHMS38	Ig heavy chain V r
8	31	100.0	121	2 E30502	Ig heavy chain V r
9	31	100.0	122	2 S20642	Ig heavy chain V r
10	31	100.0	124	2 PT0388	Ig heavy chain V r
11	31	100.0	263	2 C64339	hypothetical prote
12	31	100.0	672	2 E72391	beta-D-galactosida
13	28	90.3	107	2 PL0241	Ig heavy chain V r
14	28	90.3	107	2 S05116	Ig heavy chain V r
15	28	90.3	132	2 H96708	hypothetical prote
16	28	90.3	149	2 D82889	hypothetical prote
17	28	90.3	221	2 T32048	transcription regu
18	28	90.3	223	1 A41965	transcription regu
19	28	90.3	223	1 H85686	transcription regu
20	28	90.3	224	1 R85687	transcription regu
21	28	90.3	250	2 S28474	rfr1 protein - Vib
22	28	90.3	271	2 F82346	lipopolysaccharide
23	28	90.3	282	2 T06973	probable protoclo
24	28	90.3	286	1 JQ2154	frxC protein - Ple
25	28	90.3	286	1 S25620	frxC protein - Syn
26	28	90.3	290	2 S73108	protechlorophyllid
27	28	90.3	294	2 E86900	transcription regu
28	28	90.3	311	2 S78833	protechlorophyllid
29	28	90.3	341	2 T25051	hypothetical prote

ALIGNMENTS

RESULT 1

S46469

Ig heavy chain V region (DA-5) - human

C:Species: Homo sapiens (man)

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000

C:Accession: S46469

R:Cook, G.P.; Tomlinson, I.M.; Walter, G.; Riethman, H.; Carter, N.P.; Buluweila, L.; Nature Genet. 7, 162-168, 1994

A:Title: A map of the human immunoglobulin V(H) locus completed by analysis of the te

A:Reference number: S46460; MUID:95004581

A:Accession: S46469

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-34 <COO>

A:Cross-references: EMBL:Z29981; NID:G505463; PIDN:CAA82871.1; PID:G1335180

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

Query Match 100.0%; Score 31; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRYM 5

Db 4 DRYM 8

RESULT 2

PH1167

Ig heavy chain V region (clone 14C.2B) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PH1167

R:Schitteck, B.; Rajewsky, K.

J. Exp. Med. 176, 427-438, 1992

A:Title: Natural occurrence and origin of somatically mutated memory B cells in mice.

A:Reference number: PH1105; MUID:92364545

A:Accession: PH1167

A:Molecule type: DNA

A:Residues: 1-71 <SCH>

A:Experimental source: B cell

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

Query Match 100.0%; Score 31; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRYM 5

Db 4 DRYM 8

Db 4 DYYMN 8

RESULT 3

Ig heavy chain V region (clone 17s-cl) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PH0973
 R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
 J. Exp. Med. 176, 761-779, 1992
 A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell autoantibodies
 A:Reference number: PH0971; MUID:92381444
 A:Accession: PH0973
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-109 <TIL>
 A:Experimental source: B cell, strain [NZB x NZWJF1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 109;
 Best Local Similarity 100.0%; Pred. No. 9;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5

Db 31 DYYMN 35

RESULT 4

Ig heavy chain V-D-J region (106-10E) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 23-Jul-1999
 C:Accession: S09957
 R:Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
 Eur. J. Immunol. 20, 771-777, 1990
 A:Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodies
 A:Reference number: S09955; MUID:90269328
 A:Accession: S09957
 A:Molecule type: mRNA
 A:Residues: 1-112 <REL>
 A:Cross-references: EMBL:X51845; NID:g55244; PIDN:CRA36138.1; PID:g930213
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 112;
 Best Local Similarity 100.0%; Pred. No. 9.3;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5

Db 31 DYYMN 35

RESULT 5

Ig heavy chain V region (clone 165.60) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PH0974
 R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
 J. Exp. Med. 176, 761-779, 1992
 A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell autoantibodies
 A:Reference number: PH0971; MUID:92381444
 A:Accession: PH0974
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA

A:Residues: 1-113 <TIL>

A:Experimental source: B cell, strain [NZB x NZWJF1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 113;
 Best Local Similarity 100.0%; Pred. No. 9.3;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5

Db 31 DYYMN 35

RESULT 6

Ig heavy chain V region (clone 163-c2) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PH1027
 R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
 J. Exp. Med. 176, 761-779, 1992
 A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell autoantibodies
 A:Reference number: PH0971; MUID:92381444
 A:Accession: PH1027
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-114 <TIL>
 A:Experimental source: B cell, strain [NZB x NZWJF1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-100/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 114;
 Best Local Similarity 100.0%; Pred. No. 9.4;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5

Db 31 DYYMN 35

RESULT 7

Ig heavy chain V region (AC38 205.12) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 30-May-1997
 C:Accession: A02040
 R:Dildrop, R.; Bovens, J.; Siekevitz, M.; Beyreuther, K.; Rajewsky, K.
 EMBO J. 3, 517-523, 1984
 A:Title: A V region determinant (idiotope) expressed at high frequency in B lymphocytes
 A:Reference number: A91000; MUID:84182519
 A:Accession: A02040
 A:Molecule type: protein
 A:Residues: 1-118 <DIL>

A:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-98/Region: V segment
 F:15-98/Domain: immunoglobulin homology <IMM>
 F:99-104/Region: D segment
 F:105-118/Region: J segment
 F:22-96/Disulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 1; Length 118;
 Best Local Similarity 100.0%; Pred. No. 9.8;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5

Db 11111

Db 31 DYYMN 35

RESULT 8

Ig heavy chain V region (D42) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 23-Jul-1999

C:Accession: E30502

R:Eilat, D.; Webster, D.M.; Rees, A.R.

J. Immunol. 141, 1745-1753, 1988

A:Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 mice

A:Reference number: A30502; MUID:88315787

A:Accession: E30502

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-121 <EIL>

A:Cross-references: GB:M21909; NID:9195587; PIDN:AAA38360.1; PID:9195588

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-100/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 100.0%; Score 31; DB 2; Length 121;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5

|||||

Db 31 DYYMN 35

RESULT 9

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999

C:Accession: S20642

R:Losman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.

submitted to the EMBL Data Library, February 1992

A:Description: Relationships among antinuclear antibodies from autoimmune MRL mice reacted

A:Reference number: S20639

A:Accession: S20642

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-122 <LOS>

A:Cross-references: EMBL:X64997; NID:952604; PIDN:CAA46130.1; PID:952605

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-100/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 100.0%; Score 31; DB 2; Length 122;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5

|||||

Db 31 DYYMN 35

RESULT 10

PT0388

Ig heavy chain V region (S107/VH11 group 3-23) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C:Accession: PT0388

R:Behar, S.M.; Lustgarten, D.L.; Corbet, S.; Scharff, M.D.

J. Exp. Med. 173, 731-741, 1991

A:Title: Characterization of somatically mutated S107 VH11-encoded anti-DNA autoantibodies

A:Reference number: PT0376; MUID:91147903

A:Accession: PT0388

A:Molecule type: DNA

A:Residues: 1-124 <BEH>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-100/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 100.0%; Score 31; DB 2; Length 124;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5

|||||

Db 31 DYYMN 35

RESULT 11

C64339

hypothetical protein MJ0314 - Methanococcus jannaschii

C:Species: Methanococcus jannaschii

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000

C:Accession: C64339

R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak

rson, J.D.; Sadov, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.

Science 273, 1058-1073, 1996

A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese

A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii

A:Reference number: A64300; MUID:96337999

A:Accession: C64339

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-263 <BUL>

A:Cross-references: GB:U67486; GB:L77117; NID:91591031; PIDN:AAB98310.1; PID:91591034

C:Genetics:

A:Map position: FOR293581-294372

A:Start codon: TTG

Query Match

Best Local Similarity 100.0%; Score 31; DB 2; Length 263;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5

|||||

Db 184 DYYMN 188

RESULT 12

E72391

beta-D-galactosidase - Thermotoga maritima (strain MS88)

C:Species: Thermotoga maritima

C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000

C:Accession: E72391

R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic

garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,

C.M.

Nature 399, 323-329, 1999

A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome

A:Reference number: A72200; MUID:99287316

A:Accession: E72391

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-672 <ARN>

A:Cross-references: GB:AE001713; GB:AE000512; NID:94980809; PIDN:AAD35398.1; PID:9498

A:Experimental source: strain MS88

C:Genetics:

A:Gene: TM0310

C:Superfamily: Bacillus beta-galactosidase

Query Match

Best Local Similarity 100.0%; Score 31; DB 2; Length 672;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

us-09-724-406-20.rpr

Fri Jun 29 08:04:44 2001

C:Accession: H96708
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Cressy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719

A:Accession: H96708

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-132 <STO>

A:Cross-references: GB:AE005173; NID:g6553937; PIDN:AAF16601.1; GSPDB:GN00141

C:Genetics:

A:Gene: T26J14.5

A:Map position: 1

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Search completed: June 28, 2001, 15:58:45

Job time: 373 sec

Query Match 90.3%; Score 28; DB 2; Length 132;
 Best Local Similarity 80.0%; Pred. No. 47;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVMN 5

Db 39 DYVLN 43

Db 39 DYVLN 43

Db 39 DYVLN 43

Db 39 DYVLN 43

Db 39 DYVLN 43

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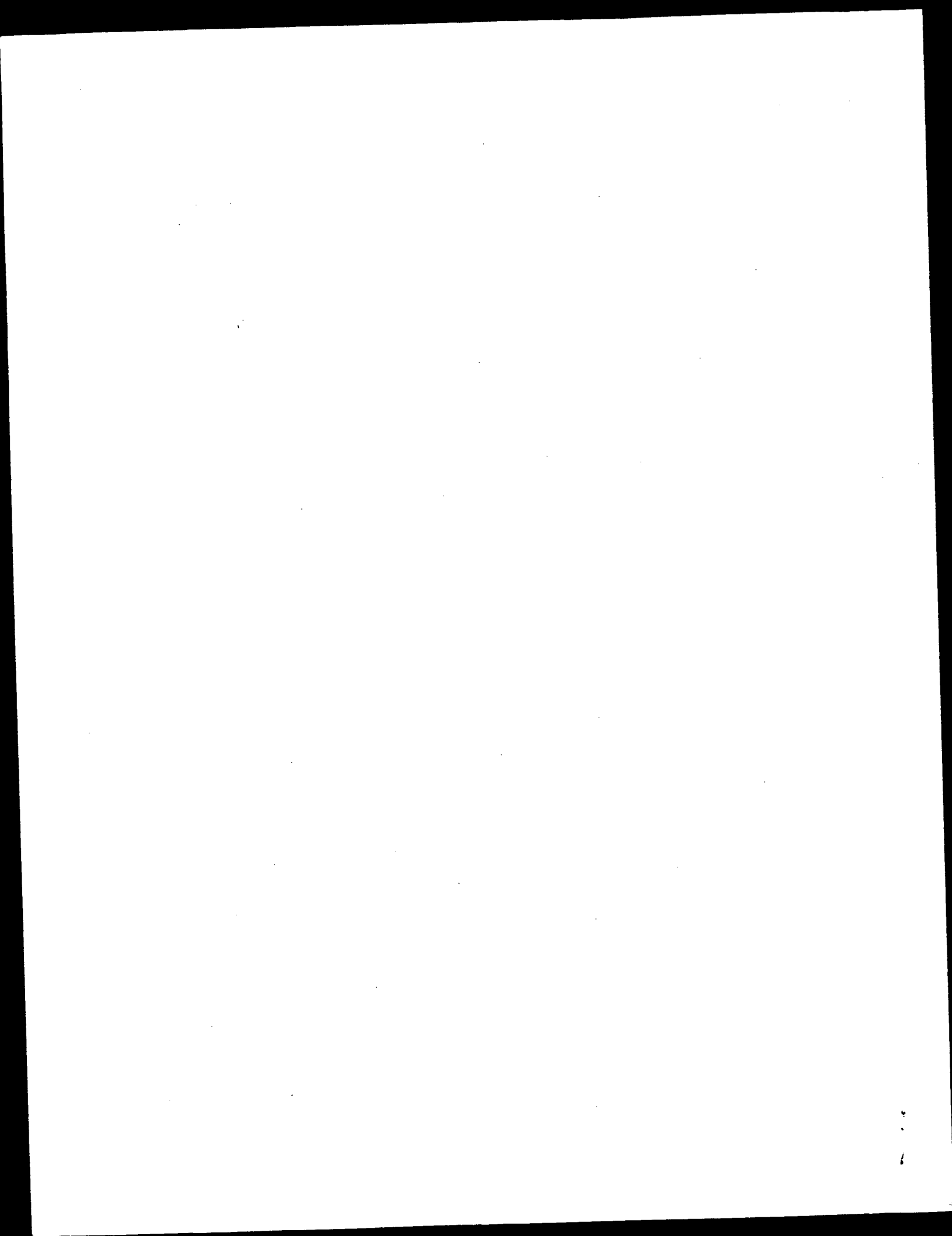
Db 39 DYVLN 43

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Db 39 DYVLN



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OM protein - protein search, using sw model

Run on: June 28, 2001, 15:54:37 ; Search time 105.36 Seconds
(without alignments)
1.626 Million cell updates/sec

Title: US-09-724-406-20
Perfect score: 31
Sequence: 1 DYMN 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	31	100.0	118	1 HV51_MOUSE	P06330 mus musculus
2	31	100.0	263	1 Y314_METJA	Q57762 methanococcus
3	28	90.3	107	1 YE13_YEAST	P39974 saccharomyc
4	28	90.3	223	1 PHOP_ECOLI	P23836 escherichia
5	28	90.3	224	1 PHOP_SALTY	P14146 salmonella
6	28	90.3	282	1 CHLL_CVAPA	P48110 cyanophora
7	28	90.3	286	1 CHLL_PLEBO	Q00237 plectonema
8	28	90.3	286	1 CHLL_SNP7	P54207 synecocyst
9	28	90.3	288	1 CHLL_SNP3	P28373 synecocyst
10	28	90.3	290	1 CHLL_PORPU	P51187 porphyra pu
11	28	90.3	350	1 Y170_METJA	Q57634 methanococc
12	28	90.3	447	1 MURE_HELPJ	Q921c6 helicobacte
13	28	90.3	456	1 VL2_HPVO7	P36745 human papil
14	28	90.3	561	1 YDDA_ECOLI	P31826 escherichia
15	28	90.3	617	1 ILVD_BUCAP	O51887 buchnera ap
16	28	90.3	651	1 PBF2_HAEIN	P44469 haemophilus
17	28	90.3	739	1 DD15_CAEEL	Q20875 caenorhabdi
18	28	90.3	754	1 ECE1_BOVIN	P42891 bos taurus
19	28	90.3	754	1 ECE1_CAVPO	P42893 cavia porce
20	28	90.3	762	1 ECE1_RAT	P42893 rattus norv
21	28	90.3	765	1 ECE2_HUMAN	O60344 homo sapien
22	28	90.3	766	1 SAK1_SCHPO	P42893 schizosacch
23	28	90.3	770	1 ECE1_HUMAN	P42892 homo sapien
24	28	90.3	787	1 ECE2_BOVIN	Q10711 bos taurus
25	28	90.3	791	1 LOW_CAMJE	O69300 campylobact
26	28	90.3	793	1 D153_HAEIN	O32629 haemophilus
27	28	90.3	795	1 D153_HAEIN	P44935 haemophilus
28	28	90.3	797	1 D151_HAEIN	P46024 haemophilus
29	28	90.3	1104	1 N1R_EMENI	P22944 emericella
30	28	90.3	1165	1 CHS3_YEAST	P29465 saccharomyc
31	28	90.3	1718	1 RPO_SHVX	Q04575 shallot vir
32	27	87.1	213	1 SODF_HELPJ	O92ke6 helicobacte
33	27	87.1	213	1 SODF_HELPJ	P43312 helicobacte

34	27	87.1	300	1 PAL_VESMC	P51528 vespula mac
35	27	87.1	336	1 PAL_VESVU	P49369 vespula vul
36	27	87.1	338	1 GALE_HAEIN	P24325 haemophilus
37	27	87.1	345	1 T2C1_HERAU	P25258 herpetosiph
38	27	87.1	371	1 RIBD_BACAM	P70814 b riboflavi
39	27	87.1	410	1 POK_METFE	P20971 methanother
40	27	87.1	426	1 VA20_VACCC	P20995 vaccinia vi
41	27	87.1	426	1 VA20_VAVR	P33843 variola vir
42	27	87.1	470	1 NRAM_IAHAL	Q07575 influenza a
43	27	87.1	470	1 NRAM_IAHKL	Q07576 influenza a
44	27	87.1	470	1 NRAM_IAHNO	P08326 influenza a
45	27	87.1	470	1 NRAM_IAHNO	Q07580 influenza a

ALIGNMENTS

RESULT 1					
HV51_MOUSE					
ID	HV51_MOUSE	STANDARD;	PRT;	118 AA.	
AC	P06330;				
DT	01-JAN-1988 (Rel. 05, Created)				
DT	01-JAN-1988 (Rel. 06, Last sequence update)				
DE	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	IG HEAVY CHAIN V REGION AC38 205.12.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE.				
RX	MEDLINE=84182515; PubMed=6201362;				
RA	Dildrop R., Bovens J., Stekevitz M., Beyreuther K., Rajewsky K.;				
RT	"A V region determinant (idiotope) expressed at high frequency in B lymphocytes is encoded by a large set of antibody structural genes.";				
RL	EMBO J. 3:517-523(1984).				
DR	PIR: A02040; MHMS38				
DR	InterPro: IPR003006; -				
DR	Pfam: PF00047; ig; 1.				
KW	Immunoglobulin V region.				
FT	DOMAIN 1 98				
FT	DOMAIN 99 104				
FT	DOMAIN 105 118				
FT	DISULFID 22 96				
FT	NON_TER 118 118				
SQ	SEQUENCE 118 AA; 12934 MW; 94F7BEB4C762A018 CRC64;				

Query Match 100.0%; Score 31; DB 1; Length 118;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 DYMN 5
Db	31 DYMN 35

RESULT 2

Y314_METJA					
ID	Y314_METJA	STANDARD;	PRT;	263 AA.	
AC	Q57762;				
DT	01-NOV-1997 (Rel. 35, Created)				
DT	01-NOV-1997 (Rel. 35, Last sequence update)				
DE	01-NOV-1997 (Rel. 35, Last annotation update)				
DE	HYPOTHETICAL PROTEIN MJ0314.				
GN	MJ0314.				
OS	Methanococcus jannaschii.				
OC	Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;				
OC	Methanococcus.				
OX	NCBI_TaxID=2190;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=JAL-1 / DSM 2661 / ATCC 43067;				

RA MEDLINE-96337999; PubMed-8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii";
RL Science 273:1058-1073(1996).
CC -1- SIMILARITY: SOME, TO M.JANNASCHII M70398.
CC
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CC
CC EMBL; U67486; AAB98310.1; -
DR TIGR; M70314; -
KW Hypothetical protein.
SQ SEQUENCE 263 RA; 30804 MW; A7520A3BBE0CC5CD CRC64;

Query Match 100.0%; Score 31; DB 1; Length 263;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYMN 5
DB 184 DYMN 188

RESULT 3
YE13_YEAST STANDARD; PRT; 107 AA.
AC P39974;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE HYPOTHETICAL 12.0 KDA PROTEIN IN DLD3 5'REGION.
GN YEL073C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C / AB972;
RA Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R.,
RA Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M.,
RA Chung E., Duncan M., Guzman E., Hartzell G., Hunnicke-Smith S.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C.,
RA Petef F.X., Roberts D., Sehl P., Schramm S., Shogen T., Smith V.,
RA Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.;
RA Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
CC
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CC
CC EMBL; U18795; AAB65014.1; -
DR SGD; S0000799; YEL073C.
KW Hypothetical protein.

SQ SEQUENCE 107 AA; 11960 MW; F5FBA3246A328ABF CRC64;

Query Match 90.3%; Score 28; DB 1; Length 107;
Best Local Similarity 80.0%; Pred. No. 16;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYMN 5
DB 39 DYLN 43

RESULT 4
PHOP_ECOLI STANDARD; PRT; 223 AA.
ID PHOP_ECOLI
AC P23836;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE TRANSCRIPTIONAL REGULATORY PROTEIN PHOP.
GN PHOP.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE-92105017; PubMed-1729240;
RA Kasahara M., Nakata A., Shinagawa H.;
RT "Molecular analysis of the Escherichia coli phoP-phoQ operon";
RL J. Bacteriol. 174:492-498(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-92105016; PubMed-1530848;
RA Groisman E.A., Heffron F., Solomon F.;
RT "Molecular genetic analysis of the Escherichia coli phoP locus";
RL J. Bacteriol. 174:486-491(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE-97426617; PubMed-9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12";
RL Science 277:1453-1474(1997).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE-97061202; PubMed-8905232;
RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiuchi T.;
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 12.7-28.0 min region on the linkage map";
RL DNA Res. 3:137-155(1996).
RN [5]
RP SEQUENCE OF 1-50 FROM N.A.
RC STRAIN-K12;
RX MEDLINE-92104952; PubMed-1729205;
RA He B., Smith J.M., Zalkin H.;
RT "Escherichia coli purB gene: cloning, nucleotide sequence, and
RT regulation by purR";
RL J. Bacteriol. 174:130-136(1992).
RN [6]
RP SEQUENCE OF 1-24 FROM N.A.
RC STRAIN-K12;
RX Green S.M., Drabble W.T.;

Submitted (MAY-1991) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM PHOQ/PHOP
 CC INVOLVED IN THE REGULATION OF ACID PHOSPHATASE.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
 CC -1- PTM: PHOSPHORYLATED BY PHOQ (PROBABLE).
 CC -1- SIMILARITY: THE N-TERMINAL REGION IS SIMILAR TO THAT OF OTHER
 CC REGULATORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS.
 CC -----
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 CC -----
 DR EMBL; D90393; BAA14390.1; -
 DR EMBL; M81433; AAA24377.1; -
 DR EMBL; AE000213; AAC74214.1; -
 DR EMBL; D90748; BAA35952.1; -
 DR EMBL; D90749; BAA35961.1; -
 DR EMBL; M74924; BAA92732.1; -
 DR EMBL; X59307; CAA41997.1; -
 DR PIR; A41965; A41965.
 DR PIR; A41966; A41966.
 DR PIR; S19213; S19213.
 DR HSSP; Q56312; 4TMY.
 DR EC02DBASE; C025.3; 6TH EDITION.
 DR EcoGene; EG10731; phop.
 DR InterPro; IPR001789; -
 DR InterPro; IPR001867; -
 DR Pfam; PF00072; response_reg; 1.
 DR Pfam; PF00486; trans_reg_C; 1.
 DR Sensory transduction; Phosphorylation; Transcription regulation;
 KW DNA-binding; Activator.
 FT MOD_RES 51 51
 FT SEQUENCE 223 AA; 25535 MW; 2EFF27E3923D43EF CRC64;
 SQ
 Query Match 90.3%; Score 28; DB 1; Length 223;
 Best Local Similarity 80.0%; Pred. No. 36;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYYMN 5
 Db 37 DYVLN 41
 |||:|
 RESULT 5
 PHOP_SALTY STANDARD; PRT; 224 AA.
 AC P14146;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE VIRULENCE TRANSCRIPTIONAL REGULATORY PROTEIN PHOP.
 GN PHOP.
 OS Salmonella typhimurium.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 CC NCBI_TaxID=602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 10428;
 RX MEDLINE=89296942; PubMed=2544889;
 RA Miller S.I., Kukral A.M., Mekalanos J.J.;
 RT "A two-component regulatory system (phoP phoQ) controls Salmonella
 RT typhimurium virulence."
 RL Proc. Natl. Acad. Sci. U.S.A. 86:5054-5058(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89386683; PubMed=2674945;
 RA Groisman E.A., Chiao E., Lipps C.J., Heffron F.;

"Salmonella typhimurium phoP virulence gene is a transcriptional
 regulator."
 RL Proc. Natl. Acad. Sci. U.S.A. 86:7077-7081(1989).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SL1344;
 RA Cano D.A., Martinez-Moya M., Casades J., Groisman E.A.,
 RA Garcia-del Portillo F.;
 RT "Attenuation of Salmonella proliferation within host cells mediated by
 RT pathogen virulence regulators."
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM PHOQ/PHOP
 CC WHICH REGULATES THE EXPRESSION OF GENES INVOLVED IN VIRULENCE AND
 CC MACROPHAGE SURVIVAL OF S.TYPHIMURIUM. MAY ACTIVATE PROMOTERS FOR
 CC PAG GENES.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
 CC -1- PTM: PHOSPHORYLATED BY PHOQ (PROBABLE).
 CC -1- SIMILARITY: THE N-TERMINAL REGION IS SIMILAR TO THAT OF OTHER
 CC REGULATORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS.
 CC -----
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 CC -----
 DR EMBL; M24424; AAA27188.1; -
 DR EMBL; M25241; AAA27187.1; -
 DR EMBL; AJ272210; CAB75591.1; -
 DR PIR; A32932; RGEBFT.
 DR HSSP; P03025; 1CDD.
 DR StyGene; SGI0293; phop.
 DR InterPro; IPR001789; -
 DR InterPro; IPR001867; -
 DR Pfam; PF00072; response_reg; 1.
 DR Pfam; PF00486; trans_reg_C; 1.
 KW Sensory transduction; Phosphorylation; Transcription regulation;
 KW DNA-binding; Activator; Virulence.
 FT MOD_RES 52 52
 FT SEQUENCE 224 AA; 25633 MW; 3A90B2FDC328C7B2 CRC64;
 SQ
 Query Match 90.3%; Score 28; DB 1; Length 224;
 Best Local Similarity 80.0%; Pred. No. 36;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYYMN 5
 Db 38 DYVLN 42
 |||:|
 RESULT 6
 CHLL_CYAPA STANDARD; PRT; 282 AA.
 AC P48110;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE PROTOCHLOROPHYLLIDE REDUCTASE IRON-SULFUR ATP-BINDING PROTEIN.
 GN CHLL OR FRXC.
 OS Cyanophora paradoxa.
 OC Cyanelle.
 OC Eukaryota; Glaucocystophyceae; Cyanophoraceae; Cyanophora.
 CC NCBI_TaxID=2762;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-LB555 / PRINGSHEIM;
 RA Stirewalt V.L., Michalowski C.B., Luffelhardt W., Bohnert H.J.,
 RA Bryant D.A.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: NOT KNOWN, PROBABLY INVOLVED IN AN ELECTRON TRANSPORT

CC SYSTEM USED IN CHLOROPHYLL BIOSYNTHESIS.
 CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE NIFH/FRXC FAMILY.
 CC -----
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 CC -----
 CC EMBL; U30821; AAA81316.1; -.
 CC HSSP; P00459; INIP.
 CC Mendel; 7873; CYAPA:chlL;1.
 CC InterPro; IPR000392; -.
 CC Pfam; PF00142; fer4_NifH; 1.
 CC PRINTS; PR00091; NITROGNASEII.
 CC PROSITE; PS00692; NIFH_FRXC_2; 1.
 CC PROSITE; PS00746; NIFH_FRXC_1; 1.
 CC Photosynthesis; Chlorophyll biosynthesis; Cyanelle; ATP-binding;
 KW Iron-sulfur; 4Fe-4S.
 FT NP_BIND 7 14 ATP (POTENTIAL).
 FT METAL 95 95 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
 FT METAL 129 129 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
 SQ SEQUENCE 282 AA; 30847 MW; BC5072D21AE28684 CRC64;
 Query Match 90.3%; Score 28; DB 1; Length 282;
 Best Local Similarity 80.0%; Pred. No. 46;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYYMN 5
 Db 234 DYYLN 238
 RESULT 7
 CHLL_PLEBO STANDARD; PRT; 286 AA.
 ID CHLL_PLEBO
 AC Q00237;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE PROTOCHLOROPHYLLIDE REDUCTASE IRON-SULFUR ATP-BINDING PROTEIN.
 GN CHLL OR FRXC.
 OS Plectonema boryanum.
 OC Bacteria; Cyanobacteria; Oscillatoriales; Plectonema.
 OX NCBI_TaxID=1184;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-IAM M-101;
 RA Fujita Y., Takahashi Y., Shonai F., Ogura Y., Matsubara H.;
 RT "Cloning, nucleotide sequences and differential expression of the nifh
 RT and nifh-like (frxc) genes from the filamentous nitrogen-fixing
 RT cyanobacterium Plectonema boryanum";
 RL Plant Cell Physiol. 32:1093-1106(1991).
 CC -!- FUNCTION: NOT KNOWN, PROBABLY INVOLVED IN AN ELECTRON TRANSPORT
 CC SYSTEM USED IN CHLOROPHYLL BIOSYNTHESIS.
 CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE NIFH/FRXC FAMILY.
 CC -----
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 CC -----
 CC EMBL; D00665; BAA00565.1; -.
 CC PIR; JQ2154; JQ2154.
 CC PIR; S36671; S36671.

DR HSSP; P00459; IN2C.
 DR InterPro; IPR000392; -.
 DR Pfam; PF00142; fer4_NifH; 1.
 DR PRINTS; PR00091; NITROGNASEII.
 DR PROSITE; PS00692; NIFH_FRXC_2; 1.
 DR PROSITE; PS00746; NIFH_FRXC_1; 1.
 KW Photosynthesis; Chlorophyll biosynthesis; ATP-binding; Iron-sulfur;
 KW 4Fe-4S.
 FT NP_BIND 7 14 ATP (BY SIMILARITY).
 FT METAL 95 95 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
 FT METAL 129 129 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
 SQ SEQUENCE 286 AA; 31220 MW; 9E74CE7F4C47EC01 CRC64;
 Query Match 90.3%; Score 28; DB 1; Length 286;
 Best Local Similarity 80.0%; Pred. No. 47;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYYMN 5
 Db 234 DYYLN 238
 RESULT 8
 CHLL_SYNP7 STANDARD; PRT; 286 AA.
 ID CHLL_SYNP7
 AC P54207;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE PROTOCHLOROPHYLLIDE REDUCTASE IRON-SULFUR ATP-BINDING PROTEIN.
 GN CHLL OR FRXC.
 OS Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
 OX NCBI_TaxID=1140;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lieman-Hurwitz J., Ronen-Tarazi M., Gabai C., Hassidim M., Schwarz R.,
 RA Kaplan A.;
 RL Submitted (SEP-1992) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: NOT KNOWN, PROBABLY INVOLVED IN AN ELECTRON TRANSPORT
 CC SYSTEM USED IN CHLOROPHYLL BIOSYNTHESIS.
 CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE NIFH/FRXC FAMILY.
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 CC -----
 CC EMBL; X67694; CAA47923.1; -.
 CC HSSP; P00459; IN2C.
 CC InterPro; IPR000392; -.
 CC Pfam; PF00142; fer4_NifH; 1.
 CC PRINTS; PR00091; NITROGNASEII.
 CC PROSITE; PS00692; NIFH_FRXC_2; 1.
 CC PROSITE; PS00746; NIFH_FRXC_1; 1.
 KW Photosynthesis; Chlorophyll biosynthesis; ATP-binding; Iron-sulfur;
 KW 4Fe-4S.
 FT NP_BIND 7 14 ATP (POTENTIAL).
 FT METAL 95 95 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
 FT METAL 129 129 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
 SQ SEQUENCE 286 AA; 31117 MW; 651121F5CD60A803 CRC64;
 Query Match 90.3%; Score 28; DB 1; Length 286;
 Best Local Similarity 80.0%; Pred. No. 47;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYYMN 5


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OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kierulff A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii.";
RL Science 273:1058-1073(1996).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE UPF0003 FAMILY.
CC
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CC
CC EMBL: U67474; AAB98155.1; -.
CC TIGR: MJ0170; -.
CC InterPro: IPR001880; -.
CC Pfam: PF00924; UPF0003; 1.
CC PROSITE: PS01246; UPF0003; 1.
CC KW Hypothetical protein; Transmembrane.
CC FT TRANSMEM 10 30 POTENTIAL.
CC TRANSMEM 130 150 POTENTIAL.
CC SEQUENCE 350 AA; 39953 MW; 4EA0E5025086E7DF CRC64;

Query Match 90.3%; Score 28; DB 1; Length 350;
Best Local Similarity 80.0%; Pred. No. 59;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVMN 5
DB 313 DYVLN 317

RESULT 12
MURE_HELPJ
ID MURE_HELPJ STANDARD; PRT; 447 AA.
AC Q92JG6;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE UDP-N-ACETYLURAMIDYL-L-GLUTAMATE--2,6-DIAMINOPIMELATE LIGASE
DE (EC 6.3.2.13) (UDP-N-ACETYLURAMIDYL-L-GLUTAMATE--2,6-DIAMINOPIMELATE LIGASE
DE DIAMINOPIMELATE-ADDING ENZYME) (UDP-MURNAC-TRIPETIDE SYNTHETASE).
DE MORE OR JHP1387.
GN Helicobacter pylori J99 (Campylobacter pylori J99).
OS Helicobacter.
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guille B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RA "Genomic sequence comparison of two unrelated isolates of the human

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RT gastric pathogen Helicobacter pylori.";
RL Nature 397:176-180(1999).
CC -1- FUNCTION: CELL WALL FORMATION. DIAMINOPIMELIC ACID ADDING ENZYME
CC (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLURAMIDYL-L-ALANYL-D-
CC GLUTAMATE + MESO-2,6-DIAMINOPIMELATE = ADP + ORTHOPHOSPHATE
CC + UDP-N-ACETYLURAMIDYL-L-ALANYL-D-GLUTAMYL-MESO-2,6-
CC DIAMINOPIMELATE.
CC -1- PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
CC -1- SIMILARITY: BELONGS TO THE MURCDF FAMILY.
CC
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CC
CC EMBL: AF001561; AAD06968.1; -.
CC InterPro: IPR000713; -.
CC Pfam: PF01225; Mur_ligase; 1.
CC KW Peptidoglycan synthesis; Cell wall; Cell division; Ligase;
CC ATP-binding.
CC FT NP_BIND 74 80 ATP (POTENTIAL).
CC SEQUENCE 447 AA; 50660 MW; 639AB9D18F3740BD CRC64;

Query Match 90.3%; Score 28; DB 1; Length 447;
Best Local Similarity 80.0%; Pred. No. 76;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVMN 5
DB 439 DYVLN 443

RESULT 13
VL2_HPV07
ID VL2_HPV07 STANDARD; PRT; 456 AA.
AC P36745;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE MINOR CAPSID PROTEIN L2.
GN L2.
OS Human papillomavirus type 7.
OC Viruses; GSDNA viruses, no RNA stage; Papovaviridae; Papillomavirus.
OX NCBI_TaxID=10620;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94265501; PubMed=8205838;
RA Delli H., Hofmann B.;
RL "Primer-directed sequencing of human papillomavirus types.";
RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).
CC
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CC
CC EMBL: X74463; CAA52480.1; -.
CC FTR: S36588; S36588.
CC InterPro: IPR000784; -.
CC Pfam: PF00513; late-protein_L2; 1.
CC KW Coat protein; Late protein.
CC SEQUENCE 456 AA; 48994 MW; 87C493D2C85E4FEB CRC64;

```


Query Match 90.3%; Score 28; DB 1; Length 456;
Best Local Similarity 80.0%; Pred. No. 78;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5
| | | | |
DB 437 DYYLN 441

RESULT 14
YDDA_ECOLI
ID YDDA_ECOLI STANDARD; PRT; 561 AA.
AC P31826; P76133; P76876;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN IN POOL-HIPA
DE INTERGENIC REGION (CDS102).
GN YDDA.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick J.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=K12;
RX MEDLINE=97251357; PubMed=9097039;
RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
RA Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M.,
RA Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T.,
RA Motomura K., Nakade S., Nakamura Y., Nishimoto H., Nishio Y.,
RA Oshima T., Saito N., Sempel G., Seki Y., Sivasubraman S.,
RA Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C.,
RA Yamamoto Y., Horiuchi T.;
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 28.0-40.1 min region on the linkage map.";
RL DNA Res. 3:363-377(1996).
RN [3]
RP SEQUENCE OF 306-561 FROM N.A.
RX STRAIN=K12;
RX Turlin E., Gasser F., Biville F.;
RL Submitted (MAY-1993) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
(ABC TRANSPORTERS).
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AE000246; AAC74569.1;
CC EMBL: X71917; CAA50732.1; ALT_INIT.
CC EMBL: D90791; BAA15167.1; ALT_INIT.
CC EMBL: D90792; BAA15170.1;
CC PIR: S33468; S33468.
CC EcoGene: EG11742; ydda.
CC InterPro: IPR001617;
CC Pfam: PF00005; ABC_tran; 1.
CC PROSITE: PS00211; ABC_TRANSPORTER; 1.

KW Hypothetical protein; ATP-binding; Transport; Transmembrane.
FT TRANSMEM 4 24 POTENTIAL.
FT TRANSMEM 32 52 POTENTIAL.
FT TRANSMEM 71 91 POTENTIAL.
FT TRANSMEM 152 172 POTENTIAL.
FT TRANSMEM 188 208 POTENTIAL.
FT TRANSMEM 291 311 POTENTIAL.
FT NP_BIND 400 407 ATP (POTENTIAL).
SQ SEQUENCE 561 AA; 64984 MW; 92B47426294413F5 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 561;
Best Local Similarity 80.0%; Pred. No. 97;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5
| | | | |
DB 109 DYYLN 113

RESULT 15
ILVD_BUCAP
ID ILVD_BUCAP STANDARD; PRT; 617 AA.
AC O51887;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE DIHYDROXY-ACID DEHYDRATASE (EC 4.2.1.9) (DAD).
GN ILVD.
OS Buchnera aphidicola (subsp. Schizaphis graminum).
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
OX NCBI_TaxID=98794;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98184963; PubMed=9516544;
RA Clark M.A., Baumann L., Baumann P.;
RT "Sequence analysis of a 34.7-kb DNA segment from the genome of
Buchnera aphidicola (endosymbiont of aphids) containing groEL, dnaA,
the atp operon, gldA, and rho.";
RL Curr. Microbiol. 36:158-163(1998).
CC -1- CATALYTIC ACTIVITY: 2,3-DIHYDROXY-3-METHYLBUTANOATE -> 3-METHYL-2-
OXOBUTANOATE + H(2)O.
CC -1- COFACTOR: BINDS A 2FE-2S CLUSTER (POTENTIAL).
CC -1- PATHWAY: FOURTH STEP IN VALINE AND ISOLEUCINE BIOSYNTHESIS.
CC -1- SIMILARITY: BELONGS TO THE ILVD / EDD FAMILY.
CC
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CC
CC EMBL: AF008210; AAC38125.1;
CC InterPro: IPR000581;
CC Pfam: PF00920; ILVD_EDD; 1.
CC PROSITE: PS00886; ILVD_EDD_1; 1.
CC PROSITE: PS00887; ILVD_EDD_2; 1.
CC
CC Branched-chain amino acid biosynthesis; Lyase; Iron-sulfur.
KW METAL 122 122 IRON-SULFUR (2FE-2S) (POTENTIAL).
FT METAL 195 195 IRON-SULFUR (2FE-2S) (POTENTIAL).
SQ SEQUENCE 617 AA; 67859 MW; 59A52ECDDFC9381 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 617;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYYMN 5
| | | | |
DB 245 DYYLN 249

Fri Jun 29 08:04:44 2001

us-09-724-406-20.rsp

Page 8

Search completed: June 28, 2001, 15:54:37
Job time: 125 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2001, 16:08:23 ; Search time 411.58 seconds
(without alignments)
1.607 Million cell updates/sec

Title: US-09-724-406-20
Perfect score: 31
Sequence: 1 DYWN 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues
Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL16.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_unclassified.*
- 13: sp_vertebrate.*
- 14: sp_virus.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	370	5	O97252
2	31	100.0	672	2	O9WYE6
3	28	90.3	87	2	O9R605
4	28	90.3	128	8	O9R604
5	28	90.3	128	8	O9R604
6	28	90.3	149	2	O9PQ44
7	28	90.3	170	5	O9NBF9
8	28	90.3	221	5	O16690
9	28	90.3	250	2	O6G956
10	28	90.3	271	2	O9KVA2
11	28	90.3	312	2	O86289
12	28	90.3	327	10	O9LSS4
13	28	90.3	341	5	O18100
14	28	90.3	390	2	O9ZMH6
15	28	90.3	399	5	O17131
16	28	90.3	405	2	O911D1
17	28	90.3	411	2	O911D2
18	28	90.3	437	10	O64514
19	28	90.3	483	2	P96066

20	28	90.3	488	3	P78972	P78972 schizosacch
21	28	90.3	499	4	Q12834	Q12834 homo sapien
22	28	90.3	499	4	O9UQI9	O9UQI9 homo sapien
23	28	90.3	499	11	O70380	O70380 rattus norv
24	28	90.3	499	11	O62623	O62623 rattus norv
25	28	90.3	499	11	O9J766	O9J766 mus musculu
26	28	90.3	507	13	O9J389	O9J389 xenopus lae
27	28	90.3	522	5	O61588	O61588 spisula sol
28	28	90.3	526	5	O24044	O24044 drosophila
29	28	90.3	533	1	O26418	O26418 methanobact
30	28	90.3	662	5	P91331	P91331 caenorhabdi
31	28	90.3	752	13	O9DCN6	O9DCN6 gallus gall
32	28	90.3	758	6	O28868	O28868 bos taurus
33	28	90.3	758	6	O28010	O28010 bos taurus
34	28	90.3	772	2	O46080	O46080 pedobacter
35	28	90.3	792	2	O32625	O32625 haemophilus
36	28	90.3	848	5	O16796	O16796 caenorhabdi
37	28	90.3	1056	5	O9VIG4	O9VIG4 drosophila
38	28	90.3	1105	5	O9VX44	O9VX44 drosophila
39	28	90.3	1169	5	O9VX45	O9VX45 drosophila
40	28	90.3	1212	5	O9UOL0	O9UOL0 plasmodium
41	28	90.3	1306	2	O9L8Z1	O9L8Z1 enterococcu
42	28	90.3	1543	14	O09498	O09498 garlic viru
43	28	90.3	1550	14	O55601	O55601 plasmodium
44	28	90.3	2013	5	O96216	O96216 plasmodium
45	28	90.3	2380	5	O96266	O96266 plasmodium

ALIGNMENTS

RESULT 1						
O97252	IC	O97252	PRELIMINARY;	PRT;	370 AA.	
ID	O97252;					
DT	01-MAY-1999	(TRENBLrel. 10, Created)				
DT	01-MAY-1999	(TRENBLrel. 10, Last sequence update)				
DT	01-MAR-2001	(TRENBLrel. 16, Last annotation update)				
DE	PF0310C PROTEIN.					
GN	PF0310C					
OS	Plasmodium falciparum (isolate 3D7).					
OC	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.					
OX	NCBI_TaxID=36329;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=3D7;					
RL	Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.					
DR	EMBL; AL034558; CAB39018.1;					
DR	HSSP; P19245; IYF					
DR	InterPro; IPR001907;					
DR	Pfam; PF00574; CLP_protease; 1.					
DR	PRINTS; PR00127; CLP_PROTEASEP.					
DR	PROSITE; PS00382; CLP_PROTEASE_HIS; UNKNOWN_1.					
SQ	SEQUENCE 370 AA; 43321 MW; 3DE959328D14CE87 CRC64;					
Query Match		100.0%;	Score 31;	DB 5;	Length 370;	
Best Local Similarity		100.0%;	Pred. No. 93;			
Matches	5;	Conservative	0;	Mismatches	0;	Gaps 0;
Qy	1	DYWN 5				
Db	338	DYWN 342				
RESULT 2						
O9WYE6	ID	O9WYE6	PRELIMINARY;	PRT;	672 AA.	
AC	O9WYE6;					
DT	01-NOV-1999	(TRENBLrel. 12, Created)				
DT	01-NOV-1999	(TRENBLrel. 12, Last sequence update)				
DT	01-MAR-2001	(TRENBLrel. 16, Last annotation update)				

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DE. BETA-D-GALACTOSIDASE.
GN TM0310.
OS Thermotoga maritima.
OC Bacteria; Thermotogales; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB8 / DSM 3109;
RX MEDLINE=99287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Utterback T.R., Malek J.A., Linder K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RA "Evidence for lateral gene transfer between Archaea and Bacteria from
RT genome sequence of Thermotoga maritima.";
RL Nature 399:323-329(1999).
DR EMBL; AE001713; AAD35398.1; -.
DR TIGR; TM0310; -.
DR InterPro; IPR003476; -.
DR Pfam; PF02449; Glyco_hydro_42; 1.
DR SEQUENCE 672 AA; 79112 MW; E7F2FB2ED1D916C CRC64;

Query Match 100.0%; Score 31; DB 2; Length 672;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYNN 5
Db 561 DYNN 565

RESULT 3
Q9R605 PRELIMINARY; PRT; 87 AA.
AC Q9R605;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2001 (TREMBlrel. 16, Last annotation update)
DE ADAPTIVE RESPONSE REGULATOR PHOP (FRAGMENT).
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93146391; PubMed=1490612;
RA Wren B.W., Colby S.M., Cubberley R.R., Pallen M.J.;
RA "Degenerate PCR primers for the amplification of fragments from genes
RT encoding response regulators from a range of pathogenic bacteria.";
RL FEMS Microbiol. Lett. 78:287-291(1992).
DR InterPro; IPR001789; -.
DR Pfam; PF00072; response_reg; 1.
DR SMART; SM00448; REC; 1.
DR SEQUENCE 87 AA; 9734 MW; 4F7B55F552FA5EDF CRC64;

Query Match 90.3%; Score 28; DB 2; Length 87;
Best Local Similarity 80.0%; Pred. No. 79;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYNN 5
Db 29 DYNN 33

RESULT 4
Q9R604 PRELIMINARY; PRT; 87 AA.
AC Q9R604;
DT 01-MAY-2000 (TREMBlrel. 13, Created)

DE. BETA-D-GALACTOSIDASE.
GN TM0310.
OS Thermotoga maritima.
OC Bacteria; Thermotogales; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB8 / DSM 3109;
RX MEDLINE=99287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Utterback T.R., Malek J.A., Linder K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RA "Evidence for lateral gene transfer between Archaea and Bacteria from
RT genome sequence of Thermotoga maritima.";
RL Nature 399:323-329(1999).
DR EMBL; AE001713; AAD35398.1; -.
DR TIGR; TM0310; -.
DR InterPro; IPR003476; -.
DR Pfam; PF02449; Glyco_hydro_42; 1.
DR SEQUENCE 672 AA; 79112 MW; E7F2FB2ED1D916C CRC64;

Query Match 90.3%; Score 28; DB 2; Length 87;
Best Local Similarity 80.0%; Pred. No. 79;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYNN 5
Db 29 DYNN 33

RESULT 4
Q9R604 PRELIMINARY; PRT; 87 AA.
AC Q9R604;
DT 01-MAY-2000 (TREMBlrel. 13, Created)

```

OC Mycoplasmataceae; Ureaplasma.
 OX NCBI_TaxID=134821;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=SEROVAR 3;
 RA MEDLINE=20500219; PubMed=11048724;
 RA Glass J.I., Lefkowitz E.J., Glass J.S., Helner C.R., Chen E.Y.,
 RA Cassell G.H.;
 RT "The complete sequence of the mucosal pathogen Ureaplasma
 RT urealyticum";
 RL Nature 407:757-762(2000).
 DR EMBL; AE002141; AAF30858.1; -;
 DR InterPro; IPR000055; -;
 DR InterPro; IPR000267; -;
 DR Pfam; PF01420; Methylase.S; 1.
 DR PROSITE; PS00144; ASN_GLN_ASE.1; UNKNOWN.1.
 SQ SEQUENCE 149 AA; 17702 MW; 4CA516DE2DCE1382 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 149;
 Best Local Similarity 80.0%; Pred. No. 1.4e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYYMN 5
 |||:|
 Db 120 DYLN 124

RESULT 7
 Q9NBF9 PRELIMINARY; PRT; 170 AA.
 ID Q9NBF9
 AC Q9NBF9
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DE 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE TRIOSEPHOSPHATE ISOMERASE (EC 5.3.1.1) (TIM) (FRAGMENT).
 GN TPI-1.

OS Philodina roseola.
 OC Eukaryota; Metazoa; Rotifera; Bdelloidea; Philodinida; Philodinidae;
 OC Philodina.
 OX NCBI_TaxID=96448;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20280140; PubMed=10817991;
 RA Welch D.M., Meselson M.;
 RT "Evidence for the evolution of bdelloid rotifers without sexual
 RT reproduction or genetic exchange";
 RL Science 288:1211-1215(2000).
 RN [2]

RP SEQUENCE FROM N.A.
 RA Mark Welch D.B., Meselson M.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE - DIHYDROXY-
 CC ACETONE PHOSPHATE (BY SIMILARITY).
 CC -1- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: TO OTHER TRIOSEPHOSPHATE ISOMERASES.
 DR EMBL; AF249994; AAF79171.1; -;
 DR InterPro; IPR000652; -;
 DR Pfam; PF00121; TIM; 1.
 DR PROSITE; PS00171; TIM; 1.
 KW Fatty acid biosynthesis; Gluconeogenesis; Glycolysis; Isomerase;
 KW Pentose shunt.
 FT NON_TER 170 170
 FT SEQUENCE 170 AA; 19016 MW; 1F4B758674AB5073 CRC64;

Query Match 90.3%; Score 28; DB 5; Length 170;
 Best Local Similarity 80.0%; Pred. No. 1.6e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYYMN 5

Db 39 DYLN 43
 |||:|

RESULT 8
 O16690 PRELIMINARY; PRT; 221 AA.
 ID O16690
 AC O16690
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE K07E8.9 PROTEIN.
 GN K07E8.9
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkneen R.,
 RA Smaildon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans";
 RL Nature 368:32-38(1994).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Jones K., Kramer J.;
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]

RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Waterston R.;
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF016678; AAB66154.1; -;
 DR InterPro; IPR003003; -;
 DR Pfam; PF01604; 7tm_5; 1.
 SQ SEQUENCE 221 AA; 24956 MW; B94C56624D5D51F3 CRC64;

Query Match 90.3%; Score 28; DB 5; Length 221;
 Best Local Similarity 80.0%; Pred. No. 2.2e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYYMN 5
 |||:|
 Db 11 DYLN 15

RESULT 9
 Q06956 PRELIMINARY; PRT; 250 AA.
 ID Q06956
 AC Q06956
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE RFBI PROTEIN.
 GN RFBI.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
 OX NCBI_TaxID=666;
 RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=O17 / BIOTYPE EL TOR / SEROTYPE OGAWA;
RX MEDLINE=92212870; PubMed=1372980;
RA Stroher U.H., Karageorgos L.E., Morona R., Manning P.A.;
RT "Serotype conversion in *Vibrio cholerae* O1";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2566-2570(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=017;
RX MEDLINE=95309704; PubMed=7540582;
RA Manning P.A., Stroher U.H., Karageorgos L.E., Morona R.;
RT "Putative O-antigen transport genes within the rfb region of *Vibrio*
RT *cholerae* O1 are homologous to those for capsule transport.";
RL Gene 158:1-7(1995).
CC -1- FUNCTION: MAY PLAY A ROLE IN LIPOPOLYSACCHARIDE TRANSPORT.
DR EMBL; X59554; CAA42140.1; -;
DR InterPro; IPR001687; -;
DR InterPro; IPR003439; -;
DR InterPro; IPR003593; -;
DR Pfam; PF000005; ABC_tran; 1.
DR SMART; SM00382; AAA; 1.
KW Polysaccharide transport; Transport.
SQ SEQUENCE 250 AA; 27563 MW; 9BBD9499D57D3677 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 250;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYNN 5
|||:
Db 242 DYLN 246

RESULT 10
Q9KVA2 PRELIMINARY; PRT; 271 AA.
AC Q9KVA2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE LIPOPOLYSACCHARIDE/O-ANTIGEN TRANSPORT PROTEIN.
GN VC0247.
OS *Vibrio cholerae*.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; *Vibrio*.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EL TOR N16961 / SEROTYPE O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Peterson J.D., Umayam L.A.,
RA Dodson R.J., Haft D.H., Hickey E.K., Tettelin H., Richardson D.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Dragoi I., Sellers P.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., White O.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen *Vibrio*
RT *cholerae*";
RL Nature 406:477-483(2000).
DR EMBL; AE004113; AAF93423.1; -;
DR TIGR; VC0247; -;
DR InterPro; IPR001687; -;
DR InterPro; IPR003439; -;
DR InterPro; IPR003593; -;
DR Pfam; PF000005; ABC_tran; 1.
DR SMART; SM00382; AAA; 1.
SQ SEQUENCE 271 AA; 29959 MW; DDB640A1E831AB93 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 271;
Best Local Similarity 80.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYNN 5
|||:
Db 263 DYLN 267

RESULT 11
O86289 PRELIMINARY; PRT; 312 AA.
AC O86289;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE REGULATORY PROTEIN.
GN CLYR.
OS *Leuconostoc mesenteroides*.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
OC *Leuconostoc*.
OX NCBI_TaxID=1245;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=195;
RX MEDLINE=98117048; PubMed=9457870;
RA Bekal S., van Beeumen J., Samyn B., Garmyn D., Henini S., Divies C.,
RA Prevost H.;
RT "Purification of *Leuconostoc mesenteroides* citrate lyase and cloning
RT and characterization of the citCDEFG gene cluster.";
RL J. Bacteriol. 180:647-654(1998).
DR EMBL; Y10621; CAA71637.1; -;
SQ SEQUENCE 312 AA; 35102 MW; 8DB478F8BD401461 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 312;
Best Local Similarity 80.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYNN 5
|||:
Db 13 DYLN 17

RESULT 12
Q9LSS4 PRELIMINARY; PRT; 327 AA.
AC Q9LSS4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE SIMILARITY TO SENESENCE-ASSOCIATED PROTEIN.
OS *Arabidopsis thaliana* (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,
RA Tabata S.;
RT "Structural analysis of *Arabidopsis thaliana* chromosome 5. XI.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB026632; BAA97503.1; -;
DR InterPro; IPR000301; -;
DR Pfam; PF00335; transmembrane4; 1.
DR PRINTS; PRO0259; TMFOUR.
SQ SEQUENCE 327 AA; 37178 MW; 505A06D6A2D39F8D CRC64;

Query Match 90.3%; Score 28; DB 10; Length 327;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYNN 5
|||:
Db 13 DYLN 17

Db 112 DYVLN 116

RESULT 13

O18100 PRELIMINARY; PRT; 341 AA.
 AC O18100;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE T21B4.6 PROTEIN.
 GN T21B4.6.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Smye R.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Korshaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
 RA Smalton N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans";
 RL Nature 368:32-38(1994).
 DR EMBL; Z81124; CAB03372.1; -.
 DR InterPro: IPR000168; -.
 DR InterPro: IPR003003; -.
 DR Pfam; PF01604; 7tm_5; 1.
 SQ SEQUENCE 341 AA; 38576 MW; A03E40826370CD5 CRC64;

Query Match 90.3%; Score 28; DB 5; Length 341;
 Best Local Similarity 80.0%; Pred. No. 3.5e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYVMN 5

Db 5 DYVLN 9

RESULT 14

Q9ZMH6 PRELIMINARY; PRT; 390 AA.
 AC Q9ZMH6;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE TYPE II DNA MODIFICATION ENZYME (METHYLTRANSFERASE).
 GN JHP0244.
 OS Helicobacter pylori J99 (Campylobacter pylori J99).
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
 OC Helicobacter.
 OX NCBI_TaxID=85963;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99120557; PubMed=9923682;
 RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
 RA Smith D.R., Noonan B., Guild B.C., deJonghe B.L., Carmel G.,
 RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
 RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
 RA Trust T.J.;

RT "Genomic sequence comparison of two unrelated isolates of the human
 RT gastric pathogen Helicobacter pylori";
 RL Nature 397:1176-1180(1999).
 DR EMBL; AE001462; RAD05820.1; -.
 DR InterPro: IPR001091; -.
 DR InterPro: IPR002052; -.
 DR InterPro: IPR002295; -.
 DR InterPro: IPR002941; -.
 DR Pfam; PF01555; N6_N4_Mtase; 1.
 DR PRINTS; PR00506; D21N6MTFRASE.
 DR PRINTS; PR00508; S21N4MTFRASE.
 DR PROSITE; PS00092; N6_MTASE; UNKNOWN-1.
 SQ SEQUENCE 390 AA; 45410 MW; 2274550598A1256C CRC64;

Query Match 90.3%; Score 28; DB 2; Length 390;
 Best Local Similarity 80.0%; Pred. No. 4e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYVMN 5

Db 328 DYVLN 332

RESULT 15

O17131 PRELIMINARY; PRT; 399 AA.
 ID O17131
 AC O17131;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE F31F4.12 PROTEIN.
 DE F31F4.12.
 GN F31F4.12.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Blanchard M., Kramer J., Elliott G., Twyman B.;
 RT "The sequence of C. elegans cosmid F31F4.";
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Waterston R.;
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF024503; AAG24095.1; -.
 DR InterPro: IPR000536; -.
 DR InterPro: IPR001628; -.
 DR PRINTS; PR00047; STROIDFINGER.
 DR SMART; SM00430; HOLI; 1.
 SQ SEQUENCE 399 AA; 46884 MW; D3763348D9CEC734 CRC64;

Query Match 90.3%; Score 28; DB 5; Length 399;
 Best Local Similarity 80.0%; Pred. No. 4.1e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYVMN 5

Db 338 DYVLN 342

Search completed: June 28, 2001, 16:08:24
Job time: 952 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2001, 16:14:37 ; Search time 362.28 Seconds
(without alignments)
3.179 Million cell updates/sec

Title: US-09-724-406-22

Perfect score: 97

Sequence: 1 FIRNKANGYTFESASVMG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_0601.*
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2: /SID58/gcgdata/geneseq/geneseq/AA1981.DAT.*
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22: /SID58/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	85.6	124	17 AAR90831	2B5 heavy chain va
2	82	84.5	124	18 AAW01594	Lead binding MAb 2
3	82	84.5	359	20 AAY29913	Human MCP-3 and mu
4	82	84.5	361	20 AAY29911	Human IP-10 and mu
5	82	84.5	374	20 AAY29916	Artificial synthe
6	81	83.5	140	13 AAR20790	Unprocessed variab
7	81	83.5	141	13 AAR30431	A5B7 antibody heav
8	81	83.5	146	13 AAR20793	CDR-grafted, human
9	81	83.5	146	13 AAR22373	CDR-grafted, human
10	81	83.5	146	13 AAR26150	A5B7 gH-2 antibody
11	81	83.5	146	13 AAR26151	A5B7 gH-2 antibody

12	81	83.5	250	17 AAW06179	Humanised A5B57 Fd
13	81	83.5	250	17 AAW06177	Murine A5B57 Fd fr
14	81	83.5	250	17 AAW41415	Human B7.1-murine
15	81	83.5	643	20 AAW82739	Clone pNG4/A5B7VH-
16	81	83.5	647	20 AAW82747	Plasmid pUC19/muA5
17	80	82.5	115	16 AAR82825	Variable heavy reg
18	80	82.5	129	21 AAY43866	Heavy chain (VH) g
19	80	82.5	142	16 AAR92828	Cl79Fv-pp variable
20	80	82.5	392	16 AAR82835	scFv-PP. Syntheti
21	79	81.4	19	16 AAR74934	H-CDR-2 of anti-id
22	79	81.4	122	16 AAR74942	Immunoglobulin hea
23	79	81.4	138	16 AAR74963	Anti-idiotypic anti
24	77	79.4	249	13 AAR21262	pSCFVNQ11 encoding
25	76	78.4	141	17 AAR92761	Human/murine chima
26	76	78.4	141	17 AAR92762	Human/murine chima
27	76	78.4	141	17 AAR92763	Human/murine chima
28	76	78.4	141	17 AAR92764	Human/murine chima
29	76	78.4	141	17 AAR92765	Human/murine chima
30	76	78.4	141	17 AAR92766	Human/murine chima
31	76	78.4	141	17 AAR92767	Human/murine chima
32	76	78.4	141	17 AAR92768	Human/murine chima
33	76	78.4	141	17 AAR92769	Human/murine chima
34	75	77.3	19	16 AAR92757	Murine anti-human
35	75	77.3	122	16 AAR74933	H-CDR-2 of anti-id
36	75	77.3	146	16 AAR74962	Immunoglobulin hea
37	73	75.3	19	18 AAW23392	Anti-idiotypic anti
38	73	75.3	100	21 AAB40069	Mutant 3 of the CD
39	73	75.3	100	21 AAB40070	Anti-hiLL12 antibod
40	73	75.3	100	21 AAB40071	Anti-hiLL12 antibod
41	72	74.2	19	18 AAW37006	Complementarity de
42	72	74.2	19	21 AAY51371	Mouse monoclonal a
43	72	74.2	119	11 AAR07316	VH domain of antib
44	72	74.2	119	15 AAR47221	Antibody heavy cha
45	72	74.2	119	17 AAW14484	Monoclonal antibod

ALIGNMENTS

RESULT 1

AAR90831

ID AAR90831 standard; Protein; 124 AA.

XX

AC AAR90831;

XX

DT 25-JUN-1996 (first entry)

XX

DE 2B5 heavy chain variable region from pCIB4615.

XX

XX delta endotoxin; Bacillus thuringiensis; western corn rootworm;

KW WCRW; maize; pesticide; brush border membrane vesicle; monoclonal;

KW antibody.

XX

OS Insecta sp.

XX

XX WO9600783-A1.

PN

XX 11-JAN-1996.

XX

PF 20-JUN-1995; 95WO-IB00497.

XX

PR 28-JUN-1994; 94US-0267641.

XX

PA (CIBA) CIBA GEIGY AG.

XX

PI Human MCP-3 and mu

XX

PI Artificial synthe

XX

DR Unprocessed variab

XX

DR A5B7 antibody heav

XX

DR CDR-grafted, human

XX

PT A5B7 gH-2 antibody

PT in plants

New monoclonal antibodies which bind insect gut proteins - used

partic. with toxin moieties for the control of insect pests, partic.

CC	01	e.g. aqueous liquid systems, in biological or environmental systems or
CC	02	in such compositions as perfumes, cosmetics, pharmaceuticals, health
CC	03	care products, skin treatment products, pesticides, herbicides,
CC	04	solvents used in the production of semi-conductor and integrated
CC	05	circuit components and production materials for electronic components.
CC	06	The products can provide for applications involving minute amounts of
CC	07	specific heavy metals.
CC	08	
XX	09	
XX	10	
XX	11	
XX	12	
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XX	99	
XX	100	

SQ Sequence 359 AA;

Query Match 84.5%; Score 82; DB 20; Length 359;
 Best Local Similarity 88.9%; Pred. No. 2.4e-05;
 Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 IRNKANGYTFESASVMG 19
 |||||:|||||
 Db 140 lrnkangytteysasvkg 157

RESULT 4

AAAY29911
 ID AAY29911 standard; Protein; 361 AA.

XX AC AAY29911;

XX DT 17-NOV-1999 (first entry)

XX DE Human IP-10 and murine scFv38 fusion protein.

XX KW Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;
 XX KW immune response; HIV; infection.

XX OS Homo sapiens.

XX OS Mus sp.

XX OS Synthetic.

XX PN WO9946392-A1.

XX PD 16-SEP-1999.

XX PF 12-MAR-1999; 99WO-US05345.

XX PR 12-MAR-1998; 98US-0077745.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Kwak LW, Biragyn A;

XX WPI; 1999-551418/46.

XX PT New fusion polypeptides comprising a chemokine and a tumour antigen or
 PT HIV antigen, used for treating cancers or treating or preventing HIV
 PT infection -

XX PS Disclosure; Page 115-116; 142pp; English.

XX CC The present invention describes fusion proteins comprising a chemokine
 CC and a tumour antigen or HIV antigen. Specifically claimed fusion
 CC proteins comprise: (1) human monocyte chemoattractant protein-3 (MCP-3) and human
 CC Muc-1; (2) human interferon-induced protein 10 (IP-10) and human
 CC (3) human macrophage-derived chemokine (MDC) and human Muc-1;
 CC SDF-1 and human Muc-1; (5) human IP-10 and HIV gp120; (6) human MCP-3 and
 CC HIV gp120; (7) human MDC and HIV gp120; and (8) human SDF-1 and HIV
 CC gp120. The fusion proteins, and nucleotide sequences encoding them, can
 CC be used for producing an immune response, e.g. an effector T cell immune
 CC response. They can also be used for treating cancer or treating or
 CC preventing HIV infection. The fusion proteins and/or nucleotide sequences
 CC can be used in in vitro diagnostic assays, as well as in screening assays
 CC for identifying unknown tumour antigen epitopes and fine mapping of
 CC tumour antigen epitopes. The present sequence represents a fusion protein
 CC from the present invention.

XX SQ Sequence 361 AA;

Query Match 84.5%; Score 82; DB 20; Length 361;
 Best Local Similarity 88.9%; Pred. No. 2.5e-05;
 Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 IRNKANGYTFESASVMG 19

Db 142 lrnkangytteysasvkg 159
 |||||:|||||

RESULT 5

AAAY29916
 ID AAY29916 standard; Protein; 374 AA.

XX AC AAY29916;

XX DT 17-NOV-1999 (first entry)

XX DE Artificial synthetic construct protein SEQ ID NO:15.

XX KW Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;
 XX KW immune response; HIV; infection.

XX OS Synthetic.

XX PN WO9946392-A1.

XX PD 16-SEP-1999.

XX PF 12-MAR-1999; 99WO-US05345.

XX PR 12-MAR-1998; 98US-0077745.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Kwak LW, Biragyn A;

XX WPI; 1999-551413/46.

XX PT New fusion polypeptides comprising a chemokine and a tumour antigen or
 PT HIV antigen, used for treating cancers or treating or preventing HIV
 PT infection -

XX PS Disclosure; Page 117-118; 142pp; English.

XX CC The present invention describes fusion proteins comprising a chemokine
 CC and a tumour antigen or HIV antigen. Specifically claimed fusion
 CC proteins comprise: (1) human monocyte chemoattractant protein-3 (MCP-3) and
 CC human Muc-1; (2) human interferon-induced protein 10 (IP-10) and human
 CC Muc-1; (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4)
 CC human SDF-1 and human Muc-1; (5) human IP-10 and HIV gp120; (6) human
 CC MCP-3 and HIV gp120; (7) human MDC and HIV gp120; and (8) human SDF-1 and
 CC HIV gp120. The fusion proteins, and nucleotide sequences encoding them,
 CC can be used for producing an immune response, e.g. an effector T cell
 CC immune response. They can also be used for treating cancer or treating
 CC or preventing HIV infection. The fusion proteins and/or nucleotide
 CC sequences can be used in in vitro diagnostic assays, as well as in
 CC screening assays for identifying unknown tumour antigen epitopes and fine
 CC mapping of tumour antigen epitopes. AAY29916 and AAZ21156 to AAZ21168 are
 CC sequences given in the SEQ ID LISTING in the present invention but which
 CC are not mentioned further within the specification.

XX SQ Sequence 374 AA;

Query Match 84.5%; Score 82; DB 20; Length 374;
 Best Local Similarity 88.9%; Pred. No. 2.6e-05;
 Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 IRNKANGYTFESASVMG 19

Db 265 lrnkangytteysasvkg 282
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RESULT 6

AAAR20790
 ID AAR20790 standard; Protein; 140 AA.

XX AC AAR20790;


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FT  Misc-difference 67..68 /note= "murine residues"
FT  Misc-difference 94..95 /note= "murine residues"
FT  Misc-difference 98 /note= "murine residue"
FT  Misc-difference 118 /note= "murine residue"
FT  Misc-difference 118 /note= "murine residue"
XX
XX  WO9201059-A.
XX
XX  23-JAN-1992.
XX
XX  05-JUL-1991; 91WO-GB01108.
XX
XX  05-JUL-1991; 91WO-GB01108.
XX  05-JUL-1990; 90GB-0014932.
XX  21-DEC-1990; 90WO-GB02017.
XX
XX  (CELL-) CELLTech LTD.
XX
XX  Adair JR, Bodmer MW, Mountain A, Owens RJ;
XX  WPI; 1992-056874/07.
XX  N-PSDB; AAQ20987.
XX
XX  New CDR-grafted anti carcinoembryonic antigen antibodies - useful
XX  in therapy and diagnosis of carcinoma
XX
XX  Claim 14; Fig 10; 70pp; English.
XX
XX  This heavy chain sequence comprises a human framework (i.e. the LAY
XX  region) which contains murine sequences (from the murine anti-CEA
XX  A5B7 Mab) in the CDRs and at other positions predicted to be
XX  important for antigen-binding and at which human and A5B7 sequences
XX  differ. (See AAQ20984 for A5B7 heavy chain coding sequence).
XX
XX  Sequence 146 AA;
XX
XX  Query Match 83.5%; Score 81; DB 13; Length 146;
XX  Best Local Similarity 84.2%; Pred. No. 1.2e-05;
XX  Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
QY  1 FIRNKANGYTFEFSASVMG 19
Db  69 fignkangytfesavskg 87
II IIIIIIIIIIIII
II IIIIIIIIIIIII

RESULT 9
AAR22373
ID  AAR22373 standard; Protein; 146 AA.
XX
XX  AAR22373;
XX
XX  19-MAY-1992 (first entry)
XX
XX  CDR-grafted, humanised heavy chain gH2.
XX
XX  murine monoclonal antibody; Mab; A5B7; humanised antibody; CEA;
XX  complementarity determining region.
XX
XX  Homo sapiens.
XX  Mus musculus.
XX
XX  Key Location/Qualifiers
XX  Peptide 1..19
XX  Protein 20..146
XX  /label= VH
XX  /note= "human LAY framework with A5B7 CDRs"
XX  45..54
XX  /label= CDR1

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FT  Region /note= "murine residues"
FT  69..87 /label= CDR2
FT  /note= "murine residues"
FT  120..129 /label= CDR3
FT  /note= "murine residues"
FT  Misc-difference 20 /note= "murine residue"
FT  Misc-difference 67..68 /note= "murine residues"
FT  Misc-difference 94..95 /note= "murine residues"
FT  Misc-difference 98 /note= "murine residues"
FT  Misc-difference 106 /note= "murine residue"
FT  Misc-difference 111 /note= "murine residue"
FT  Misc-difference 118 /note= "murine residue"
FT  Misc-difference 118 /note= "murine residue"
XX
XX  WO9201059-A.
XX
XX  23-JAN-1992.
XX
XX  05-JUL-1991; 91WO-GB01108.
XX
XX  05-JUL-1991; 91WO-GB01108.
XX  05-JUL-1990; 90GB-0014932.
XX  21-DEC-1990; 90WO-GB02017.
XX
XX  (CELL-) CELLTech LTD.
XX
XX  Adair JR, Bodmer MW, Mountain A, Owens RJ;
XX  WPI; 1992-056874/07.
XX  N-PSDB; AAQ20988.
XX
XX  New CDR-grafted anti carcinoembryonic antigen antibodies - useful
XX  in therapy and diagnosis of carcinoma
XX
XX  Claim 14; Fig 11; 70pp; English.
XX
XX  This heavy chain sequence comprises a human framework (i.e. the LAY
XX  region) which contains murine sequences (from the murine anti-CEA
XX  A5B7 Mab) in the CDRs and at other positions predicted to be
XX  important for antigen-binding and at which human and A5B7 sequences
XX  differ. (See AAQ20984 for A5B7 heavy chain coding sequence).
XX
XX  Sequence 146 AA;
XX
XX  Query Match 83.5%; Score 81; DB 13; Length 146;
XX  Best Local Similarity 84.2%; Pred. No. 1.2e-05;
XX  Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
QY  1 FIRNKANGYTFEFSASVMG 19
Db  69 fignkangytfesavskg 87
II IIIIIIIIIIIII
II IIIIIIIIIIIII

RESULT 10
AAR26150
ID  AAR26150 standard; Protein; 146 AA.
XX
XX  AAR26150;
XX
XX  03-FEB-1993 (first entry)
XX
XX  A5B7 gH-2 antibody grafted heavy chain.
XX
XX  humanised antibody; chimaeric; carcino-embryonic antigen; therapy;

```

diagnosis; carcinomas; CDR; IgG; human; murine; ss.

Chimaeric.
Key Location/Qualifiers
Region 26..35
/note= "grafted murine CDR1"
Region 50..65
/note= "grafted murine CDR2"
Region 95-102
/note= "grafted murine CDR3"

W09201059-A.

23-JAN-1992.

05-JUL-1991; 91WO-GB01108.

05-JUL-1991; 91WO-GB01108.

05-JUL-1990; 90GB-0014932.

21-DEC-1990; 90WO-GB02017.

(CELL-) CELTECH LTD.

Adair JR, Bodmer MW, Mountain A, Owens RJ;

WPI; 1992-284316/34.

N-PSDB; AAQ27354.

Humanised antibody molecules - comprising murine and human regions, specific for carcino-embryonic antigen, useful for diagnosis and therapy

Example 4; Figure 10; 71pp; English.

This sequence is CDR-grafted A5B7 human antibody having murine CDRs at amino acids 26-35 (CDR1), 50-65 (CDR2), and 95-102 (CDR3) and additional murine framework residues at 1, 48, 49, 72, 73, 76, and 93. The LAY framework was chosen when making the coding construct (AAQ27354) as it shows the highest homology to A5B7. The antibody has specificity for carcinoembryonic antigen, produced by tumours, and the Ab is thus useful in both therapy and diagnosis of certain carcinomas.

Sequence 146 AA;

Query Match 83.5%; Score 81; DB 13; Length 146;

Best Local Similarity 84.2%; Pred. No. 1.2e-05;

Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FIRNKANGYTFESASVMG 19

Db 69 fignkangytfesavskg 87

RESULT 11

AA26151

ID AAR26151 standard; Protein; 146 AA.

AC AAR26151;

03-FEB-1993 (first entry)

A5B7 gH-2 antibody grafted heavy chain.

humanised antibody; chimaeric; carcino-embryonic antigen; therapy;

diagnosis; carcinomas; CDR; IgG; human; murine; ss.

Chimaeric.

Key Location/Qualifiers

Region 26..35

FT Region /note= "grafted murine CDR1"

FT 50..65

FT /note= "grafted murine CDR2"

FT 95-102

FT /note= "grafted murine CDR3"

XX W09201059-A.

XX 23-JAN-1992.

XX 05-JUL-1991; 91WO-GB01108.

XX 05-JUL-1991; 91WO-GB01108.

XX 05-JUL-1990; 90GB-0014932.

XX 21-DEC-1990; 90WO-GB02017.

XX (CELL-) CELTECH LTD.

XX Adair JR, Bodmer MW, Mountain A, Owens RJ;

XX WPI; 1992-284316/34.

XX N-PSDB; AAQ27355.

XX Humanised antibody molecules - comprising murine and human regions, specific for carcino-embryonic antigen, useful for diagnosis and therapy

XX Example 4; Figure 10; 71pp; English.

XX This sequence is CDR-grafted A5B7 human antibody having murine CDRs at amino acids 26-35 (CDR1), 50-65 (CDR2), and 95-102 (CDR3) and additional murine framework residues at 1, 48, 49, 72, 73, 76, 82b, 86 and 93. The LAY framework was chosen when making the coding construct (AAQ27354) as it shows the highest homology to A5B7. The antibody has specificity for carcinoembryonic antigen, produced by tumours, and the Ab is thus useful in both therapy and diagnosis of certain carcinomas.

XX Sequence 146 AA;

Query Match 83.5%; Score 81; DB 13; Length 146;

Best Local Similarity 84.2%; Pred. No. 1.2e-05;

Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FIRNKANGYTFESASVMG 19

Db 69 fignkangytfesavskg 87

RESULT 12

AAW06179

ID AAW06179 standard; Protein; 250 AA.

XX AAW06179;

17-FEB-1997 (first entry)

Humanised A5B57 Fd fragment.

ribonuclease; human; bovine; pancreatic; anti-tumour therapy; ADEPT;

mustard-ribonucleotide; antibody directed enzyme prodruug therapy;

anti-neoplastic; prodrug; reverse polarity; ion pair interaction;

reduced immunogenicity; non-selective triggering; primer;

polymerase chain reaction; PCR; Hp-RNase; Fd; F(ab')2.

XX Synthetic.

XX WO9620011-A1.

XX 04-JUL-1996.

XX 21-DEC-1995; 95WO-GB02991.

```

XX PR 16-AUG-1995; 95GB-0016810.
XX PR 23-DEC-1994; 94GB-0026192.
XX PA (ZENE ) ZENECA LTD.
XX
XX PI Blakey DC, Boyle FT, Davies DH, Eggelte HJ, Heaton DW;
XX PI Hennem JF, Hennequin LFA, Marsham PR, Rabin BR, Slater AM;
XX PI Tarragona-Fiola A, Taylorson CJ;
XX
XX DR WPI; 1996-321650/32.
XX DR N-PSDB; AAT42509.
XX
XX PT Two component system for anti-tumour therapy - comprising targeting
XX PT moiety linked to mutated enzyme which can transform an
XX PT anti-neoplastic prodrug
XX
XX PS Example 6; Page 121-122; 182pp; English.
XX
XX CC A two-component system for anti-tumour therapy comprises a targeting
XX CC moiety linked to a mutated enzyme which can transform an anti-neoplastic
XX CC prodrug. The system is based on antibody directed enzyme prodrug therapy
XX CC (ADEPT) using a non-naturally occurring mutant form of a host enzyme,
XX CC pref. human pancreatic ribonuclease (HP-RNase), (see AAT42478-83). The
XX CC targeting moiety can be an antibody, in partic. murine monoclonal
XX CC antibody A5B7 (which binds to human carcinoembryonic antigen). A5B7 is
XX CC suitable for targeting colorectal carcinoma. Fragments, esp. F(ab')2,
XX CC of the antibody can be conjugated to HP-RNase. A5B7 Fd and L chain
XX CC fragments were isolated by PCR using cDNA isolated from A5B7 hybridoma
XX CC cells. The present sequence is that of a humanised A5B7 Fd fragment.
XX
XX SQ Sequence 250 AA;
XX
XX Query Match 83.5%; Score 81; DB 17; Length 250;
XX Best Local Similarity 84.2%; Pred. No. 2.3e-05;
XX Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FIRNKANGYTTTSPSVMG 19
Db 69 fignkangytteysavkg 87
|| |||||:|||||
|| |||||:|||||

RESULT 13
AAW06177
ID AAW06177 standard; Protein; 250 AA.
XX
XX AC AAW06177;
XX
XX DT 17-FEB-1997 (first entry)
XX
XX DE Murine A5B7 Fd fragment.
XX
XX KW ribonuclease; human; bovine; pancreatic; anti-tumour therapy; ADEPT;
XX KW mustard-ribonucleotide; antibody directed enzyme prodrug therapy;
XX KW anti-neoplastic; prodrug; reverse polarity; ion pair interaction;
XX KW reduced immunogenicity; non-selective triggering; primer;
XX KW polymerase chain reaction; PCR; HP-RNase; Fd; F(ab')2.
XX
XX OS Synthetic.
XX
XX PN W09620011-A1.
XX
XX PD 04-JUL-1996.
XX
XX PF 21-DEC-1995; 95WO-GB02991.
XX
XX PR 16-AUG-1995; 95GB-0016810.
XX PR 23-DEC-1994; 94GB-0026192.
XX
XX PA (ZENE ) ZENECA LTD.
XX
XX PI Blakey DC, Boyle FT, Davies DH, Eggelte HJ, Heaton DW;

PI Hennem JF, Hennequin LFA, Marsham PR, Rabin BR, Slater AM;
PI Tarragona-Fiola A, Taylorson CJ;
XX
XX DR WPI; 1996-321650/32.
XX DR N-PSDB; AAT42507.
XX
XX PT Two component system for anti-tumour therapy - comprising targeting
XX PT moiety linked to mutated enzyme which can transform an
XX PT anti-neoplastic prodrug
XX
XX PS Example 6; Page 118-119; 182pp; English.
XX
XX CC A two-component system for anti-tumour therapy comprises a targeting
XX CC moiety linked to a mutated enzyme which can transform an anti-neoplastic
XX CC prodrug. The system is based on antibody directed enzyme prodrug therapy
XX CC (ADEPT) using a non-naturally occurring mutant form of a host enzyme,
XX CC pref. human pancreatic ribonuclease (HP-RNase), (see AAT42478-83). The
XX CC targeting moiety can be an antibody, in partic. murine monoclonal
XX CC antibody A5B7 (which binds to human carcinoembryonic antigen). A5B7 is
XX CC suitable for targeting colorectal carcinoma. Fragments, esp. F(ab')2,
XX CC of the antibody can be conjugated to HP-RNase. A5B7 Fd and L chain
XX CC fragments were isolated by PCR using cDNA isolated from A5B7 hybridoma
XX CC cells. The present sequence is that of the murine A5B7 Fd fragment.
XX
XX SQ Sequence 250 AA;
XX
XX Query Match 83.5%; Score 81; DB 17; Length 250;
XX Best Local Similarity 84.2%; Pred. No. 2.3e-05;
XX Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FIRNKANGYTTTSPSVMG 19
Db 69 fignkangytteysavkg 87
|| |||||:|||||
|| |||||:|||||

RESULT 14
AAW41415
ID AAW41415 standard; Protein; 473 AA.
XX
XX AC AAW41415;
XX
XX DT 02-JUN-1998 (first entry)
XX
XX DE Human B7.1-murine A5B7 F(ab')2 fusion protein.
XX
XX KW Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy;
XX KW cancer diagnosis; complementarity determining region.
XX
XX OS Chimeric - Homo sapiens.
XX OS Chimeric - Mus sp.
XX
XX PN W09742329-A1.
XX
XX PD 13-NOV-1997.
XX
XX PF 29-APR-1997; 97WO-GB01165.
XX
XX PR 14-FEB-1997; 97GB-0003103.
XX PR 04-MAY-1996; 96GB-0009405.
XX
XX PA (ZENE ) ZENECA LTD.
XX
XX PI Copley CG, Edge MD, Emery SC;
XX
XX DR WPI; 1997-558987/51.
XX DR N-PSDB; AAV17340.
XX
XX PT Anti-carcinoembryonic antigen antibody 806.077 Ab - used for
XX PT diagnosis and therapy of cancer
XX
XX PS Reference Example 3; Page 190-193; 208pp; English.
XX

```


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OM protein - protein search, using sw model

Run on: June 28, 2001, 16:01:14 ; Search time 138.34 Seconds
(without alignments)
2.767 Million cell updates/sec

Title: US-09-724-406-22

Perfect score: 97

Sequence: 1 FIRNKANGYTEFSASVMG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 2014635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2_6/ptodata/2/1aa/5A-COMB.pep.*
- 2: /cgn2_6/ptodata/2/1aa/5B-COMB.pep.*
- 3: /cgn2_6/ptodata/2/1aa/6A-COMB.pep.*
- 4: /cgn2_6/ptodata/2/1aa/6B-COMB.pep.*
- 5: /cgn2_6/ptodata/2/1aa/PCTUS-COMB.pep.*
- 6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	83	85.6	124	1	US-08-442-542-6
2	83	85.6	124	3	US-08-765-469-6
3	82	84.5	124	4	US-08-767-128-38
4	81	83.5	140	2	US-08-449-287-4
5	81	83.5	146	2	US-08-449-287-10
6	81	83.5	146	2	US-08-449-287-12
7	80	82.5	116	1	US-08-401-908-1
8	79	81.4	19	1	US-08-318-9708-6
9	76	78.4	19	2	US-08-765-783A-85
10	76	78.4	141	2	US-08-765-783A-29
11	76	78.4	141	2	US-08-765-783A-41
12	76	78.4	141	2	US-08-765-783A-45
13	76	78.4	141	2	US-08-765-783A-49
14	76	78.4	141	2	US-08-765-783A-51
15	76	78.4	141	2	US-08-765-783A-55
16	76	78.4	141	2	US-08-765-783A-59
17	76	78.4	141	2	US-08-765-783A-63
18	76	78.4	141	2	US-08-765-783A-65
19	76	78.4	141	3	US-08-921-100-29
20	76	78.4	141	3	US-08-921-100-45
21	76	78.4	141	3	US-08-921-100-49
22	76	78.4	141	3	US-08-921-100-51
23	76	78.4	141	3	US-08-921-100-55
24	76	78.4	141	3	US-08-921-100-59
25	76	78.4	141	3	US-08-921-100-63
26	76	78.4	141	3	US-08-921-100-65
27	76	78.4	141	3	US-08-921-100-65

28	76	78.4	141	3	US-08-880-142-29	Sequence 29, Appl
29	76	78.4	141	3	US-08-880-142-41	Sequence 41, Appl
30	76	78.4	141	3	US-08-880-142-45	Sequence 45, Appl
31	76	78.4	141	3	US-08-880-142-49	Sequence 49, Appl
32	76	78.4	141	3	US-08-880-142-51	Sequence 51, Appl
33	76	78.4	141	3	US-08-880-142-55	Sequence 55, Appl
34	76	78.4	141	3	US-08-880-142-59	Sequence 59, Appl
35	76	78.4	141	3	US-08-880-142-63	Sequence 63, Appl
36	76	78.4	141	3	US-08-880-142-65	Sequence 65, Appl
37	76	78.4	141	3	US-08-902-201-29	Sequence 29, Appl
38	76	78.4	141	3	US-08-902-201-41	Sequence 41, Appl
39	76	78.4	141	3	US-08-902-201-45	Sequence 45, Appl
40	76	78.4	141	3	US-08-902-201-49	Sequence 49, Appl
41	76	78.4	141	3	US-08-902-201-51	Sequence 51, Appl
42	76	78.4	141	3	US-08-902-201-55	Sequence 55, Appl
43	76	78.4	141	3	US-08-902-201-59	Sequence 59, Appl
44	76	78.4	141	3	US-08-902-201-63	Sequence 63, Appl
45	76	78.4	141	3	US-08-902-201-65	Sequence 65, Appl

ALIGNMENTS

RESULT 1
US-08-442-542-6
; Sequence 6, Application US/08442542
; Patent No. 5686600
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine B.
; TITLE OF INVENTION: Antibodies which Bind to Insect Gut
; TITLE OF INVENTION: Proteins and their Use
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,542
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/267,641
; FILING DATE: 28-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REFERENCE/DOCKET NUMBER: CGC 1750
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8615
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-442-542-6

Query Match 85.6%; Score 83; DB 1; Length 124;
Best Local Similarity 84.2%; Pred. No. 9.3e-07;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FIRNKANGYTEFSASVMG 19

Db 50 FIRKANGYTTTEYSASVKG 68
|||:|||||:|||||

RESULT 2

US-08-765-469-6
; Sequence 6, Application US/08765469
; Patent No. 6069301
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine B.
; APPLICANT: Kozziel, Michael G.
; TITLE OF INVENTION: Antibodies which Bind to Insect Gut
; TITLE OF INVENTION: Proteins and their Use
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,469
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/267,641
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: CGC 1750
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8615
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-765-469-6

Query Match 85.6%; Score 83; DB 3; Length 124;
Best Local Similarity 84.2%; Pred. No. 9.3e-07;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FIRKANGYTTTEFSASVMG 19
|||:|||||:|||||

Db 50 FIRKANGYTTTEYSASVKG 68

RESULT 3

US-08-767-128-38
; Sequence 38, Application US/08767128
; Patent No. 6111079
; GENERAL INFORMATION:
; APPLICANT: WYLIE, DWANE E.
; APPLICANT: LOPEZ, OSVALDO
; APPLICANT: MURRAY, PETER JOSEPH
; APPLICANT: GOEBEL, PETER
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6111079 West Center, 90 South Seventh St

CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,128
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 04-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09258
FILING DATE: 05-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/541,373
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,798
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.49USF1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/371-5278
TELEFAX: 612/332-9081
TELEX:
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-767-128-38

Query Match 84.5%; Score 82; DB 4; Length 124;
Best Local Similarity 88.9%; Pred. No. 1.4e-06;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 IRNKANGYTTTEFSASVMG 19
|||:|||||:|||||

Db 51 IRNKANGYTTTEYSASVKG 68

RESULT 4

US-08-449-287-4
; Sequence 4, Application US/08449287
; Patent No. 5877293
; GENERAL INFORMATION:
; APPLICANT: ADAIR, John Robert
; APPLICANT: BODMER, Mark William
; APPLICANT: MOUNTAIN, Andrew
; APPLICANT: OWENS, Raymond John
; TITLE OF INVENTION: CDR Grafted Anti-CEA Antibodies and
; TITLE OF INVENTION: Their Production
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.

```

; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,287
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/154,389
; FILING DATE:
; APPLICATION DATA:
; APPLICATION NUMBER: PCT GB91/01108
; FILING DATE: 05-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9014932.9
; FILING DATE: 21-DEC-1990
; APPLICATION NUMBER: PCT GB90/02017
; FILING DATE: 05-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 40283/110 CARA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 9041136
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-449-287-4

```

```

Query Match 83.5%; Score 81; DB 2; Length 140;
Best Local Similarity 84.2%; Pred. No. 2.3e-06;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FIRKANGYTTFESASVVG 19
Db 69 FIGNKANGYTTFESASVKG 87

RESULT 5
US-08-449-287-10
; Sequence 10, Application US/08449287
; Patent No. 5877293
; GENERAL INFORMATION:
; APPLICANT: ADAIR, John Robert
; APPLICANT: BODMER, Mark William
; APPLICANT: MOUNTAIN, Andrew
; APPLICANT: OWENS, Raymond John
; TITLE OF INVENTION: CDR Grafted Anti-CEA Antibodies and
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

```

```

; APPLICATION NUMBER: US/08/449,287
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/154,389
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT GB91/01108
; FILING DATE: 05-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9014932.9
; FILING DATE: 05-JUL-1990
; APPLICATION DATA:
; APPLICATION NUMBER: PCT GB90/02017
; FILING DATE: 21-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 40283/110 CARA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 9041136
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-449-287-10

Query Match 83.5%; Score 81; DB 2; Length 146;
Best Local Similarity 84.2%; Pred. No. 2.4e-06;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FIRKANGYTTFESASVVG 19
Db 69 FIGNKANGYTTFESASVKG 87

RESULT 6
US-08-449-287-12
; Sequence 12, Application US/08449287
; Patent No. 5877293
; GENERAL INFORMATION:
; APPLICANT: ADAIR, John Robert
; APPLICANT: BODMER, Mark William
; APPLICANT: MOUNTAIN, Andrew
; APPLICANT: OWENS, Raymond John
; TITLE OF INVENTION: CDR Grafted Anti-CEA Antibodies and
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,287
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/154,389
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT GB91/01108

```

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-401-908-1

Query Match 82.5%; Score 80; DB 1; Length 116;
Best Local Similarity 78.9%; Pred. No. 2.7e-06;
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FIRNKANGYTFEFSASVMG 19
Db 50 FIRDRANGYTFEYSASVKG 68
|||||

RESULT 8
US-08-318-970B-6
Sequence 6, Application US/08318970B
Patent No. 5589573
GENERAL INFORMATION:
APPLICANT: Hideaki Hagiwara, et al.
TITLE OF INVENTION: AMINO ACID SEQUENCES OF ANTI-IDIOTYPIC
TITLE OF INVENTION: ANTIBODIES AGAINST ANTI-CANCER HUMAN MONOCLONAL ANTIBODY
TITLE OF INVENTION: AND DNA BASE SEQUENCES ENCODING THOSE SEQUENCES
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Office of Sherman and Shalloway
STREET: 413 N. Washington Street
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: Dell System 210; Intel 80 285 Microprocessor
OPERATING SYSTEM: MS DOS 3.3
SOFTWARE: Word Perfect, Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,970B
FILING DATE: October 6, 1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Richard A. Steinberg
REGISTRATION NUMBER: 26,588
REFERENCE/DOCKET NUMBER: S-2371
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 549-2282
TELEFAX: (703) 836-0106
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: H-CDR2-3
OTHER INFORMATION: hypervariable region
US-08-318-970B-6

Query Match 81.4%; Score 79; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.8e-07;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FIRNKANGYTFEFSASVMG 19
Db 1 FIRNKANGYTFEYSASVKG 19
|||||

RESULT 9
US-08-765-783A-85
Sequence 85, Application US/08765783A
Patent No. 5994524

FILING DATE: 05-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9014932.9
FILING DATE: 05-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT GB90/02017
FILING DATE: 21-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 40283/110 CARA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-449-287-12

Query Match 83.5%; Score 81; DB 2; Length 146;
Best Local Similarity 84.2%; Pred. No. 2.4e-06;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FIRNKANGYTFEFSASVMG 19
Db 69 FIGNKANGYTFEYSASVKG 87
|||||

RESULT 7
US-08-401-908-1
Sequence 1, Application US/08401908
Patent No. 5684146
GENERAL INFORMATION:
APPLICANT: Yoshinobu Okuno et al.
TITLE OF INVENTION: A DNA WHICH CODES FOR THE VARIABLE REGION OF
TITLE OF INVENTION: ANTIBODY
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/401,908
FILING DATE: March 10, 1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 116
TYPE: amino acid

```

; GENERAL INFORMATION:
; APPLICANT: Matsushima, Kouji
; APPLICANT: Matsumoto, Yoshihiro
; APPLICANT: Yamada, Yoshiki
; APPLICANT: Sato, Koh
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yamazaki, Tatsumi
; TITLE OF INVENTION: Reshaped Human Antibody to
; TITLE OF INVENTION: Interleukin-8
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,783A
; FILING DATE: 07-MAR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 35029-20001.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX:
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-765-783A-85

Query Match 78.4%; Score 76; DB 2; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.5e-06;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 IRNKANGYTTTFSASVMG 19
Db 2 IRNKANGYTTREYSASVKG 19

RESULT 10
US-08-765-783A-29
; Sequence 29, Application US/08765783A
; Patent No. 5994524
; GENERAL INFORMATION:
; APPLICANT: Matsushima, Kouji
; APPLICANT: Matsumoto, Yoshihiro
; APPLICANT: Yamada, Yoshiki
; APPLICANT: Sato, Koh
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yamazaki, Tatsumi
; TITLE OF INVENTION: Reshaped Human Antibody to
; TITLE OF INVENTION: Interleukin-8
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington

```

```

; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,783A
; FILING DATE: 07-MAR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 35029-20001.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX:
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 141 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Signal Sequence
; LOCATION: 1...19
; OTHER INFORMATION:
; US-08-765-783A-29

Query Match 78.4%; Score 76; DB 2; Length 141;
Best Local Similarity 83.3%; Pred. No. 1.6e-05;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 IRNKANGYTTTFSASVMG 19
Db 70 IRNKANGYTTREYSASVKG 87

RESULT 11
US-08-765-783A-41
; Sequence 41, Application US/08765783A
; Patent No. 5994524
; GENERAL INFORMATION:
; APPLICANT: Matsushima, Kouji
; APPLICANT: Matsumoto, Yoshihiro
; APPLICANT: Yamada, Yoshiki
; APPLICANT: Sato, Koh
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yamazaki, Tatsumi
; TITLE OF INVENTION: Reshaped Human Antibody to
; TITLE OF INVENTION: Interleukin-8
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0

```


SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: Signal Sequence
LOCATION: 1...19
OTHER INFORMATION:
US-08-765-783A-49

Query Match 78.4%; Score 76; DB 2; Length 141;
Best Local Similarity 83.3%; Pred. No. 1.6e-05;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 IRNKANGYTTEFSASVMG 19
|||||I:||||I
Db 70 IRNKANGYTREYSASVKG 87

RESULT 14

US-08-765-783A-51
Sequence 51, Application US/08765783A
Patent No. 5994524

GENERAL INFORMATION:

APPLICANT: Matsumoto, Kouji
APPLICANT: Matsumoto, Yoshihiro
APPLICANT: Yamada, Yoshiaki
APPLICANT: Sato, Koh
APPLICANT: Tsuchiya, Masayuki
APPLICANT: Yamazaki, Tatsumi
TITLE OF INVENTION: Reshaped Human Antibody to
Interleukin-8
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW, suite 5500
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,783A
FILING DATE: 07-MAR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 35029-20001.20
TELEPHONE: 202-887-1500
TELEFAX: 202-822-0168
TELEX:

INFORMATION FOR SEQ ID NO: 51:

SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
FEATURE:

NAME/KEY: Signal Sequence
LOCATION: 1...19
OTHER INFORMATION:
US-08-765-783A-51

Query Match 78.4%; Score 76; DB 2; Length 141;
Best Local Similarity 83.3%; Pred. No. 1.6e-05;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 IRNKANGYTTEFSASVMG 19
|||||I:||||I
Db 70 IRNKANGYTREYSASVKG 87

RESULT 15

US-08-765-783A-55
Sequence 55, Application US/08765783A
Patent No. 5994524

GENERAL INFORMATION:

APPLICANT: Matsumoto, Kouji
APPLICANT: Matsumoto, Yoshihiro
APPLICANT: Yamada, Yoshiaki
APPLICANT: Sato, Koh
APPLICANT: Tsuchiya, Masayuki
APPLICANT: Yamazaki, Tatsumi
TITLE OF INVENTION: Reshaped Human Antibody to
Interleukin-8
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW, suite 5500
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,783A
FILING DATE: 07-MAR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 35029-20001.20
TELEPHONE: 202-887-1500
TELEFAX: 202-822-0168
TELEX:

INFORMATION FOR SEQ ID NO: 55:

SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
FEATURE:

NAME/KEY: Signal Sequence
LOCATION: 1...19
OTHER INFORMATION:
US-08-765-783A-55

Query Match 78.4%; Score 76; DB 2; Length 141;
Best Local Similarity 83.3%; Pred. No. 1.6e-05;

Matches	15;	Conservative	1;	Mismatches	2;	Indels	0;	Gaps	0;
Qy	2	IRNKANGYTTTFSASVNG	19						
Db	70	IRNKANGYTTREISASVKG	87						

Search completed: June 28, 2001, 16:01:14
Job time: 522 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2001, 15:58:45 ; Search time 234.85 Seconds
(without alignments)
6.163 Million cell updates/sec

Title: US-09-724-406-22

Perfect score: 97

Sequence: 1 FIRNKANGYTFESASVMG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_68.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88	90.7	81	2 D33936	Ig heavy chain V r
2	88	90.7	119	2 S24492	Ig heavy chain V r
3	88	90.7	119	2 S24493	Ig heavy chain V r
4	88	90.7	119	2 S24491	Ig heavy chain V r
5	88	90.7	119	2 S24525	Ig heavy chain V r
6	88	90.7	119	2 S24520	Ig heavy chain V r
7	88	90.7	119	2 S24518	Ig heavy chain V r
8	88	90.7	119	2 S24511	Ig heavy chain V r
9	88	90.7	119	2 S24494	Ig heavy chain V r
10	88	90.7	119	2 S24490	Ig heavy chain V r
11	88	90.7	119	2 S24517	Ig heavy chain V r
12	88	90.7	119	2 D30540	Ig heavy chain V r
13	88	90.7	123	2 S32186	Ig heavy chain V r
14	83	85.6	118	2 E30540	Ig heavy chain V r
15	82	84.5	91	2 S24523	Ig heavy chain V r
16	82	84.5	101	2 PU0002	Ig heavy chain V r
17	82	84.5	105	2 PU0255	Ig heavy chain V r
18	82	84.5	113	2 PH1029	Ig heavy chain V r
19	82	84.5	114	2 PH1027	Ig heavy chain V r
20	82	84.5	119	2 S24522	Ig heavy chain V r
21	82	84.5	119	2 S24513	Ig heavy chain V r
22	82	84.5	119	2 S24515	Ig heavy chain V r
23	82	84.5	119	2 S24517	Ig heavy chain V r
24	82	84.5	122	1 AVMSX2	Ig heavy chain V r
25	82	84.5	124	2 PT0388	Ig heavy chain V r
26	82	84.5	126	2 S16280	Ig heavy chain (38
27	82	84.5	145	2 S03844	Ig heavy chain pre
28	79	81.4	101	2 PU0003	Ig heavy chain V r
29	79	81.4	119	2 S24519	Ig heavy chain V r

ALIGNMENTS

RESULT 1

D33936
Ig heavy chain V region (VM201) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 09-May-1997
C:Accession: D33936

R:Meek, K.; Johansson, B.; Schulman, J.; Bona, C.; Capra, J.D.
Proc. Natl. Acad. Sci. U.S.A. 86, 4664-4668, 1989

A:Title: Nucleotide changes in sequential variants of influenza virus hemagglutinin g

A:Reference number: A33936; MUID:89282831

A:Accession: D33936

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-81 <MEE>

A:Cross-references: GB:J04579

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 90.7%; Score 88; DB 2; Length 81;
Best Local Similarity 89.5%; Pred. No. 1.4e-07;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FIRNKANGYTFESASVMG 19

|||||:|||||

Db 13 FIRNKANGYTFESASVKG 31

RESULT 2

S24492
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S24492

R:Kaartinen, M.

submitted to the EMBL Data Library, October 1991

A:Reference number: S24490

A:Accession: S24492

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-119 <KAA>

A:Cross-references: EMBL:X66649; NID:951217; PIDN:CAA47211.1; PID:951218

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-119/Domain: immunoglobulin homology <IMM>

Query Match 90.7%; Score 88; DB 2; Length 119;

Best Local Similarity 89.5%; Pred. No. 2.1e-07;

Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FIRNKANGYTFESASVMG 19

A:Cross-references: EMBL:X66668; NID:g51254; PIDN:CAA47230.1; PID:g51255
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-119/Domain: immunoglobulin homology <IMM>

Query Match 90.7%; Score 88; DB 2; Length 119;
Best Local Similarity 89.5%; Pred. No. 2.1e-07;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 FIRNKANGYTTTFSASVMG 19
Db 69 FIRNKANGYTTTFSASVKG 87
|||||:|||||:|||||

RESULT 6
S24520
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S24520
R:Kaartinen, M.
submitted to the EMBL Data Library, October 1991
A:Reference number: S24490
A:Accession: S24520
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-119 <KAA>
A:Cross-references: EMBL:X66663; NID:g51245; PIDN:CAA47225.1; PID:g51246
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-119/Domain: immunoglobulin homology <IMM>

Query Match 90.7%; Score 88; DB 2; Length 119;
Best Local Similarity 89.5%; Pred. No. 2.1e-07;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 FIRNKANGYTTTFSASVMG 19
Db 69 FIRNKANGYTTTFSASVKG 87
|||||:|||||:|||||

RESULT 7
S24518
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S24518
R:Kaartinen, M.
submitted to the EMBL Data Library, October 1991
A:Reference number: S24490
A:Accession: S24518
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-119 <KAA>
A:Cross-references: EMBL:X66661; NID:g51241; PIDN:CAA47223.1; PID:g51242
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-119/Domain: immunoglobulin homology <IMM>

Query Match 90.7%; Score 88; DB 2; Length 119;
Best Local Similarity 89.5%; Pred. No. 2.1e-07;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 FIRNKANGYTTTFSASVMG 19
Db 69 FIRNKANGYTTTFSASVKG 87
|||||:|||||:|||||

RESULT 8
S24511

A:Cross-references: EMBL:X66650; NID:g51219; PIDN:CAA47212.1; PID:g51220
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-119/Domain: immunoglobulin homology <IMM>

Query Match 90.7%; Score 88; DB 2; Length 119;
Best Local Similarity 89.5%; Pred. No. 2.1e-07;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 FIRNKANGYTTTFSASVMG 19
Db 69 FIRNKANGYTTTFSASVKG 87
|||||:|||||:|||||

RESULT 4
S24491
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S24491
R:Kaartinen, M.
submitted to the EMBL Data Library, October 1991
A:Reference number: S24490
A:Accession: S24491
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-119 <KAA>
A:Cross-references: EMBL:X66648; NID:g51215; PIDN:CAA47210.1; PID:g51216
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-119/Domain: immunoglobulin homology <IMM>

Query Match 90.7%; Score 88; DB 2; Length 119;
Best Local Similarity 89.5%; Pred. No. 2.1e-07;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 FIRNKANGYTTTFSASVMG 19
Db 69 FIRNKANGYTTTFSASVKG 87
|||||:|||||:|||||

RESULT 5
S24525
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S24525
R:Kaartinen, M.
submitted to the EMBL Data Library, October 1991
A:Reference number: S24490
A:Accession: S24525
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-119 <KAA>

Query Match 90.7%; Score 88; DB 2; Length 119;
Best Local Similarity 89.5%; Pred. No. 2.1e-07;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 FIRNKANGYTTTFSASVMG 19
Db 69 FIRNKANGYTTTFSASVKG 87
|||||:|||||:|||||

RESULT 5
S24525
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S24525
R:Kaartinen, M.
submitted to the EMBL Data Library, October 1991
A:Reference number: S24490
A:Accession: S24525
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-119 <KAA>

Ig heavy chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
 C:Accession: S24511
 R:Kaartinen, M.
 submitted to the EMBL Data Library, October 1991
 A:Reference number: S24490
 A:Accession: S24511
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-119 <KAA>
 A:Cross-references: EMBL:X66659; NID:g51237; PIDN:CAA47221.1; PID:g51238
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:34-119/Domain: immunoglobulin homology <IMM>

Query Match 90.7%; Score 88; DB 2; Length 119;
 Best Local Similarity 89.5%; Pred. No. 2.1e-07;
 Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FIRNKANGYTTTFSSASVVG 19
 Db 69 FIRNKANGYTTTFSSASVVG 87
 |||||
 RESULT 9
 S24494
 Ig heavy chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
 C:Accession: S24494
 R:Kaartinen, M.
 submitted to the EMBL Data Library, October 1991
 A:Reference number: S24490
 A:Accession: S24494
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-119 <KAA>
 A:Cross-references: EMBL:X66651; NID:g51221; PIDN:CAA47213.1; PID:g51222
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:34-119/Domain: immunoglobulin homology <IMM>

Query Match 90.7%; Score 88; DB 2; Length 119;
 Best Local Similarity 89.5%; Pred. No. 2.1e-07;
 Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FIRNKANGYTTTFSSASVVG 19
 Db 69 FIRNKANGYTTTFSSASVVG 87
 |||||
 RESULT 10
 S24490
 Ig heavy chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
 C:Accession: S24490
 R:Kaartinen, M.
 submitted to the EMBL Data Library, October 1991
 A:Reference number: S24490
 A:Accession: S24490
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-119 <KAA>
 A:Cross-references: EMBL:X66647; NID:g51213; PIDN:CAA47209.1; PID:g51214
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:34-119/Domain: immunoglobulin homology <IMM>

Query Match 90.7%; Score 88; DB 2; Length 119;
 Best Local Similarity 89.5%; Pred. No. 2.1e-07;
 Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FIRNKANGYTTTFSSASVVG 19
 Db 69 FIRNKANGYTTTFSSASVVG 87
 |||||
 RESULT 11
 S24517
 Ig heavy chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
 C:Accession: S24517; S24541
 R:Kaartinen, M.
 submitted to the EMBL Data Library, October 1991
 A:Reference number: S24490
 A:Accession: S24517
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-119 <KAA>
 A:Cross-references: EMBL:X66660; NID:g51239; PIDN:CAA47222.1; PID:g51240; EMBL:X66669
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:34-119/Domain: immunoglobulin homology <IMM>

Query Match 90.7%; Score 88; DB 2; Length 119;
 Best Local Similarity 89.5%; Pred. No. 2.1e-07;
 Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FIRNKANGYTTTFSSASVVG 19
 Db 69 FIRNKANGYTTTFSSASVVG 87
 |||||
 RESULT 12
 D30540
 Ig heavy chain V region (174.3F4) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Feb-1989 #sequence_revision 10-Feb-1989 #text_change 16-Aug-1996
 C:Accession: D30540
 R:Clafin, J. L.; Berry, J.
 J. Immunol. 141, 4012-4019, 1988
 A:Title: Genetics of the phosphocholine-specific antibody response to Streptococcus p
 A:Reference number: A30534; MUID:89035545
 A:Accession: D30540
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
 A:Molecule type: mRNA
 A:Residues: 1-119 <CLA>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-100/Domain: immunoglobulin homology <IMM>

Query Match 90.7%; Score 88; DB 2; Length 119;
 Best Local Similarity 89.5%; Pred. No. 2.1e-07;
 Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FIRNKANGYTTTFSSASVVG 19
 Db 50 FIRNKANGYTTTFSSASVVG 68
 |||||
 RESULT 13
 S32186
 Ig heavy chain V region - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 23-Jul-1999
 C:Accession: S32186
 R:izul, S.
 submitted to the EMBL Data Library, February 1993

Fri Jun 29 08:04:48 2001

us-09-724-406-22.rpr

Db 42 IRNKANGYTFEYSASVKG 59

Search completed: June 28, 2001, 15:58:45
Job time: 373 sec

A:Reference number: S32185
A:Accession: S32186
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-123 <IZU>
A:Cross-references: EMBL:X70093; NID:g288249; PIDN:CAA49698.1; PID:g288250
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-100/Domain: immunoglobulin homology <IMM>

Query Match 90.7%; Score 88; DB 2; Length 123;
Best Local Similarity 89.5%; Pred. No. 2.2e-07;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FIRNKANGYTFEFSASVGM 19
|||||
Db 50 FIRNKANGYTFEYSASVKG 68

RESULT 14
E30540
Ig heavy chain V region (252.8G3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 10-Feb-1989 #sequence_revision 10-Feb-1989 #text_change 16-Aug-1996
C:Accession: E30540
R:Clafalin, J.L.; Berry, J.
J: Immunol. 141, 4012-4019, 1988
A:Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneumoniae
A:Reference number: A30534; MUID:89035545
A:Accession: E30540
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-118 <CLA>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-100/Domain: immunoglobulin homology <IMM>

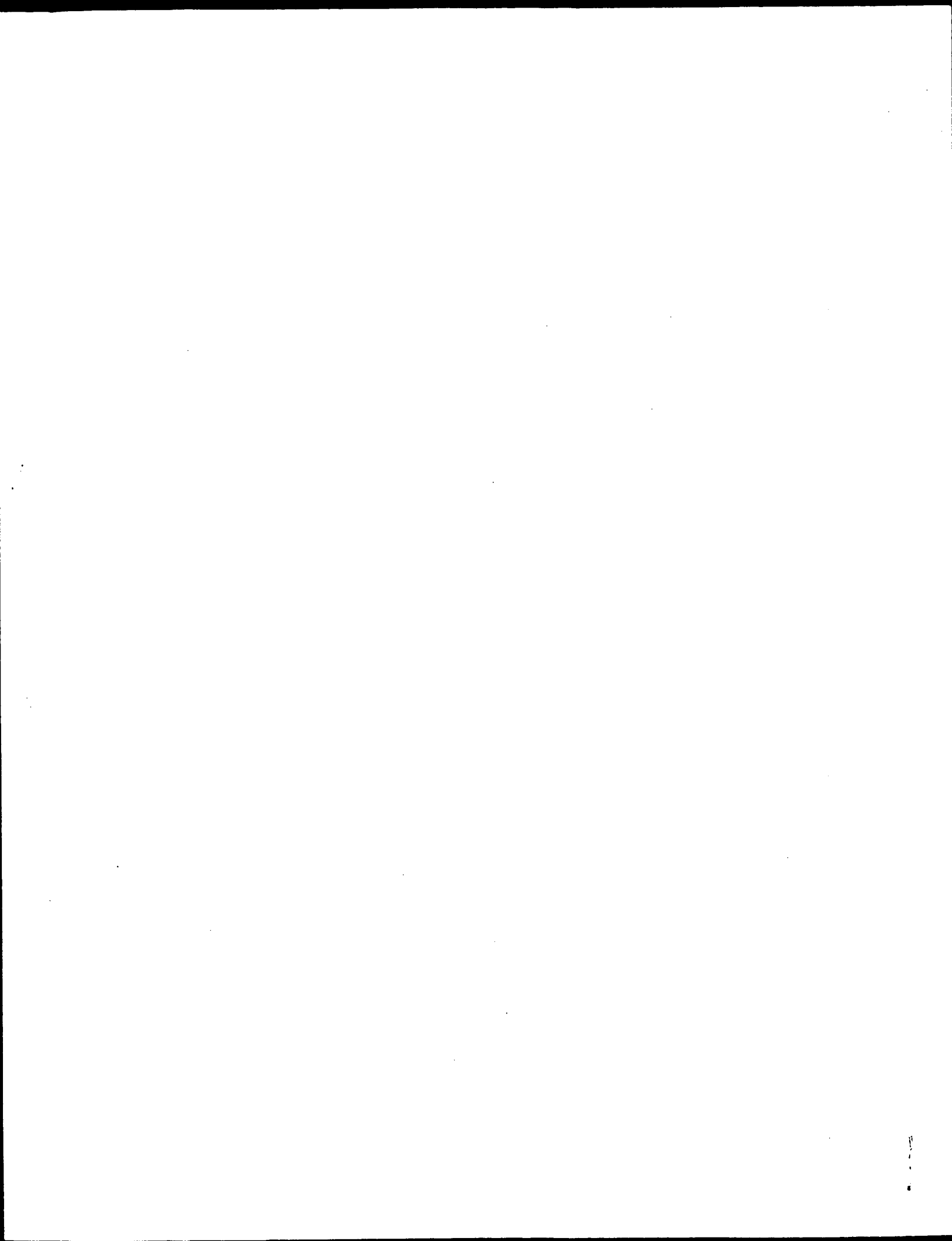
Query Match 85.6%; Score 83; DB 2; Length 118;
Best Local Similarity 84.2%; Pred. No. 1.4e-06;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FIRNKANGYTFEFSASVGM 19
|||||
Db 50 FIRNKANGYTFEYSASVKG 68

RESULT 15
S24523
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S24523
R:Kaartinen, M.
Submitted to the EMBL Data Library, October 1991
A:Reference number: S24490
A:Accession: S24523
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-91 <RAA>
A:Cross-references: EMBL:X66666; NID:g51251; PIDN:CAA47228.1; PID:g388532
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:6-91/Domain: immunoglobulin homology <IMM>

Query Match 84.5%; Score 82; DB 2; Length 91;
Best Local Similarity 88.9%; Pred. No. 1.6e-06;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 IRNKANGYTFEFSASVGM 19
|||||



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2001, 15:54:37 ; Search time 105.36 Seconds
(without alignments)
6.177 Million cell updates/sec

Title: US-09-724-406-22
Perfect score: 97
Sequence: 1 FIRNKANGYTFESASVMG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72	74.2	117	1 HV17_MOUSE	P01786 mus muscu
2	71	73.2	122	1 HV21_MOUSE	P01790 mus muscu
3	71	73.2	123	1 HV18_MOUSE	P01787 mus muscu
4	71	73.2	123	1 HV19_MOUSE	P01788 mus muscu
5	71	73.2	123	1 HV22_MOUSE	P01791 mus muscu
6	71	73.2	123	1 HV25_MOUSE	P01794 mus muscu
7	66	68.0	122	1 HV20_MOUSE	P01789 mus muscu
8	62	63.9	123	1 HV23_MOUSE	P01792 mus muscu
9	59	60.8	123	1 HV24_MOUSE	P01793 mus muscu
10	55	56.7	144	1 HV26_MOUSE	P01795 mus muscu
11	47	48.5	142	1 HV01_RAT	P01805 mus muscu
12	46	47.4	115	1 HV32_MOUSE	P01801 mus muscu
13	41	42.3	113	1 HV27_MOUSE	P01796 mus muscu
14	41	42.3	113	1 HV28_MOUSE	P01797 mus muscu
15	41	42.3	113	1 HV29_MOUSE	P01798 mus muscu
16	41	42.3	113	1 HV30_MOUSE	P01799 mus muscu
17	41	42.3	115	1 HV33_MOUSE	P01802 mus muscu
18	41	42.3	381	1 GVPC_HALME	Q02228 halobacteri
19	41	42.3	639	1 TETM_STRLI	Q02652 streptomyce
20	41	42.3	690	1 VATI_DEIRA	Q9rwh3 deinococcus
21	40	41.2	113	1 HV31_MOUSE	P01800 mus muscu
22	40	41.2	824	1 HELI_HSV60	P52356 human herpe
23	40	41.2	824	1 HELI_HSV62	P52450 human herpe
24	40	41.2	1183	1 CNA_STRAU	Q53654 staphylococ
25	39	40.2	252	1 YAGI_ECOLI	P77300 escherichia
26	39	40.2	352	1 STSV_CATRO	P18417 catharanthu
27	39	40.2	358	1 TRMU_CHLTR	O84289 chlamydia t
28	39	40.2	401	1 HAT2_YEAST	P39984 saccharomyc
29	39	40.2	666	1 COI4_BRAJA	P98057 bradyrhizob
30	39	40.2	993	1 FLT3_HUMAN	P36888 homo sapien
31	39	40.2	1267	1 VLS_REOVJ	P17377 reovirus (t
32	39	40.2	2244	1 PYRL_SCHPO	Q09794 schizosacch
33	38.5	39.7	450	1 HEMN_BRAJA	O31381 bradyrhizob

34 38.5 39.7 658 1 LYTB_STRPN
35 38 39.2 131 1 RS17_SCHPO
36 38 39.2 136 1 R17A_YEAST
37 38 39.2 136 1 R17B_YEAST
38 38 39.2 146 1 RS17_NEUCR
39 38 39.2 237 1 OPAC_NEIGO
40 38 39.2 331 1 YI19_SYNY3
41 38 39.2 527 1 SECY_PEA
42 38 39.2 889 1 GLK2_MOUSE
43 38 39.2 907 1 AVRA_PSESG
44 38 39.2 908 1 GLK2_HUMAN
45 38 39.2 908 1 GLK2_RAT

Q9z4p7 streptococc
O42984 schizosacch
P02407 saccharomyc
P14127 saccharomyc
P27770 neurospora
Q04880 neisseria g
P73709 synchocyst
Q9xqu4 pismu sativ
P39087 mus musculu
P14377 pseudomonas
Q13002 homo sapien
P42260 rattus norv

ALIGNMENTS

RESULT 1
HV17_MOUSE
ID HV17_MOUSE STANDARD; PRT; 117 AA.
AC P01786;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION MOPC 47A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=80049769; PubMed=115869;
RA Robinson E.A., Appella E.;
RT "Amino acid sequence of a mouse myeloma immunoglobulin heavy chain
(MOPC 47 A) with a 100-residue deletion.";
RL J. Biol. Chem. 254:11418-11430(1979).
CC -!- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA
LINKED BY A DISULFIDE BOND. IN CONTRAST, NORMAL MOUSE IGA
MOLECULES CONTAIN TWO LIGHT AND TWO HEAVY CHAINS AND LACK A
LIGHT-HEAVY CHAIN DISULFIDE BOND.
CC PIR: A02069; ALMS47.
DR HSSP: P01789; 2MCP.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
KW Immunoglobulin V region.
FT NON_TER 117
SQ SEQUENCE 117 AA; 12975 MW; 0C74BE8BB154BDF4 CRC64;

Query Match 74.2%; Score 72; DB 1; Length 117;
Best Local Similarity 86.7%; Pred. No. 1.4e-05;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FIRNKANGYTFESA 15
|||||:|||||:11
Db 50 FIRNKABGYTFESA 64

RESULT 2
HV21_MOUSE
ID HV21_MOUSE STANDARD; PRT; 122 AA.
AC P01790;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION M511.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.

Fri Jun 29 08:04:48 2001

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RX MEDLINE=81054880; PubMed=6776528;
RA Robinson E.A., Appella E.;
RT "Complete amino acid sequence of a mouse immunoglobulin alpha chain
RL (MOPC 511).";
CC Proc. Natl. Acad. Sci. U.S.A. 77:4909-4913(1980).
CC -|- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS PHOSPHORYLCHOLINE.
DR PIR: A02070; AVMT5.
DR HSP: P01789; 2MCP.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
DR Immunoglobulin V region.
KW NON_TER 122 122
FT SEQUENCE 122 AA; 13652 MW; 9F4837731EA50207 CRC64;

Query Match 73.2%; Score 71; DB 1; Length 122;
Best Local Similarity 82.4%; Pred. No. 2.2e-05;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 RNKANGYTTTFSASVMG 19
DB 52 RNKANDYTTTFSASVKG 68
||||| ||||:|||||

RESULT 4
ID HV18_MOUSE STANDARD; PRT; 123 AA.
AC P01787;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION HPCM3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RA Barstad P.;
RL thesis (1975). California Institute of Technology / Pasadena, U.S.A.
CC -|- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS PHOSPHORYLCHOLINE.
DR PIR: A02070; AVMT5.
DR HSP: P01789; 2MCP.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
DR Mus musculus (Mouse).
KW Immunoglobulin V region.
KW NON_TER 123 123
FT SEQUENCE 123 AA; 13805 MW; 9D581401912F7000 CRC64;

Query Match 73.2%; Score 71; DB 1; Length 123;
Best Local Similarity 82.4%; Pred. No. 2.3e-05;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 RNKANGYTTTFSASVMG 19
DB 52 RNKANDYTTTFSASVKG 68
||||| ||||:|||||

RESULT 5
ID HV22_MOUSE STANDARD; PRT; 123 AA.
AC P01791;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION HPCM6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.;
RL "IgG antibodies to phosphorylcholine exhibit more diversity than
RT their IgM counterparts.";
CC Nature 291:29-34(1981).
CC -|- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS PHOSPHORYLCHOLINE.
DR PIR: A02070; AVMT5.
DR HSP: P01789; 2MCP.
DR InterPro: IPR003006; -.
DR Immunoglobulin V region; Hybridoma.
KW

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```

DR Pfam: PF00047; ig: 1.
KW Immunoglobulin V region; Hybridoma.
FT NON_TER 123 123
SQ SEQUENCE 123 AA; 13895 MW; 81361892ECBF7000 CRC64;

Query Match
Best Local Similarity 73.2%; Score 71; DB 1; Length 123;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 RNKANGYTTTFSASVGM 19
Db 52 RNKANDYTTTFSASVKG 68

RESULT 6
HV25_MOUSE
ID HV25_MOUSE STANDARD; PRT; 123 AA.
AC P01794;
DT 21-JUL-1986 (Rel. 01, Created)
DE 21-JUL-1986 (Rel. 01, Last sequence update)
DE IG HEAVY CHAIN V REGION HPCG14.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81197602; PubMed=7231520;
RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.;
RT "IgG antibodies to phosphorylcholine exhibit more diversity than
RL their IGM counterparts."
RL Nature 291:29-34(1981).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
DR BINDS PHOSPHORYLCHOLINE.
DR PIR: A02070; AVMS75.
DR HSP: P01789; 2MCP.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; ig: 1.
KW Immunoglobulin V region; Hybridoma.
FT NON_TER 123 123
SQ SEQUENCE 123 AA; 13807 MW; A7584FE098B7785D CRC64;

Query Match
Best Local Similarity 73.2%; Score 71; DB 1; Length 123;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 RNKANGYTTTFSASVGM 19
Db 52 RNKANDYTTTFSASVKG 68

RESULT 7
HV20_MOUSE
ID HV20_MOUSE STANDARD; PRT; 122 AA.
AC P01789;
DT 21-JUL-1986 (Rel. 01, Created)
DE 21-JUL-1986 (Rel. 01, Last sequence update)
DE IG HEAVY CHAIN V REGION M603.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80199926; PubMed=6769593;
RA Early P., Huang H., Davis M., Calame K., Hood L.;
RT "An immunoglobulin heavy chain variable region gene is generated from
RL three segments of DNA: VH, D and JH."
RL Cell 19:981-992(1980).

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RN RP SEQUENCE OF 1-120.
RX MEDLINE=75017346; PubMed=4213527;
RA Rudikoff S., Potter M.;
RT "Variable region sequence of the heavy chain from a phosphorylcholine
RL binding myeloma protein."
RL Biochemistry 13:4033-4038(1974).
RN [3]
RX X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF FAB FRAGMENT.
RX MEDLINE=75065510; PubMed=4530984;
RA Segal D.M., Padlan E.A., Cohen G.H., Rudikoff S., Potter M.,
RA Davies D.R.;
RT "The three-dimensional structure of a phosphorylcholine-binding mouse
RL immunoglobulin Fab and the nature of the antigen binding site."
RL Proc. Natl. Acad. Sci. U.S.A. 71:4298-4302(1974).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
DR BINDS PHOSPHORYLCHOLINE.
DR PIR: A02070; AVMS75.
DR PDB: 1MCP; 15-JUL-92.
DR PDB: 2MCP; 15-JUL-92.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; ig: 1.
KW Immunoglobulin V region; 3D-structure.
FT SITE 33 33
FT H-BOND WITH THE PHOSPHATE GROUP OF PHOS-
FT PHORYLCHOLINE.
FT H-BOND WITH THE PHOSPHATE GROUP OF PHOS-
FT PHORYLCHOLINE.
FT STRAND 3 7
FT STRAND 11 12
FT TURN 14 15
FT STRAND 17 25
FT HELIX 29 31
FT STRAND 33 39
FT TURN 41 42
FT STRAND 46 50
FT TURN 54 55
FT STRAND 61 61
FT TURN 64 66
FT STRAND 67 67
FT TURN 68 69
FT STRAND 70 75
FT TURN 76 79
FT STRAND 80 86
FT HELIX 90 92
FT STRAND 94 103
FT STRAND 107 112
FT STRAND 116 120
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13626 MW; BA2C864438B64F0F CRC64;

Query Match
Best Local Similarity 68.0%; Score 66; DB 1; Length 122;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 RNKANGYTTTFSASVGM 19
Db 52 RNKNGKYTTTFSASVKG 68

RESULT 8
HV23_MOUSE
ID HV23_MOUSE STANDARD; PRT; 123 AA.
AC P01792;
DT 21-JUL-1986 (Rel. 01, Created)
DE 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION HPCG8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

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Fri Jun 29 08:04:48 2001

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93358330; PubMed=6101208;
RA Kim S., Davis M., Sinn E., Patten P., Hood L.;
RT "Antibody diversity: somatic hypermutation of rearranged VH genes.";
RL Cell 27:573-581(1981).
RN [2]
RP SEQUENCE OF 20-142.
RX MEDLINE=76222762; PubMed=819932;
RA Rudikoff S., Potter M.;
RT "Size differences among immunoglobulin heavy chains from
phosphorylcholine-binding proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 73:2109-2112(1976).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN
THAT BINDS PHOSPHORYLCHOLINE.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
CC EMBL; J00516; AAC18867.1; -.
DR PIR; A02071; AVMS67.
DR HSSP; P01789; 2MCP.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 144 IG HEAVY CHAIN V REGION M167.
FT CONFLICT 125 125 N -> D (IN REF. 2).
FT NON_TER 144 144
FT SEQUENCE 144 AA; 16219 MW; BECBA42C956CF769 CRC64;
SQ
Query Match 56.7%; Score 55; DB 1; Length 144;
Best Local Similarity 64.7%; Pred. No. 0.016;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 3 RNKANGYTFESASVMG 19
Db 71 RSKAHDYTFESASVKG 87
|:::|:::|:::|
RESULT 11
ID HV01_RAT STANDARD; PRT; 142 AA.
AC P01805;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION IR2 PRECURSOR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83064537; PubMed=6292865;
RA Hellman L., Pettersson U., Engstrom A., Karlsson T., Bennich H.;
RT "Structure and evolution of the heavy chain from rat immunoglobulin
E.";
RL Nucleic Acids Res. 10:6041-6049(1982).
CC -1- MISCELLANEOUS: THE MRNA WAS ISOLATED FROM AN ICE-SECRETING
IMMUNOCYTOMA THAT ARISES SPONTANEOUSLY IN LOU/C/WSL RATS.
CC
CC PIR; A02075; EVTR2.
DR HSSP; P01789; 2MCP.

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RP SEQUENCE.
RX MEDLINE=81197602; PubMed=7231520;
RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.;
RT "IgG antibodies to phosphorylcholine exhibit more diversity than
their IgM counterparts.";
RL Nature 291:29-34(1981).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BINDS PHOSPHORYLCHOLINE.
CC
CC PIR; A02070; AVMS5.
DR HSSP; P01789; 2MCP.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
DR Immunoglobulin V region; Hybridoma.
KW NON_TER 123 123
FT SEQUENCE 123 AA; 13879 MW; 4559D3106CAF7D8D CRC64;
SQ
Query Match 63.9%; Score 62; DB 1; Length 123;
Best Local Similarity 76.5%; Pred. No. 0.00082;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 3 RNKANGYTFESASVMG 19
Db 52 RNKAFDYTFESASVKG 68
|:::|:::|:::|
RESULT 9
ID HV24_MOUSE STANDARD; PRT; 123 AA.
AC P01793;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION HPCG13.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81197602; PubMed=7231520;
RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.;
RT "IgG antibodies to phosphorylcholine exhibit more diversity than
their IgM counterparts.";
RL Nature 291:29-34(1981).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BINDS PHOSPHORYLCHOLINE.
CC
CC PIR; A02070; AVMS5.
DR HSSP; P01789; 2MCP.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
DR Immunoglobulin V region; Hybridoma.
KW NON_TER 123 123
FT SEQUENCE 123 AA; 13808 MW; 6599F256CCEDE50 CRC64;
SQ
Query Match 60.8%; Score 59; DB 1; Length 123;
Best Local Similarity 70.8%; Pred. No. 0.0027;
Matches 12; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 3 RNKANGYTFESASVMG 19
Db 52 RNKYDYTFESASVKG 68
|:::|:::|:::|
RESULT 10
ID HV26_MOUSE STANDARD; PRT; 144 AA.
AC P01795;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION M167 PRECURSOR.

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DR InterPro: IPR003006; -.
KW Immunoglobulin V region; Signal.
FT SIGNAL 19
FT CHAIN 20 142 IG HEAVY CHAIN V REGION IR2.
FT NON_TER 142 142
SQ SEQUENCE 142 AA; 16024 MW; DE29E6CFE745DF3B CRC64;

Query Match 48.5%; Score 47; DB 1; Length 142;
Best Local Similarity 50.0%; Pred. No. 0.38;
Matches 9; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 IRNKANGYTTTFSASVVG 19
   ||||| | : | |
DB 70 IRNKANNVAYVYKSLAG 87

RESULT 12
HV32_MOUSE
ID HV32_MOUSE STANDARD; PRT; 115 AA.
AC P01801;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION J606.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=82099361; PubMed=6798111;
RA Johnson N., Stankard J., Paul L., Hood L.;
RT "The complete V domain amino acid sequences of two myeloma inulin-
RT binding proteins."
RL J. Immunol. 128:302-307(1982).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS INULIN.
DR PIR: C92811; AVMS06.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region.
FT DISULFID 22 98 BY SIMILARITY.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12810 MW; B67AD6638A121A5F CRC64;

Query Match 47.4%; Score 46; DB 1; Length 115;
Best Local Similarity 50.0%; Pred. No. 0.45;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 IRNKANGYTTTFSASVVG 19
   ||||| | : | |
DB 51 IRLKSNYATHVAESVKG 68

RESULT 13
HV27_MOUSE
ID HV27_MOUSE STANDARD; PRT; 113 AA.
AC P01796;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION A4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=78158406; PubMed=417344;
RA Vrana M., Rudikoff S., Potter M.;

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RT "Sequence variation among heavy chains from inulin-binding myeloma
RT proteins."
RL Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS INULIN.
DR PIR: A93818; AVMSAB.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region.
FT DISULFID 22 98 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12675 MW; 76658C121C598285 CRC64;

Query Match 42.3%; Score 41; DB 1; Length 113;
Best Local Similarity 44.4%; Pred. No. 3.2;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 IRNKANGYTTTFSASVVG 19
   ||||| | : | |
DB 51 IRLKSHNYATHVAESVKG 68

RESULT 14
HV28_MOUSE
ID HV28_MOUSE STANDARD; PRT; 113 AA.
AC P01797;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION U61.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=78158406; PubMed=417344;
RA Vrana M., Rudikoff S., Potter M.;
RT "Sequence variation among heavy chains from inulin-binding myeloma
RT proteins."
RL Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS INULIN.
DR PIR: B93818; AVMS61.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region.
FT DISULFID 22 98 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12671 MW; 76634C121C598285 CRC64;

Query Match 42.3%; Score 41; DB 1; Length 113;
Best Local Similarity 44.4%; Pred. No. 3.2;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 IRNKANGYTTTFSASVVG 19
   ||||| | : | |
DB 51 IRLKSHNYATHVAESVKG 68

RESULT 15
HV29_MOUSE
ID HV29_MOUSE STANDARD; PRT; 113 AA.
AC P01798;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION E109.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=78158406; PubMed=417344;
 RA Vrana M., Rudikoff S., Potter M.;
 RT "Sequence variation among heavy chains from inulin-binding myeloma
 RL proteins."; Acad. Sci. U.S.A. 75:1957-1961(1978).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
 CC BINDS INULIN.
 DR PIR; C93818; AVMS09.
 DR InterPro: IPR003006; -.
 DR Pfam: PF00047; ig: 1.
 KW Immunoglobulin V region. BY SIMILARITY.
 FT DISULFID 22 98
 FT NON_TER 113 113
 SQ SEQUENCE 113 AA; 12647 MW; EE50F2F20EDB129B CRC64;

Query Match 42.3%; Score 41; DB 1; Length 113;
 Best Local Similarity 44.4%; Pred. No. 3.2;
 Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Oy 2 IRNKANGYTFEFSASVMG 19
 |||::||::|||
 Db 51 IRLKSHNYATHYAESVKG 68

Search completed: June 28, 2001, 15:54:38
 Job time: 126 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2001, 16:08:24 ; Search time 411.58 Seconds
(without alignments)
6.108 Million cell updates/sec

Title: us-09-724-406-22

Perfect score: 97
Sequence: 1 FIRKANGYTTFSASVWG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues
Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL16:

- 1: sp-archaea:*
- 2: sp-bacteria:*
- 3: sp-fungi:*
- 4: sp-human:*
- 5: sp-invertebrate:*
- 6: sp-mammal:*
- 7: sp-mhc:*
- 8: sp-organelle:*
- 9: sp-plant:*
- 10: sp-phage:*
- 11: sp-rodent:*
- 12: sp-unclassified:*
- 13: sp-vertebrate:*
- 14: sp-virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	67	69.1	80	4	075727
2	47	48.5	76	4	075733
3	46	47.4	295	1	026691
4	46	47.4	877	10	042497
5	46	47.4	2516	2	09RN43
6	45	46.4	808	5	09V995
7	44	45.4	86	4	075740
8	44	45.4	131	4	09UL88
9	42	43.3	117	5	P91362
10	42	43.3	346	2	007414
11	42	43.3	1792	5	097417
12	42	43.3	1792	5	09V4M6
13	41	42.3	635	2	09EWR9
14	41	42.3	702	5	09VSH4
15	41	42.3	745	3	09HE61
16	41	42.3	1320	2	09X2Y4
17	40.5	41.8	463	3	09P4E8
18	40	41.2	199	14	09QCY8
19	40	41.2	418	2	09HWP4

20	40	41.2	453	2	09KQS1
21	40	41.2	487	2	050901
22	40	41.2	493	5	017454
23	40	41.2	516	5	017455
24	40	41.2	530	10	082811
25	40	41.2	547	2	007475
26	40	41.2	584	2	09KEB2
27	40	41.2	655	2	09RXY9
28	40	41.2	824	14	057139
29	40	41.2	1146	5	09N8Q9
30	40	41.2	1282	2	046348
31	39.5	40.7	196	10	09FGT3
32	39.5	40.7	995	5	09W2L7
33	39	40.2	81	4	075736
34	39	40.2	224	10	09SNW25
35	39	40.2	245	1	09YAP5
36	39	40.2	261	2	09RGL9
37	39	40.2	283	10	09LYX4
38	39	40.2	301	2	053796
39	39	40.2	311	14	09DVR8
40	39	40.2	427	10	09SZ39
41	39	40.2	471	5	09U6D6
42	39	40.2	474	2	09PAX0
43	39	40.2	590	10	09LYK7
44	39	40.2	607	5	09GZF2
45	39	40.2	868	14	09QEV5

ALIGNMENTS

RESULT 1

075727 ID 075727 PRELIMINARY; PRT; 80 AA.
AC 075727;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
GN VH.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM H.A.

RC TISSUE=INTESTINE;

RA Fischer M., Kueppers R.;

RT "Human IgA and IgM secreting intestinal plasma cells carry heavily

RL mutated VH region genes.";

RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.

CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX

CC DOMAIN.

DR EMBL; AJ009524; CAA08731.1; -

DR InterPro; IPR003006; -

DR InterPro; IPR003596; -

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

FT NON_TER 1

FT NON_TER 80

SQ SEQUENCE 80 AA; 9351 MW; B5A34A4210437AAE CRC64;

Query Match 69.1%; Score 67; DB 4; Length 80;

Best Local Similarity 72.2%; Pred. No. 0.00044;

Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 IRKANGYTTFSASVWG 19

Db 19 IRKANGYTTFSASVWG 36

RESULT 2

	Query Match	47.4%;	Score 46;	DB 1;	Length 295;	
	Best Local Similarity	52.9%;	Pred. No. 7.1;	Mismatches	5; Indels	0; Gaps
	Matches	9; Conservative				
OY	1 FIRNKANGYTTEFSASV 17					
	: :					
DB	254 FIRNNADGVASSFRAAV 270					
	: :					
RESULT	4					
Q42497	PRELIMINARY;					
ID	Q42497					
AC	Q42497					
DT	01-NOV-1996 (TrEMBLrel. 01, Created)					
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)					
DT	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)					
DE	NITRATE REDUCTASE.					
DN	NIAL.					
GN	Chlorella vulgaris.					
OS	Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;					
OC	Chlorellaceae; Chlorella.					
NCBI_TaxID=3077;						
RN	[1]					
RP	SEQUENCE FROM N.A.					
EX	MEDLINE-96257211; PubMed-8666264;					
RA	Dawson H.N., Pendleton L.C., Solomonson L.P., Cannons A.C.;					
RT	"Cloning and characterization of the nitrate reductase-encoding gene					
RT	from Chlorella vulgaris: structure and identification of transcription					
RT	start points and initiator sequences.";					
RL	Gene 171:139-145(1996).					
CC	-!- SIMILARITY: TO CYTOCHROME B5 DOMAIN.					
DR	EMBL; U39931; AAC49460.1; -.					
DR	EMBL; U39930; AAC49459.1; -.					
DR	HSP; P17571; 2CNDU.					
DR	Mendel; 7718; Chlva; Nial; 7718.					
DR	InterPro; IPR000572; -.					
DR	InterPro; IPR001195; -.					
DR	InterPro; IPR001433; -.					
DR	InterPro; IPR001834; -.					
DR	Pfam; PF00173; heme_1; 1.					
DR	Pfam; PF00174; oxidored_molyb; 1.					
DR	Pfam; PF00175; oxidored_fad; 1.					
DR	Pfam; PF00970; Cyt.reductase; 1.					
DR	PRINTS; PR00406; CYTB5RDFTASE.					
DR	PRINTS; PR00363; CYTOCHROME B5.					
DR	PRINTS; PR00407; EUMOPTERIN.					
DR	PROSITE; PS00191; CYTOCHROME_B5_1; 1.					
DR	PROSITE; PS0255; CYTOCHROME_B5_2; 1.					
KW	Heme.					
SQ	SEQUENCE 877 AA; 96010 MW; 09248C1B3337371C CRC64;					
	Query Match	47.4%;	Score 46;	DB 10;	Length 877;	
	Best Local Similarity	75.0%;	Pred. No. 24;	Mismatches	2; Indels	0; Gaps
	Matches	9; Conservative				
OY	5 KANGYTTEFSAS 16					
	: :					
DB	22 KANGYTEASAA 33					
RESULT	5					
Q9RNA3	PRELIMINARY;					
ID	Q9RNA3					
AC	Q9RNA3					
DT	01-MAY-2000 (TrEMBLrel. 13, Created)					
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)					
DT	01-JUN-2000 (TrEMBLrel. 14, Last annotation update)					
DE	TCOA.					
GN	Xenorhabdus luminescens (Xenorhabdus luminescens).					
OS	Photobacterium; Proteobacteria; gamma subdivision; Enterobacteriaceae;					
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;					


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OC Photorhabdus.
OX NCBI_TaxID=29488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-W-14;
RA Merlo D.J., Wegrich L.M., Roberts J.L., Petell J.K.;
RT "Expression of Photorhabdus luminescens tcda gene in maize confers
RL corn rootworm tolerance.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF188483; AAR05542.1; -
DR InterPro: IPR001589; -
DR PROSITE: PS00019; ACTININ.1; UNKNOWN.1.
SQ SEQUENCE 2516 AA; 282953 MW; 8250A0650B614B99 CRC64;

Query Match 47.4%; Score 46; DB 2; Length 2516;
Best Local Similarity 64.3%; Pred. No. 78;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 KANGYTTTFFSASVM 18
Db 2159 EATGYVMEFSANVM 2172
:| | | | | | | | | |

RESULT 6
ID Q9V995 PRELIMINARY; PRT; 808 AA.
AC Q9V995;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (T-EMBLrel. 16, Last annotation update)
DE CG15236 PROTEIN.
GN CG15236.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Brokstein P., Brotter P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Matel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacht J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kimms I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

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RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL: AE003790; AAF57401.1; -
DR FlyBase: FBgn033108; CG15236.
DR InterPro: IPR001781; -
DR PROSITE: PS000094; -; 1.
SQ SEQUENCE 808 AA; 87716 MW; 04AC2B699DA5F9AD CRC64;

Query Match 46.4%; Score 45; DB 5; Length 808;
Best Local Similarity 44.4%; Pred. No. 32;
Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 FIRKANGYTTTFFSASVM 18
Db 640 FFRSSYNDYSSEFNGSVV 657
:| | | | | | | | | |

RESULT 7
ID 075740 PRELIMINARY; PRT; 86 AA.
AC 075740;
DT 01-NOV-1998 (T-EMBLrel. 08, Created)
DT 01-NOV-1998 (T-EMBLrel. 08, Last sequence update)
DT 01-MAR-2001 (T-EMBLrel. 16, Last annotation update)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
GN VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=INTESTINE;
RA Fischer M., Kueppers R.;
RT "Human Iga and Igm secreting intestinal plasma cells carry heavily
RL mutated VH region genes.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN
DR EMBL: AJ009539; CAA08744.1; -
DR InterPro: IPR003006; -
DR InterPro: IPR003596; -
DR Pfam: PF00047; Iq; 1.
DR SMART: SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 86
SQ SEQUENCE 86 AA; 9625 MW; F529E1FBCF8CBEB3 CRC64;

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Query Match 45.4%; Score 44; DB 4; Length 86;
Best Local Similarity 44.4%; Pred. No. 3.9;
Matches 8; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 2 IRNKANGYTTTFFSASVM 19
Db 21 IKSKTDGTTDYAAPVK 38
:| | | | | | | | | |

RESULT 8
ID Q9UL88 PRELIMINARY; PRT; 131 AA.
AC Q9UL88;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (T-EMBLrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).

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Fri Jun 29 08:04:49 2001

us-09-724-406-22.rspt

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035026; AAD56262.1; -.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 131
FT NON_TER 131
SQ SEQUENCE 131 AA; 14142 MW; 96E7D668E375DEA0 CRC64;

Query Match 45.4%; Score 44; DB 4; Length 131;
Best Local Similarity 44.4%; Pred. No. 6.3;
Matches 8; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

OY 2 IRNKANGYTTTFSASVMG 19
DB 51 IKSXTDGGTDDYAPVKG 68
ID P91362 PRELIMINARY; PRT; 117 AA.
AC P91362;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE COSMID F59A3.
GN F59A3.10.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Alnscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Cooley T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkneen R.,
RA Smalton N., Smith A., Sonnenhammer E., Staden R., Sulston J.,
RA Thierri-Mieg J., Thomas K., Vaubin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
RT *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.;
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Wu X., Le T.T.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U80448; AAB37824.1; -.

SQ SEQUENCE 117 AA; 13808 MW; 8113F031205E2C3A CRC64;

Query Match 43.3%; Score 42; DB 5; Length 117;
Best Local Similarity 60.0%; Pred. No. 12;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 FIRKANGYTTTFS 15
DB 50 FLRQTAGGATTYFSA 64
ID O07414 PRELIMINARY; PRT; 346 AA.
AC O07414;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE HYPOTHETICAL 37.7 KDA PROTEIN.
GN RV0170 OR MFC128.10.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-H37RV;
RA MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekai F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squires R., Sulston J.E.,
RA Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
DR EMBL; 297050; CAB09753.1; -.
DR Tuberculist; RV0170; -.
DR InterPro; IPR003399; -.
DR Pfam; PF02470; mce; 1.
KW Hypothetical protein.
SQ SEQUENCE 346 AA; 37727 MW; 0B6F5BC6E612805F CRC64;

Query Match 43.3%; Score 42; DB 2; Length 346;
Best Local Similarity 63.6%; Pred. No. 41;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 4 NKANGYTTTFS 14
DB 34 DRTNGYTTTFS 44
ID O97417 PRELIMINARY; PRT; 1792 AA.
AC O97417;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE MYOSIN V.
GN DIDUM OR CG2146.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.

Query Match	43.3%	Score 42;	DB 5;	Length 1792;
Best Local Similarity	50.0%	Pred. No. 2.5e+02;		
Matches	8;	Conservative	4;	Mismatches 4; Indels 0; Gaps 0;

OY	2	IRNKANGYTTFASV	17
	:	:	:
DB	1383	IRNKSNGTSADVGANV	1398
<hr/>			
RESULT	12		
Q9V4M6			
ID	Q9V4M6	PRELIMINARY;	PRT; 1792 AA.
AC	Q9V4M6;		
DT	01-MAY-2003	(TrEMBLrel. 13,	Created)
DT	01-MAR-2001	(TrEMBurel. 16,	Last sequence update)
DT	01-MAR-2001	(TrEMBurel. 16,	Last annotation update)
DE	DIDUM PROTEIN.		
DE	DIDUM OR CG2146.		
GNN	Drosophila melanogaster	(Fruit fly).	
OS	Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;		
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OX	Ephyridioidea; Drosophilidae; Drosophila.		
NCBI_TaxID=7227;	[1]		
RN	SEQUENCE FROM N.A.		
RP	STRAIN=BERKELEY;		
RC	MEDLINE=20_96006; PubMed=10731132;		
RR	Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,		
RR	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,		
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,		
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,		
RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,		
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,		
RA	Abri1 J.J., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,		
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,		
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,		
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,		
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,		

RA	Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.B., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lascko P., Lei Y., Levitsky A.C., Li J., Li Z., Liang Y., Lin X., Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Modary C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.C., Pacle J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Sidon-Klamis I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svrlkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasarman D.A., Weinstein G.M., Weissbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.
RT	"The genome sequence of <i>Drosophila melanogaster</i> ."
RL	Science 287:2135-2195(2000).
DR	EMBL; AE003841; AAF59241.2; -.
DR	HSP; P08799; IMMN.
DR	FlyBase; FBgn0015933; didum.
DR	InterPro; IPRO000048; -.
DR	InterPro; IPRO01609; -.
DR	InterPro; IPRO02710; -.
DR	Pfam; PF00063; myosin_head; 1.
DR	Pfam; PF00612; IQ; 6.
DR	Pfam; PF01843; DIL; 2.
DR	PRINTS; PR00193; MYOSINHEAVY.
SQ	SEQUENCE 1792 AA; 207260 MW; A34A6FA70271CB43 CRC64;
Query Match	43.3%; Score 42; DB 5; Length 1792;
Best Local Similarity	50.0%; Pred. No. 2.6e+02;
Matches	8; Conservative 4; Mismatches 4; Indels 0; Gaps
Qy	2 IRNKANGYTTFSSASV 17 ::: s : :
Db	1383 IRNKSNGTSADVCAWV 1398 ::: s : :
RESULT 13	
ID	Q9EWR9 PRELIMINARY; PROT; 635 AA.
OC	O9EWR9;
DC	01-MAR-2001 (TrEMBLrel. 16, Created)
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE	TETRACYCLINE RESISTANCE PROTEIN.
GN	TEM.
OS	Streptomyces coelicolor.
OC	Bacteria; Firmicutes; Actinobacteriae; Actinobacteridae;
OC	Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX	NCBI_TaxID=1902;
RN	[1]
RN	SEQUENCE FROM N.A.
RC	STRAIN=A3(2);
CC	Seeger K.J., Harris D.;
RL	Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN=A3(2);
CC	Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RL	Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN	[3]

Query Match 43.3%; Score 42; DB 5; Length 1792;
Best Local Similarity 50.0%; Pred. No. 2.6e+02;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

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QY      2  IRNKANGYTTEFSASV  17
        ||||| : : | : |
Db     1383  IRNKSNGTSDVGVANV  1398
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RESULT 13

Q9EWR9	ID	Q9EWR9	PRELIMINARY;	PRT;	635 AA.
AC	QC	Q9EWR9;			
DT	DT	01-MAR-2001	(TremBLrel. 16, Created)		
DT	DT	01-WAR-2001	(TremBLrel. 16, Last sequence update)		
DT	DT	01-MAR-2001	(TremBLrel. 16, Last annotation update)		
DE	DE	TETRAYCLINE RESISTANCE PROTEIN.			
OS	OS	TEM.			
OC	OS	Streptomyces coelicolor.			
OC	OC	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;			
OX	OC	Actinomycetales; Streptomycineae; Streptomycetaceae; Str			
[1]	RN	NCBI_TaxID=1902;			
RN	RN	[1]			
RP	RP	SEQUENCE FROM N.A.			
RA	RC	STRAIN=A3(2);			
RL	RC	Seeger K.J.; Harris D.;			
RN	RL	Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.			
[2]	RN	[2]			
RP	RP	SEQUENCE FROM N.A.			
RA	RC	STRAIN=A3(2);			
RL	RC	Cerdeno A.M.; Parkhill J., Barrell B.G., Rajandream M.A.;			
RN	RL	Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.			
[3]	RN	[3]			

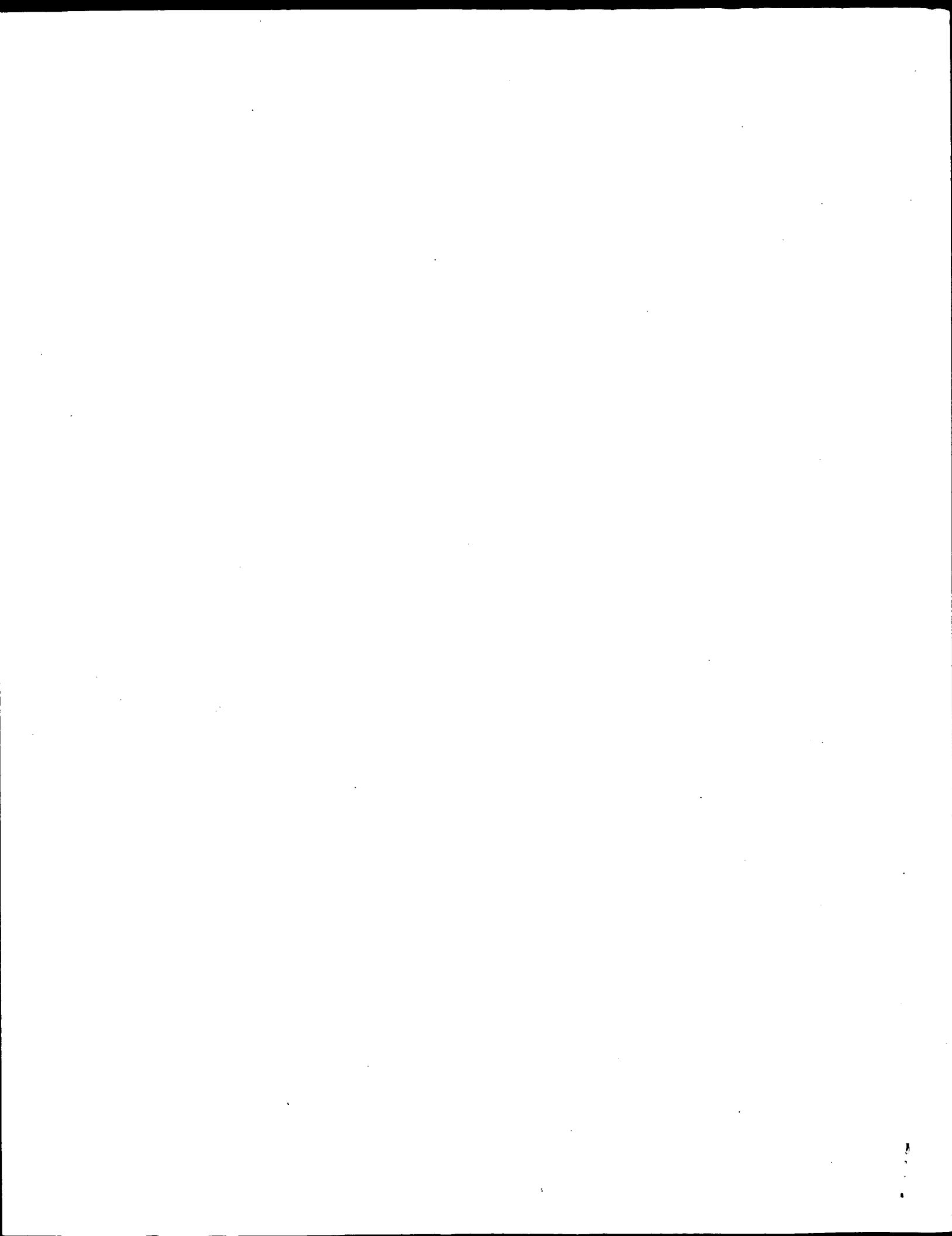
SEQUENCE FROM N.A.
STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
Redenbach M., Kieser H.M., Denapatte D., Eichner A., Cullum J.,
Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
MOL. Microbiol. 21:77-96(1996).
EMBL; AL445945; CAC14348.1; -.
Cyclin.
SEQUENCE 635 AA; 66884 MW; FD8DEBC2BF2310FF CRC64;

		Pred. NO. 1.2e+02;		
Best Local Similarity	47.1%	Mismatches	5:	Gaps
Matches	8:	Conservative	Indels	0:
QY	1 FIRNKANGYTTEFSASV	17		
	: : :			
Dd	288 FLRRSDGRTTVEGSRV	304		

Q9VSH4	PRELIMINARY;	PRT;	702 AA.
ID	Q9VSH4		
AC	Q9VSH4;		
DT	01-WAY-2000 (TREMBLrel. 13, Created)		
DT	01-WAY-2000 (TREMBLrel. 13, Last sequence update)		
DT	01-WAR-2001 (TREMBLrel. 16, Last annotation update)		
DE	CG7185 PROTEIN.		
GN	CG7185.		
OS	Drosophila melanogaster (Fruit fly).		
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;		
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC	Ephydroidea; Drosophilidae; Drosophila.		
OX	NCBI_TaxID=7227;		
RN	[1]		
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RP	STRAIN=BERKELEY.		
RX	MEDLINE=20196006; PubMed=10731132;		
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,		
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,		
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,		
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,		
RA	Randown R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,		
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,		
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RA	Baxendale S.A., Beeson J., Bonin M., Borodovsky M., Boudreau N.,		
RA	Brett D., Brown J., Brunelle A., Busch C., Butler L.,		
RA	Butterfield R., Caciopre R., Chan A.M., Chao M., Chiu J.,		
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RA	Conrad M., Corbett R., Coulte K., Currely M., Daczkowski R.,		
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RA Borkova D., Botchan M.R., Bouck J., Brookstein P., Brottier P.,
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 RA Gloděk A., Gong F., Correll J.H., Gu Z., Guan P., Harris M.,
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 RA Shue B.C., Siden-kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissensbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

Search completed: June 28, 2001, 16:08:25
Job time: 953 sec



	XX	21-NOV-1996.	
	DD		
	PPD	16-MAY-1996; 96WO-US07113.	
	XXX		
	XXXX	18-MAY-1995; 95US-0443540.	
	XXXXX	(UNWI) UNIV MICHIGAN.	
	XPA	Glick GD, Swanson PC;	
	XX	WPI; 1997-011854/Ol.	
	XX	N-PSDB; AAT43740.	
	XX	Anti-DNA antibody which specifically binds DNA hairpin - useful to develop prods. for diagnosis and treatment of disorders, e.g. glomerulonephritis or systemic lupus erythematosus	
	XX	Example; Fig 7; 102pp; English.	
	CC	The present sequence is the heavy chain variable region of the anti-DNA monoclonal antibody (Mab) 1lf8, which has a high affinity for single stranded DNA, low or no affinity for double stranded DNA and specifically binds a DNA hairpin. The Mab can be used diagnose disorders associated with the pathological complexation of DNA,	
	CCC	e.g. inflammatory glomerulonephritis and systemic lupus erythematosus. It can also be used to generate reagents to screen for pharmaceutical agents, and treat and/or prevent an above disorder.	
	CCCC	Calf thymus DNA was used to immunise a MRL-lpr mouse, spleen cells from which were then fused with Sp2/0 myeloma cells to give hybridomas producing the anti-DNA Mab. 1f8 was found to react strongly with single stranded DNA and poly(dT).	
	XX	Sequence 115 AA;	
	ISQ		
		Query Match 63.3%; Score 57; DB 18; Length 115; Best Local Similarity 83.3%; Pred. No. 0.13; Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
	OY	3 PYGNPHYYAMDY 14 93 pygnygyyamyd 104	
	Ddb		
		RESULT 2	
	AARW07438	AAW07438 standard; Protein; 123 AA.	
	ID	AAW07438	
	XX		
	AC	AAW07438;	
	DT	12-AUG-1997 (first entry)	
	DE	Anti-DNA antibody 1lf8 group heavy chain variable region.	
	KK	Heavy chain; variable region; anti-DNA; monoclonal; antibody; 1lf8 group; hairpin; diagnosis; inflammatory glomerulonephritis; systemic lupus erythematosus; screening; treatment; prevention; SLE; disease; consensus; putative.	
	OS	Synthetic.	
	Key	Location/Qualifiers	
	Ft	Region 1..30 /label= framework_I	
	Ft	FT Region 31..35 /label= CDR_I	
	Ft	FT Region 36..49 /label= framework_II	
	Ft	FT Region 50..66 /label= CDR_II	
	Ft	FT Region 67..98	


```

PF 14-JAN-1997; 97FR-0000300.
XX
PR 14-JAN-1997; 97FR-0000300.
XX
XX (UYBO-) UNIV BOURGOGNE.
XX
PI Bourgeois C, Kohli E, Pothier P;
XX
DR WPI; 1998-390320/34.
XX
XX New peptide(s) recognising viral epitope with tropism to mucosa -
PT useful for, e.g. diagnosing, preventing and treating viral
PT infection(s)
XX
XX Claim 8; Fig 3; 5lpp; French.
XX
XX AAW70905-46 represent peptide sequences that can recognise, by
CC antigen-antibody type reactions, at least 1 epitope of a pathogenic
CC virus having tropism for the mucosa. AAW70905-16 and AAW70929-46 are
CC analogous to CDR regions of monoclonal antibodies specific for
CC respiratory syncytial virus (RSV). AAW70917-28 are analogous to CDR
CC regions of monoclonal antibodies specific for site III or IV of the
CC VP6 protein of rota virus (RV). The peptides can neutralise viral
CC infections and may also inhibit fusion between infected and uninfected
CC cells or cells and viruses. They provide passive or active protection
CC and/or inhibit transcription of the virus, so are useful as antiviral
CC agents or for prophylaxis, in human or veterinary medicine. The peptides
CC can be labelled and used to diagnose infection or contamination by the
CC virus. The peptides are particularly directed against RSV or RS but may
CC also be used against papilloma, adeno, entero, polio, influenza or
CC immune deficiency viruses.
XX
SQ Sequence 14 AA;

Query Match 54.4%; Score 49; DB 19; Length 14;
Best Local Similarity 57.1%; Pred. No. 0.25;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 DPPYGNPHYAMDY 14
||| : : ||||
Db 1 dpdyndnyfyamdy 14

RESULT 4
AAW70931
ID AAW70931 standard; peptide; 14 AA.
XX
AC AAW70931;
XX
DT 14-OCT-1998 (first entry)
XX
DE CDR3 of the heavy chain of monoclonal antibody RS-18B2.
XX
KW Pathogenic virus; tropism; mucosa; CDR region; monoclonal antibody;
KW respiratory syncytial virus; RSV; VP6 protein; rota virus; RV;
KW viral infection; inhibit; fusion; protection; transcription;
KW antiviral agent; prophylaxis; diagnosis; infection; contamination.
XX
OS Synthetic.
OS Mus sp.
XX
XX FR2758331-A1.
XX
PD 17-JUL-1998.
XX
XX 14-JAN-1997; 97FR-0000300.
XX
XX 14-JAN-1997; 97FR-0000300.
XX
XX (UYBO-) UNIV BOURGOGNE.
XX
PI Bourgeois C, Kohli E, Pothier P;

Query Match 54.4%; Score 49; DB 19; Length 14;
Best Local Similarity 57.1%; Pred. No. 0.25;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 DPPYGNPHYAMDY 14
||| : : ||||
Db 1 dpdyndnyfyamdy 14

RESULT 5
AAW70913
ID AAW70913 standard; peptide; 23 AA.
XX
AC AAW70913;
XX
DT 14-OCT-1998 (first entry)
XX
DE Peptide PEP3H, homologous to heavy chain CDR3 of antibody RS-348.
XX
KW Pathogenic virus; tropism; mucosa; CDR region; monoclonal antibody;
KW respiratory syncytial virus; RSV; VP6 protein; rota virus; RV;
KW viral infection; inhibit; fusion; protection; transcription;
KW antiviral agent; prophylaxis; diagnosis; infection; contamination.
XX
OS Synthetic.
OS Mus sp.
XX
XX FR2758331-A1.
XX
PD 17-JUL-1998.
XX
XX 14-JAN-1997; 97FR-0000300.
XX
XX 14-JAN-1997; 97FR-0000300.
XX
XX (UYBO-) UNIV BOURGOGNE.
XX
PI Bourgeois C, Kohli E, Pothier P;
XX
XX WPI; 1998-390320/34.
XX
XX New peptide(s) recognising viral epitope with tropism to mucosa -
PT useful for, e.g. diagnosing, preventing and treating viral
PT infection(s)
XX

```


CC that can be used in the treatment of HIV infection.

XX Sequence 225 AA;

Query Match 50.6%; Score 45.5; DB 15; Length 225;
Best Local Similarity 75.0%; Pred. No. 14;
Matches 9; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 3 PYGN-PHYAMD I3
||||:|||||
Db 103 pygndayyyamd I14

RESULT 8

AAB61541
ID AAB61541 standard; Protein; 269 AA.

XX AC AAB61541;

XX DT 03-APR-2001 (first entry)

XX DE 3DX sfv protein sequence.

XX KW 3DX; single chain antibody; ScFv; modular protein binding domain; MPBD;
XX KW protein-protein interaction.

XX OS Unidentified.

XX FN WO200101137-A1.

XX PD 04-JAN-2001.

XX PF 29-JUN-2000; 2000WO-US17929.

XX PR 30-JUN-1999; 99US-0141896.

XX PA (CHIL-) CHILDRENS MEDICAL CENT.
XX PA (BLOO-) CENT BLOOD RES.

XX PI Mayer BJ, Saksele K, Kirchausen T;

XX WPI; 2001-123027/13.

XX DR N-PSDB; AAF28599.

XX PT New fusion proteins, useful for validating protein-protein interaction
XX PT causing a specific biological activity, comprises a single chain
XX PT antibody instead of a modular protein binding domain

XX Example 1; Fig 1; 34pp; English.

XX CC The present invention relates to fusion proteins containing a single
XX CC chain antibody (sfv) in place of a modular protein binding domain (MPBD),
XX CC or an antibody epitope in place of the linear binding epitope for a MPBD.
XX CC The fusion proteins can be used in assays to identify protein-protein
XX CC interactions. The present sequence is the protein sequence for 3DX
XX CC antibody. 3DX is derived from 9E10. 3DX was used in the method of the
XX CC present invention.

XX Sequence 269 AA;

Query Match 50.6%; Score 45.5; DB 22; Length 269;
Best Local Similarity 75.0%; Pred. No. 17;
Matches 9; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 4 YGNPHY-AMDY 14
|||:|||||
Db 110 ygntyyyamdy 121

RESULT 9

AAG27978

ID AAG27978 standard; Protein; 304 AA.

XX AC AAG27978;

XX DT 17-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 33024.

XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX KW termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301439.

XX PR 25-FEB-1999; 99US-0121825.

XX PR 05-MAR-1999; 99US-0123180.

XX PR 09-MAR-1999; 99US-0123548.

XX PR 23-MAR-1999; 99US-0125788.

XX PR 25-MAR-1999; 99US-0126264.

XX PR 23-MAR-1999; 99US-0126785.

XX PR 01-APR-1999; 99US-0127462.

XX PR 06-APR-1999; 99US-0128234.

XX PR 08-APR-1999; 99US-0128714.

XX PR 16-APR-1999; 99US-0129845.

XX PR 19-APR-1999; 99US-0130077.

XX PR 21-APR-1999; 99US-0130449.

XX PR 23-APR-1999; 99US-0130510.

XX PR 23-APR-1999; 99US-0130891.

XX PR 28-APR-1999; 99US-0131449.

XX PR 30-APR-1999; 99US-0132048.

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XX PR 04-MAY-1999; 99US-0132484.

XX PR 05-MAY-1999; 99US-0132485.

XX PR 06-MAY-1999; 99US-0132486.

XX PR 06-MAY-1999; 99US-0132487.

XX PR 07-MAY-1999; 99US-0132863.

XX PR 11-MAY-1999; 99US-0134256.

XX PR 14-MAY-1999; 99US-0134218.

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XX PR 21-MAY-1999; 99US-0135353.

XX PR 24-MAY-1999; 99US-0135629.

XX PR 25-MAY-1999; 99US-0136021.

XX PR 27-MAY-1999; 99US-0136392.

XX PR 28-MAY-1999; 99US-0136782.

XX PR 01-JUN-1999; 99US-0137222.

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XX PR 08-JUN-1999; 99US-0138094.

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XX PR 18-JUN-1999; 99US-0139460.

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 PR 02-AUG-1999; 99US-0146389.
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 PR 23-AUG-1999; 99US-0149902.

PR 23-AUG-1999; 99US-0149930.
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 PR 27-AUG-1999; 99US-0151065.
 PR 27-AUG-1999; 99US-0151066.
 PR 27-AUG-1999; 99US-0151080.
 PR 30-AUG-1999; 99US-0151303.
 PR 31-AUG-1999; 99US-0151438.
 PR 01-SEP-1999; 99US-0151930.
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 PR 28-OCT-1999; 99US-0161993.
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Query Match 50.6%; Score 45.5; DB 21; Length 304;
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 Db 96 pygfpvdpfhytgwdy 110

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 AC AAG27977;
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 DT 17-OCT-2000 (first entry)
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 DE Arabidopsis thaliana protein fragment SEQ ID NO: 33023.

XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
XX EPI033405-A2.
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XX 25-FEB-2000; 2000EP-0301439.
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Query Match      50.6%; Score 45.5; DB 21; Length 349;
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XX 17-OCT-2000 (first entry)
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XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX KW
XX termination sequence.
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Query Match 50.6%; Score 45.5; DB 21; Length 422;
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Matches 8; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

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Db 214 pygfpvdpghgwdy 228

RESULT 12

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DT 26-FEB-1999 (first entry)

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KW ScFvCD19; anti-CD19; single chain; antibody; B-cell marker; CD19; T cell;
 KW retroviral vector; gene therapy; tumour-associated antigen; cancer.

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OS Homo sapiens.

XX

PN DE19720152-A1.

XX

PD 05-NOV-1998.

XX

PF 02-MAY-1997; 97DE-1020152.

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PR 02-MAY-1997; 97DE-1020152.

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 XX WPI; 1998-584686/50.
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 XX Claim 8; Page 5; 10pp; German.
 XX This sequence represents a novel human recombinant anti-CD19 single chain
 CC antibody, ScFvCD19 which recognizes the extracellular domain of the
 CC B-cell marker CD19. This sequence is used in a retroviral vector system
 CC for gene transfer and expression in primary human T cells which involves
 CC a retroviral vector containing cDNA corresponding to a therapeutic gene,
 CC a promoter selected from the SV40 immediate early promoter or the human
 CC IL-2 or MHC I promoter and a selectable marker, and a packaging cell
 CC line (i.e. a modified retroviral packaging line for enhanced transfer
 CC into primary human T lymphocytes). This vector system in which the cDNA
 CC encodes a single-chain antibody (scFv) specific for a tumour-associated
 CC antigen can be used for gene therapy of cancer, especially by isolating
 CC T cells from the patient's blood, stimulating the T cells in vitro,
 CC introducing the retroviral vector into the T cells and returning the T
 CC cells to the patient, preferably by intravenous injection.
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 AC AAW82315;
 XX 26-FEB-1999 (first entry)
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 XX retroviral vector; tumour-associated antigen; cancer; immunoglobulin;
 KW CD8 alpha chain; hinge region; theta chain; transmembrane domain;
 KW intracellular domain; T-cell receptor-CD3 complex.
 XX OS Homo sapiens.
 OS Synthetic.
 XX DE19720152-A1.
 PN 05-NOV-1998.
 PD 02-MAY-1997; 97DE-1020152.
 XX 02-MAY-1997; 97DE-1020152.
 XX (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
 XX Bargou R, Schroeder A, Schwenkenbecher J;
 XX WPI; 1998-584686/50.
 XX N-PSDB; AAV73324.
 XX Retroviral vector system for gene therapy - by expression of
 PT therapeutic gene in T cells
 XX Claim 9; Page 6; 10pp; German.
 XX This sequence represents a novel chimeric CD19/CTCR protein which is
 CC composed of an immunoglobulin leader sequence, an anti-CD19 single chain
 CC antibody fragment (ScFvCD19), a hinge region from the C8 alpha-chain
 CC and the transmembrane and intracellular domain of the T-cell
 CC receptor-CD3 complex theta chain. This sequence is used in a retroviral
 CC vector system for gene transfer and expression in primary human T cells
 CC which involves a retroviral vector containing cDNA corresponding to a
 CC therapeutic gene, a promoter selected from the SV40 immediate early
 CC promoter or the human IL-2 or MHC I promoter and a selectable marker, and
 CC a packaging cell line (i.e. a modified retroviral packaging line for
 CC enhanced transfer into primary human T lymphocytes). This vector system
 CC in which the cDNA encodes a single-chain antibody (scFv) specific for a
 CC tumour-associated antigen can be used for gene therapy of cancer,
 CC especially by isolating T cells from the patient's blood, stimulating the
 CC T cells in vitro, introducing the retroviral vector into the T cells and
 CC returning the T cells to the patient, preferably by intravenous
 CC injection.
 XX SQ Sequence 483 AA;
 Query Match 50.0%; Score 45; DB 19; Length 483;
 Best Local Similarity 87.5%; Pred. No. 37;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 7 PHYVAMDY 14
 Db 125 PYVYAMDY 132
 RESULT 14
 AAB48937
 ID AAB48937 standard; Protein; 125 AA.
 AC AAB48937;
 XX 16-MAR-2001 (first entry)
 DT Anti-TrkA murine monoclonal antibody MNAC13 light chain variable region.
 DE Murine monoclonal antibody MNAC13; heavy chain variable region; VH;
 KW human TrkA antagonist; NGF receptor; nerve growth factor;
 KW neurological pathology; acute pain; chronic pain; analgesic; neuroma;
 KW cancer; TrkA-expressing tumour; gene therapy; in vivo imaging;
 KW diagnosis.
 XX OS Mus sp.
 OS WO200073344-A2.
 PN 07-DEC-2000.
 PD 26-MAY-2000; 2000WO-IT00218.
 PF 26-MAY-1999; 99IT-RM00333.
 PR (SIRS-) SIRS SOC ITAL RICERCA SCI SRL.
 PA Novak MM;
 XX WPI; 2001-061515/07.
 XX N-PSDB; AAC87642.
 DR Monoclonal antibody and its derivatives specific to high affinity
 PT tyrosine kinase receptor of nerve growth factor useful for treating and
 PT diagnosing neuropathological disorders such as pain, neuromas, TrkA
 PT expressing neoplastic tumors -
 XX Claim 3; Page -; 33pp; English.

XX The invention relates to a murine monoclonal antibody, MNAC13, which
 CC recognises the human nerve growth factor (NGF) receptor tyrosine
 CC kinase, TrkA, and acts as an antagonist of NGF/TrkA binding. MNAC13
 CC has a light chain variable region (VL) as given in AAB48936, and a heavy
 CC chain variable region (VH) as given in AAB48937. The invention also
 CC encompasses synthetic derivatives of monoclonal antibody MNAC13, such as
 CC the single chain antibody, scFvMNAC13 (AAB48934), which comprises the
 CC VL and VH regions of MNAC13 in one polypeptide chain. The invention
 CC additionally relates to pharmaceutical compositions comprising the
 CC antibody or antibody derivatives of the invention, engineered eukaryotic
 CC cells able to express the MNAC13 antibody or its derivatives, and a
 CC diagnostic composition comprising the antibody or its derivatives for in
 CC vivo imaging. NGF antagonist (inhibitor of binding of NGF to TrkA
 CC receptor) The MNAC13 monoclonal antibody and its derivatives are useful
 CC for treating neurological pathologies such as acute or chronic pain,
 CC neuromas, and TrkA-expressing neoplastic tumours. A composition
 CC comprising MNAC13 or its derivatives with a diagnostically acceptable
 CC carrier is useful for in vivo imaging diagnostics. The present
 CC sequence represents the heavy chain variable region of the anti-TrkA
 CC murine monoclonal antibody MNAC13.
 CC Note: The present sequence is derived from that of the single chain
 CC antibody scFvMNAC13 shown on pages 32-33 and the information given in
 CC claim 3.

SQ Sequence 125 AA;

Query Match 48.9%; Score 44; DB 22; Length 125;
 Best Local Similarity 63.6%; Pred. No. 13;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 4 YGNPHYVAMDY 14
 ||| : |||
 Db 101 ygndffypmgy 111

RESULT 15

AAB48934
 ID AAB48934 standard; Protein: 295 AA.

XX AAB48934;

XX 16-MAR-2001 (first entry)

XX Anti-TrkA single chain antibody scFvMNAC13.

KW Single chain antibody: murine monoclonal antibody MNAC13; scFvMNAC13;
 KW human TrkA antagonist; NGF receptor; nerve growth factor;
 KW neurological pathology; acute pain; chronic pain; analgesic; neuroma;
 KW cancer; TrkA-expressing tumour; gene therapy; in vivo imaging;
 KW diagnosis.

OS Mus sp.
 OS Synthetic.

XX WO200073344-A2.

XX 07-DEC-2000.

XX 26-MAY-2000; 2000WO-IT00218.

XX 26-MAY-1999; 99IT-RW00333.

XX (SIRS-) SIRS SOC ITAL RICERCA SCI SRL.

XX Novak MM;

XX WPI: 2001-061515/07.

XX N-PSDB; AAC87642.

XX Monoclonal antibody and its derivatives specific to high affinity
 PT tyrosine kinase receptor of nerve growth factor useful for treating and

PT diagnosing neuropathological disorders such as pain, neuromas, TrkA
 PT expressing neoplastic tumors

XX Claim 8; Page 32-33; 33pp; English.

XX The invention relates to a murine monoclonal antibody, MNAC13, which
 CC recognises the human nerve growth factor (NGF) receptor tyrosine
 CC kinase, TrkA, and acts as an antagonist of NGF/TrkA binding. MNAC13
 CC has a light chain variable region (VL) as given in AAB48936, and a heavy
 CC chain variable region (VH) as given in AAB48937. The invention also
 CC encompasses synthetic derivatives of monoclonal antibody MNAC13, such as
 CC the single chain antibody, scFvMNAC13 (AAB48934), which comprises the
 CC VL and VH regions of MNAC13 in one polypeptide chain. The invention
 CC additionally relates to pharmaceutical compositions comprising the
 CC antibody or antibody derivatives of the invention, engineered eukaryotic
 CC cells able to express the MNAC13 antibody or its derivatives, and a
 CC diagnostic composition comprising the antibody or its derivatives for in
 CC vivo imaging. NGF antagonist (inhibitor of binding of NGF to TrkA
 CC receptor) The MNAC13 monoclonal antibody and its derivatives are useful
 CC for treating neurological pathologies such as acute or chronic pain,
 CC neuromas, and TrkA-expressing neoplastic tumours. A composition
 CC comprising MNAC13 or its derivatives with a diagnostically acceptable
 CC carrier is useful for in vivo imaging diagnostics. The present
 CC sequence represents the anti-TrkA single chain antibody scFvMNAC13.

SQ Sequence 295 AA;

Query Match 48.9%; Score 44; DB 22; Length 295;
 Best Local Similarity 63.6%; Pred. No. 32;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 4 YGNPHYVAMDY 14
 ||| : |||
 Db 252 ygndffypmgy 262

Search completed: June 28, 2001, 16:14:37
 Job time: 1325 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2001, 16:01:14 ; Search time 138.34 seconds
(without alignments)
2.039 Million cell updates/sec

Title: US-09-724-406-24
Perfect score: 90
Sequence: 1 DPYGNPHYAMDY 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*

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- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	63.3	115	3	US-08-881-037-22
2	57	63.3	121	3	US-08-881-037-67
3	52	57.8	108	1	US-08-436-463-17
4	42	46.7	123	2	US-08-561-521-9
5	42	46.7	123	2	US-08-561-521-11
6	42	46.7	123	5	PCT-US95-01219-9
7	42	46.7	123	5	PCT-US95-01219-11
8	42	46.7	140	5	PCT-US95-01219-4
9	42	46.7	140	5	PCT-US95-01219-17
10	42	46.7	142	5	US-08-561-521-17
11	42	46.7	142	5	PCT-US95-01219-17
12	41	45.6	2476	2	US-08-276-967-2
13	40	44.4	209	3	US-08-793-229-28
14	40	44.4	209	3	US-09-285-957-28
15	40	44.4	846	1	US-07-731-157A-5
16	40	44.4	846	1	US-08-541-780-5
17	39	43.3	209	2	US-08-793-229-29
18	39	43.3	209	3	US-09-285-957-29
19	39	43.3	246	1	US-08-197-834-7
20	39	43.3	284	3	US-08-793-229-31
21	39	43.3	284	3	US-09-285-957-31
22	39	43.3	348	4	US-09-113-536-2
23	39	43.3	348	5	PCT-US95-05785-2
24	39	43.3	399	2	US-08-282-197C-54
25	39	43.3	609	2	US-08-716-301-4
26	39	43.3	844	1	US-07-731-157A-6
27	39	43.3	844	2	US-08-541-780-6

28	39	43.3	3898	2	US-08-876-991-2
29	39	43.3	3898	2	US-09-059-853-2
30	38.5	42.8	481	4	US-08-843-859-4
31	38	42.2	27	6	5196510-1
32	38	42.2	113	2	US-08-273-146-59
33	38	42.2	115	1	US-08-468-661-1
34	38	42.2	115	1	US-08-466-272A-1
35	38	42.2	115	1	US-08-478-857-1
36	38	42.2	115	2	US-08-471-771-1
37	38	42.2	115	3	US-09-130-783-1
38	38	42.2	138	3	US-08-603-024-2
39	38	42.2	139	1	US-08-253-877C-8
40	38	42.2	139	1	US-08-253-877C-19
41	38	42.2	139	2	US-08-452-164A-8
42	38	42.2	139	2	US-08-452-164A-19
43	38	42.2	139	3	US-08-603-024-18
44	38	42.2	239	6	5455030-13
45	38	42.2	720	1	US-07-731-157A-2

ALIGNMENTS

RESULT 1
US-08-881-037-22
; Sequence 22, Application US/08881037
; Patent No. 6080588
; GENERAL INFORMATION:
; APPLICANT: Click, Gary D.
; APPLICANT: Swanson, Patrick C.
; TITLE OF INVENTION: DNA BINDING ANTIBODIES
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1318
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Pat-ent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/881,037
; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/443,540
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kanski, Antoinette F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: 203442110710
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX:
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-881-037-22

Query Match 63.3%; Score 57; DB 3; Length 115;
Best Local Similarity 83.3%; Pred. No. 0.16;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1

APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-561-521-9

Query Match 46.7% Score 42; DB 2; Length 123;
Best Local Similarity 72.7% Pred. No. 22;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 YGNPHYAMDY 14
||| |||||
Db 102 YGNYGVYAMDY 112

RESULT 5

US-08-561-521-11
Sequence 11, Application US/08561521
Patent No 5840299

GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
FILING DATE:
CLASSIFICATION: 424

Prior Application Data:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994

ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-561-521-11

Query Match 46.7% Score 42; DB 2; Length 123;
Best Local Similarity 72.7% Pred. No. 22;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 YGNPHYAMDY 14
||| |||||
Db 102 YGNYGVYAMDY 112

RESULT 6

PCT-US95-01219-9
Sequence 9, Application PC/TUS9501219
GENERAL INFORMATION:

APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
CLASSIFICATION:

Prior Application Data:
APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994

ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-01219-9

Query Match 46.7% Score 42; DB 5; Length 123;
Best Local Similarity 72.7% Pred. No. 22;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 YGNPHYAMDY 14
||| |||||
Db 102 YGNYGVYAMDY 112

RESULT 7

PCT-US95-01219-11
Sequence 11, Application PC/TUS9501219
GENERAL INFORMATION:

APPLICANT: Bendig, Mary M.

us-09-724-406-24.ra1

Fri Jun 29 08:04:51 2001

```

; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01219
; FILING DATE: 25-JAN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/186,269
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-01219-11

Query Match 46.7%; Score 42; DB 5; Length 123;
Best Local Similarity 72.7%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 3; Indels 3; Gaps 0;

QY 4 YGNPHYVYAMDY 14
   ||| |||||
Db 102 YGNVGYVYAMDY 112

RESULT 8
US-08-561-521-4
; Sequence 4, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01219
; FILING DATE: 25-JAN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/186,269
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-01219-11
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/561,521
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,269A
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-561-521-4

Query Match 46.7%; Score 42; DB 2; Length 140;
Best Local Similarity 72.7%; Pred. No. 26;
Matches 8; Conservative 0; Mismatches 3; Indels 3; Gaps 0;

QY 4 YGNPHYVYAMDY 14
   ||| |||||
Db 121 YGNVGYVYAMDY 131

RESULT 9
PCT-US95-01219-4
; Sequence 4, Application PC/TUS9501219
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01219
; FILING DATE: 25-JAN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/186,269
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
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;
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-01219-4

Query Match 46.7%; Score 42; DB 5; Length 140;
Best Local Similarity 72.7%; Pred. No. 26;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 YGNPHYVAMDY 14
||| |||||
Db 121 YGNYGVYAMDY 131

RESULT 10
US-08-561-521-17
; Sequence 17, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/561,521
; FILING DATE:

CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,269A
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 142 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-561-521-17

Query Match 46.7%; Score 42; DB 2; Length 142;
Best Local Similarity 72.7%; Pred. No. 26;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 YGNPHYVAMDY 14
||| |||||
Db 121 YGNYGVYAMDY 131

RESULT 11

PCT-US95-01219-17
; Sequence 17, Application PC/TUS9501219
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01219
; FILING DATE: 25-JAN-1995

CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/186,269
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 142 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-01219-17

Query Match 46.7%; Score 42; DB 5; Length 142;
Best Local Similarity 72.7%; Pred. No. 26;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 YGNPHYVAMDY 14
||| |||||
Db 121 YGNYGVYAMDY 131

RESULT 12
US-08-276-967-2
; Sequence 2, Application US/08276967
; Patent No. 5851817
; GENERAL INFORMATION:
; APPLICANT: Hardy, Daniel M.
; APPLICANT: Garbers, David L.
; TITLE OF INVENTION: Species-Specific Egg-Binding Proteins of
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,967
FILING DATE: Submitted Herewith
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UTSD:418\KIT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1400
TELEFAX: 713-789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2476 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-276-967-2

Query Match 45.6%; Score 41; DB 2; Length 2476;
Best Local Similarity 60.0%; Pred. No. 7.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 YGNPHYAMD 13
||:|||||
DB 804 YGDPHYLTFFD 813

RESULT 13
US-08-793-229-28
Sequence 28, Application US/08793229
Patent No. 5891703
GENERAL INFORMATION:
APPLICANT: VAN DER LAAN, Jan Metske
APPLICANT: RIEMENS, Adriana Marina
APPLICANT: QUAX, Wilhelmus Johannes
TITLE OF INVENTION: Mutated Penicillin G Acylase Genes
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,229
FILING DATE: 23-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/03249
FILING DATE:
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 97075
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)913-0001
TELEFAX: (312)913-0002
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 209 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-793-229-28

Query Match 44.4%; Score 40; DB 2; Length 209;
Best Local Similarity 70.0%; Pred. No. .75;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 YGNPHYAMD 13
||:|||||
DB 14 YGMPHYIYAND 23

RESULT 14
US-09-285-957-28
Sequence 28, Application US/09285957
Patent No. 6033823
GENERAL INFORMATION:
APPLICANT: VAN DER LAAN, Jan Metske
APPLICANT: RIEMENS, Adriana Marina
APPLICANT: QUAX, Wilhelmus Johannes
TITLE OF INVENTION: Mutated Penicillin G Acylase Genes
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/285,957
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/793,229
FILING DATE:
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 97075
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)913-0001
TELEFAX: (312)913-0002
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 209 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-285-957-28

Query Match 44.4%; Score 40; DB 3; Length 209;
Best Local Similarity 70.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 YGNPHYAMD 13
||:|||||
DB 14 YGMPHYIYAND 23

RESULT 15
US-07-731-157A-5
Sequence 5, Application US/07731157A
Patent No. 5457032
GENERAL INFORMATION:
APPLICANT: Quax, Wilhelmus J.


```

; APPLICANT: Misset, Onno
; APPLICANT: Van der Laan, Jan M.
; APPLICANT: Lenting, Herman B.M.
; TITLE OF INVENTION: Mutated beta-lactam acylase genes
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM
; STREET: FIVE PALO ALTO SQUARE, 4TH FLOOR
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/731,157A
; FILING DATE: 19910509
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 90200962
; FILING DATE: 18-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: RAE-VENTER PH.D., BARBARA
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: GBRO-027/000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-494-7622
; TELEFAX: 415-857-0663
; TELEX: 380816 COOLEY PA
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 846 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli
; PUBLICATION INFORMATION:
; AUTHORS: Schumacher, G
; AUTHORS: Sizmann, D
; AUTHORS: Haug, H
; AUTHORS: Buckel, P
; AUTHORS: Bock, A
; TITLE: Penicillin acylase from E.coli: unique
; TITLE: gene-protein realtion.
; JOURNAL: Nucleic Acids Res.
; VOLUME: 14
; PAGES: 5713-5727
; DATE: 1986
; US-07-731-157A-5

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Query Match          44.4%; Score 40; DB 1; Length 846;
Best Local Similarity 70.0%; Pred. No. 3.3e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY      4 YGNPHYVAMD 13
      |||||
Db      40 YGMPHYVAND 49

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Search completed: June 28, 2001, 16:01:15
Job time: 523 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run On: June 28, 2001, 15:58:45 ; Search time 234.85 Seconds
(without alignments)
4.541 Million cell updates/sec

Title: US-09-724-406-24
Perfect score: 90
Sequence: 1 DPPYGNPHYAMDY 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*

- 1: pir1:*
- 2: pir2:*
- 3: pir3:*
- 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	57.8	15	2 PH1610	Ig H chain V-D-J r
2	52	57.8	94	2 PH0996	Ig heavy chain V r
3	51	56.7	113	2 S26468	Ig heavy chain V r
4	49	54.4	14	2 PH1608	Ig H chain V-D-J r
5	49	54.4	125	2 PH0100	Ig heavy chain V r
6	48	53.3	119	2 C53285	Ig heavy chain V a
7	48	53.3	139	2 A25912	Ig heavy chain pre
8	48	53.3	470	2 T49278	hypothetical prote
9	46	51.1	14	2 PH1615	Ig H chain V-D-J r
10	46	51.1	115	2 PC6026	acetylcoline recep
11	45	50.0	123	2 F48677	Ig heavy chain V-D
12	45	50.0	123	2 G48677	Ig heavy chain V-D
13	45	50.0	123	2 E48677	Ig heavy chain pre
14	45	50.0	136	1 GLMS21	ribulose-bisphosph
15	45	50.0	171	1 RK525J	Ig H chain V-D-J r
16	44	48.9	13	2 PH1593	Ig H chain V-D-J r
17	44	48.9	16	2 PH1604	Ig heavy chain V r
18	44	48.9	118	2 A49026	Ig heavy chain V r
19	44	48.9	124	2 C27888	Ig heavy chain pre
20	44	48.9	140	2 S04575	Ig heavy chain pre
21	44	48.9	149	2 S30752	Ig heavy chain pre
22	44	48.9	1090	2 S59077	Ig heavy chain pre
23	43.5	48.3	2573	2 D71614	cellulose 1,4-beta
24	43	47.8	114	2 PH1597	hypothetical prote
25	43	47.8	119	2 E25114	Ig H chain V-D-J r
26	43	47.8	329	2 G71140	Ig heavy chain V r
27	43	47.8	381	2 A54415	hypothetical prote
28	43	47.8	647	2 S48471	transcription fact
29	43	47.8	878	2 T17245	probable membrane
					hypothetical prote

30	43	47.8	1080	2 A71485	probable pbp2-tran
31	43	47.8	2809	2 T30213	G-cadherin - sea u
32	42	46.7	45	2 PL0094	Ig heavy chain V r
33	42	46.7	77	2 D43331	sor 3'-region hypo
34	42	46.7	114	2 PH1027	Ig heavy chain V r
35	42	45.7	497	2 H83886	hypothetical prote
36	42	45.7	973	2 T35238	probable secreted
37	41.5	45.1	363	2 G81439	site-specific DNA-
38	41.5	45.1	856	2 G70483	pyruvate,water dik
39	41	45.6	14	2 PH1601	Ig H chain V-D-J r
40	41	45.6	17	2 PH1607	Ig H chain V-D-J r
41	41	45.6	110	2 S26323	Ig heavy chain V r
42	41	45.6	218	2 T36033	probable hydrolase
43	41	45.6	222	2 T36465	hypothetical prote
44	41	45.6	261	2 A84128	hypothetical prote
45	41	45.6	265	2 S32652	transcription fact

ALIGNMENTS

RESULT 1

PH1610

Ig H chain V-D-J region (wild-type clone 337) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C:Accession: PH1610

R:Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less m

A:Reference number: PH1580; MUID:93301609

A:Accession: PH1610

A:Molecule type: DNA

A:Residues: 1-15 <LEV>

A:Experimental source: bone marrow pre-B lymphocyte

C:Keywords: immunoglobulin

Query Match 57.8%; Score 52; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 0.032;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 GNPHYAMDY 14

Db 6 GSPHYAMDY 15

RESULT 2

PH0996

Ig heavy chain V region (clone 165.3m) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PH0996

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective

A:Reference number: PH0971; MUID:92381444

A:Accession: PH0996

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-94 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match

Best Local Similarity 57.8%; Score 52; DB 2; Length 94;

Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DPPYGNPHYAMDY 14

Db 80 DPPLRLLYYAMDY 93

Fri Jun 29 08:04:52 2001

us-09-724-406-24.rpr

C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;15-98/Domain: immunoglobulin homology <IMM>
 F;31-35/Region: complementarity-determining 1
 F;50-66/Region: complementarity-determining 2
 F;99-112/Region: complementarity-determining 3

Query Match 54.4%; Score 49; DB 2; Length 125;
 Best Local Similarity 72.7%; Pred. No. 0.95; Indels 0; Gaps 0;
 Matches 8; Conservative 2; Mismatches 1;

QY 4 YGNPHYVAMDY 14
 ||| : |||||
 Db 102 YGSRNYAMDY 112

RESULT 6

C53285
 Ig heavy chain V and J regions, monoclonal antibody OHP7D7.2.3 - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
 C;Accession: C53285
 R;Sawada, J.; Mizusawa, S.; Terao, T.; Naito, M.; Kurosawa, Y.
 Mol. Immunol. 28, 1063-1072, 1991
 A;Title: Molecular characterization of monoclonal anti-steroid antibodies: primary st
 and their pH-reactivity profiles.
 A;Reference number: A53285; MUID:92017897
 A;Accession: C53285
 A;Status: preliminary
 A;Molecule type: mRNA; protein
 A;Residues: 1-119 <SAW>
 A;Cross-references: GB:D12734; NID:g220548; PIDN:BAA02226.1; PID:g220549
 A;Note: sequence extracted from NCBI backbone (NCBI:63297, NCBI:63302)
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 53.3%; Score 48; DB 2; Length 119;
 Best Local Similarity 80.0%; Pred. No. 1.3; Indels 0; Gaps 0;
 Matches 8; Conservative 1; Mismatches 1;

QY 5 GNPHYVAMDY 14
 || : |||||
 Db 99 GNRYYVAMDY 108

RESULT 7

A25912
 Ig heavy chain precursor V region (W3129) - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 23-Jul-1999
 C;Accession: A25912
 R;Borden, P.; Kabat, E.A.
 Proc. Natl. Acad. Sci. U.S.A. 84, 2440-2443, 1987
 A;Title: Nucleotide sequence of the cDNAs encoding the variable region heavy and ligh
 A;Reference number: A94147; MUID:87175689
 A;Accession: A25912
 A;Molecule type: mRNA
 A;Residues: 1-139 <BOR>
 A;Cross-references: GB:M15873; NID:g195268; PIDN:AAA38228.1; PID:g195269
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;1-18/Domain: signal sequence #status predicted <SIG>
 F;19-139/Product: Ig heavy chain V region W3129 #status predicted <VAR>
 F;33-116/Domain: immunoglobulin homology <IMM>

Query Match 53.3%; Score 48; DB 2; Length 139;
 Best Local Similarity 80.0%; Pred. No. 1.5; Indels 0; Gaps 0;
 Matches 8; Conservative 1; Mismatches 1;

RESULT 3

S26468
 Ig heavy chain V region - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
 C;Accession: S26468
 R;Kavaler, J.
 submitted to the EMBL Data Library, April 1991

A;Reference number: S26459
 A;Accession: S26468
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-113 <KAV>
 A;Cross-references: EMBL:X59107; NID:g51944; PIDN:CAA41833.1; PID:g51945
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;11-94/Domain: immunoglobulin homology <IMM>

Query Match 56.7%; Score 51; DB 2; Length 113;
 Best Local Similarity 83.3%; Pred. No. 0.41; Indels 0; Gaps 1;
 Matches 10; Conservative 0; Mismatches 0;

QY 3 PYGNPHYVAMDY 14
 |||| : |||||
 Db 96 PYGN--YVAMDY 105

RESULT 4

PH1608
 Ig H chain V-D-J region - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
 C;Accession: PH1608
 R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
 J. Exp. Med. 178, 317-329, 1993
 A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
 A;Reference number: PH1580; MUID:93301609
 A;Accession: PH1608
 A;Molecule type: DNA
 A;Residues: 1-14 <LEV>
 A;Experimental source: bone marrow pre-B lymphocyte, wild-type clone 335
 A;Accession: PH1603
 A;Molecule type: DNA
 A;Residues: 1-14 <LEV2>
 A;Experimental source: bone marrow pre-B lymphocyte, wild-type clone 324
 C;Keywords: immunoglobulin

Query Match 54.4%; Score 49; DB 2; Length 14;
 Best Local Similarity 80.0%; Pred. No. 0.089; Indels 0; Gaps 0;
 Matches 8; Conservative 1; Mismatches 1;

QY 5 GNPHYVAMDY 14
 || : |||||
 Db 5 GNSYYVAMDY 14

RESULT 5

PH0100
 Ig heavy chain V region (anti-cyclosporin E) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 21-Jan-2000
 C;Accession: PH0100
 R;Schmitter, D.; Poch, O.; Zeder, G.; Heinrich, G.F.; Koehler, H.P.; Quesniaux, V.F.J.;
 Mol. Immunol. 27, 1029-1038, 1990
 A;Title: Analysis of the structural diversity of monoclonal antibodies to cyclosporine.
 A;Reference number: PH0087; MUID:91042649
 A;Accession: PH0100
 A;Molecule type: mRNA
 A;Residues: 1-125 <SCH>

QY 5 GNPHYAMDY 14
I: |||||

Db 119 GDHYAMDY 128

RESULT 8

T49278
hypothetical protein T21J18.90 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C:Accession: T49278
R:Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Rudd, S.
submitted to the Protein Sequence Database, April 2000
A:Reference number: 225021
A:Accession: T49278
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-470 <RIE>
A:Cross-references: EMBL:AL132963; GSPDB:GN00061; ATSP:T21J18.90
A:Experimental source: cultivar Columbia; BAC clone T21J18
C:Genetics:
A:Gene: ATSP:T21J18.90
A:Map position: 3
A:Introns: 35/2; 71/3; 123/3; 157/2; 174/2; 238/3; 269/1; 290/3; 342/2; 369/3; 406/2

Query Match 53.3%; Score 48; DB 2; Length 470;
Best Local Similarity 63.8%; Pred. No. 5.7;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YGNPHYAMDY 14
I: |||||

Db 83 YGLPYVVDY 93

RESULT 9

PH1615
Ig H chain V-D-J region (clone B-less 22) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C:Accession: PH1615
R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A:Reference number: PH1580; MUID:93301609
A:Accession: PH1615
A:Molecule type: DNA
A:Residues: 1-14 <LEV>
A:Experimental source: bone marrow pre-B lymphocyte
C:Keywords: immunoglobulin

Query Match 51.1%; Score 46; DB 2; Length 14;
Best Local Similarity 88.9%; Pred. No. 0.26;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 NPHYAMDY 14
I: |||||

Db 6 NPIYAMDY 14

RESULT 10

PC6026
acetylcholine receptor monoclonal antibody A7 heavy chain variable region - mouse (fragme
C:Species: Mus musculus (house mouse)
C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jan-2000
C:Accession: PC6026
R:Meng, F.; Yang, K.; Graus, Y.; de Baets, M.
Chinese J. Microbiol. Immunol. 16, 45-48, 1996
A:Title: Pathogenicity and sequence analysis of a mouse anti-AChR monoclonal antibody A7
A:Reference number: PC6026
A:Accession: PC6026
A:Molecule type: mRNA

A:Residues: 1-115 <MEN>

A:Cross-references: EMBL:X80962
C:Comment: This protein induces acetylcholine receptor loss and muscular weakness in m
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 51.1%; Score 46; DB 2; Length 115;
Best Local Similarity 77.8%; Pred. No. 2.6;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 NPHYAMDY 14
I: |||||

Db 96 SPIYAMDY 104

RESULT 11

F48677
Ig heavy chain V-D-J region (44.1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 17-Mar-1999
C:Accession: F48677
R:Tassignon, J.; Brait, M.; Jamila, I.; Urbain, J.; Gottlieb, P.; Brown, A.; Hasemann
Proc. Natl. Acad. Sci. U.S.A. 90, 9508-9512, 1993
A:Title: Molecular characterization of monoclonal CRI-A-positive anti-arsonate antio
A:Reference number: A48677; MUID:94022404
A:Accession: F48677
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-123 <TAS>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 50.0%; Score 45; DB 2; Length 123;
Best Local Similarity 63.6%; Pred. No. 4;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 YGNPHYAMDY 14
I: |||||

Db 102 FGGVYAMDY 112

RESULT 12

G48677
Ig heavy chain V-D-J region (419.1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 17-Mar-1999
C:Accession: G48677
R:Tassignon, J.; Brait, M.; Jamila, I.; Urbain, J.; Gottlieb, P.; Brown, A.; Hasemann
Proc. Natl. Acad. Sci. U.S.A. 90, 9508-9512, 1993
A:Title: Molecular characterization of monoclonal CRI-A-positive anti-arsonate antio
A:Reference number: A48677; MUID:94022404
A:Accession: G48677
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-123 <TAS>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 50.0%; Score 45; DB 2; Length 123;
Best Local Similarity 63.6%; Pred. No. 4;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 YGNPHYAMDY 14
I: |||||

Db 102 FGGVYAMDY 112

RESULT 13

E48677

Ig heavy chain V-D-J region (48) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 17-Mar-1999
C:Accession: E48677
R:Tassignon, J.; Brait, M.; Jamila, I.; Urbain, J.; Gottlieb, P.; Brown, A.; Hasemann, C.
Proc. Natl. Acad. Sci. U.S.A. 90, 9508-9512, 1993
A:Title: Molecular characterization of monoclonal CRI-A-positive anti-arsonate antibodies
A:Reference number: A48677; MUID:94022404
A:Accession: E48677
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-123 <TAS>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 50.0%; Score 45; DB 2; Length 123;
Best Local Similarity 63.6%; Pred. No. 4;
Matches 7; Conservative 2; Mismatches 0; Gaps 0;

Qy 4 YGNPHYAMDY 14
:| :|||||
Db 102 FGGGYVAMDY 112

RESULT 14

GLMS21
Ig heavy chain precursor V region (MOPC 21) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 22-Jun-1999
C:Accession: E90809; A93184; A02066
R:Bochwell, A.L.M.; Faskind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore, D.
Cell 24, 625-637, 1981
A:Title: Heavy chain variable region contribution to the NP(b) family of antibodies: some
A:Reference number: A90809; MUID:81234548
A:Accession: E90809
A:Molecule type: mRNA
A:Residues: 1-136 <BOT>
A:Cross-references: GB:J00522; NID:g195052; PIDN:AAD15290.1; PID:g195055
R:Adetugbo, K.; Milstein, C.; Secher, D.S.
Nature 265, 299-304, 1977
A:Title: Molecular analysis of spontaneous somatic mutants.
A:Reference number: A93184; MUID:77100368
A:Contents: myeloma protein MOPC 21
A:Accession: A93184
A:Molecule type: protein
A:Residues: 17-74,'D','76-77','H','79-88','ND','91-114','H','116-119','W','121-136 <ADE>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-16/Domain: signal sequence (fragment) #status predicted <SIG>
F:17-136/Product: Ig heavy chain V region (MOPC 21) #status experimental <MAT>
F:31-114/Domain: immunoglobulin homology <IMM>
F:115-119/Region: D segment
F:120-136/Region: J segment (JH4)
F:38-112/Disulfide bonds: #status experimental

Query Match 50.0%; Score 45; DB 1; Length 136;
Best Local Similarity 72.7%; Pred. No. 4.4;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 YGNPHYAMDY 14
:| :|||||
Db 115 WGNPHYAMDY 125

RESULT 15

RKSZSJ
Ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - Japanese black pine
C:Species: Pinus thunbergiana (Japanese black pine)
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 18-Jun-1999

C:Accession: S02046
R:Yamamoto, N.; Kano-Murakami, Y.; Matsuo, M.; Ohashi, Y.; Tanaka, Y.
Nucleic Acids Res. 16, 11830, 1988
A:Title: Nucleotide sequence of a full length cDNA clone of ribulose biphosphate car
A:Reference number: S02046; MUID:85098344
A:Accession: S02046
A:Molecule type: mRNA
A:Residues: 1-171 <YAM>
A:Cross-references: EMBL:X13408; NID:g20957; PIDN:CAA31774.1; PID:g20958
C:Superfamily: ribulose-bisphosphate carboxylase small chain
C:Keywords: Calvin cycle; carbon dioxide fixation; carbon-carbon lyase; carboxy-lyase
F:1-51/Domain: transit peptide (chloroplast) #status predicted <TNP>
F:52-171/Product: ribulose-bisphosphate carboxylase small chain #status predicted <MA

Query Match 50.0%; Score 45; DB 1; Length 171;
Best Local Similarity 46.2%; Pred. No. 5.7;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 PPYGNPHYAMDY 14
||:|||| :|
Db 56 PPFGNPKFETLSY 68

Search completed: June 28, 2001, 15:58:45
Job time: 373 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2001, 15:54:38 ; Search time 105.36 Seconds
(without alignments)
4.552 Million cell updates/sec

Title: US-09-724-406-24
Perfect score: 90
Sequence: 1 DPPYGNPHYANDY 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues
Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	45	50.0	136	1	P01793 mus musculus
2	45	50.0	171	1	RBS_PINTH
3	44	48.9	1090	1	GUXB_CELFI
4	43	47.8	647	1	YIK1_YEAST
5	42	46.7	77	1	P29088 acidianus a
6	41.5	46.1	856	1	YPSA_ACIAM
7	41	45.6	265	1	OC3B_HUMAN
8	41	45.6	360	1	OC3A_HUMAN
9	41	45.6	407	1	MURG_MYCLE
10	41	45.6	1592	1	GTF2_STRDO
11	41	45.6	2476	1	ZAN_PIG
12	40.5	45.0	221	1	SFR9_HUMAN
13	40	44.4	482	1	PGFU_ECOLI
14	40	44.4	608	1	PPCK_NEOFR
15	40	44.4	834	1	TF1B_MOUSE
16	40	44.4	835	1	TF1B_HUMAN
17	40	44.4	846	1	PAC_ECOLI
18	39.5	43.9	3530	1	MY15_HUMAN
19	39	43.3	107	1	COTT_BACSU
20	39	43.3	180	1	RBS1_PETSP
21	39	43.3	180	1	RBS2_PETSP
22	39	43.3	230	1	PRP2_SOYBN
23	39	43.3	252	1	GSPN_ABBHY
24	39	43.3	348	1	GALE_HUMAN
25	39	43.3	660	1	PRIA_BORBU
26	39	43.3	837	1	XYNZ_CLOTM
27	39	43.3	841	1	YAGX_ECOLI
28	39	43.3	844	1	PAC_KLUCI
29	39	43.3	3898	1	POIG_HCVA
30	38.5	42.8	481	1	KRL_HSV1
31	38	42.2	124	1	V124_ASFB7
32	38	42.2	124	1	V124_ASFL5
33	38	42.2	124	1	V125_ASFL5

34	38	42.2	162	1	CBP6_YEAST
35	38	42.2	311	1	7B4C_PSESP
36	38	42.2	366	1	1C03_HUMAN
37	38	42.2	366	1	1C04_HUMAN
38	38	42.2	381	1	ORIA_DROME
39	38	42.2	772	1	CPTM_RAT
40	38	42.2	877	1	INCE_CHICK
41	38	42.2	919	1	EXL3_HUMAN
42	38	42.2	960	1	VP41_LYCES
43	38	42.2	976	1	VP41_ARATH
44	37.5	41.7	87	1	UV15_SCHPO
45	37.5	41.7	1569	1	GLI3_XENLA

ALIGNMENTS

RESULT 1
HV16_MOUSE STANDARD; PRT; 136 AA.
ID HV16_MOUSE
AC P01793;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION MOPC 21 PRECURSOR (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.D.M., Paskin M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
RN [2]
RP SEQUENCE OF 17-136.
RX MEDLINE=77100368; PubMed=401950;
RA Adetugbo K., Milstein C., Secher D.S.;
RL "Molecular analysis of spontaneous somatic mutants.";
RL Nature 265:299-304(1977).
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CC or send an email to license@isb-sib.ch).
CC EMBL; J00522; AAD15290.1; -
CC PIR; A02066; GIMS21.
DR InterPro: IPR003006; -
DR Pfam: PF00047; ig; 1.
DR Immunoglobulin V region; Signal.
FT NON_TER 1
FT SIGNAL <1 16
FT CHAIN 17 136 IG HEAVY CHAIN V REGION MOPC 21.
FT DOMAIN 115 119 D SEGMENT.
FT DOMAIN 120 136 JH4 SEGMENT.
FT DISULFID 38 112
FT CONFLICT 75 78 HYAD -> DYAH (IN REF. 2).
FT CONFLICT 89 90 DN -> ND (IN REF. 2).
FT CONFLICT 115 115 W -> H (IN REF. 2).
FT CONFLICT 120 120 Y -> W (IN REF. 2).
FT NON_TER 136 136
SQ SEQUENCE 136 AA; 15071 MW; 2276A98DBDBF7016 CRC64;

Query Match 50.0%; Score 45; DB 1; Length 136;
Best Local Similarity 72.7%; Pred. No. 2.2;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 YGNPHYVAMY 14
:||| |||||
Db 115 WGNPHYVAMY 125

RESULT 2
RBS_PINTH STANDARD; PRT; 171 AA.

AC P10053;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (EC 4.1.1.39)
DE (RUBISCO SMALL SUBUNIT).
GN RBES.
OS Pinus thunbergii (Green pine) (Japanese black pine).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=3350;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89098345; PubMed=3267239;
RA Yamamoto N., Matsuo M., Kano Murakami Y., Tanaka Y., Ohashi Y.;
RT "Mouse spleen derived cDNA clones containing per repeat sequence.";
RL Nucleic Acids Res. 16:11831-11831(1988).
CC -1- FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF
CC D-RIBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC
CC CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION OF
CC THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH
CC REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME
CC ACTIVE SITE.
CC -1- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2) =
CC 2 3-PHOSPHO-D-GLYCERATE.
CC -1- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + O(2) =
CC 3-PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCOLATE.
CC -1- SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -1- SIMILARITY: BELONGS TO THE RUBISCO SMALL CHAIN FAMILY.
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CC
CC EMBL; X13408; CAA31774.1; -.
CC PIR; S02046; RKSZSJ.
CC HSSP; P00866; IRLC.
CC Mendel; 447; PINTH; rbcS;1.
CC InterPro; IPR000894; -.
CC PRAM; PF00101; RuBisCO_small; 1.
CC PRINTS; PR00152; RUBISCO_SMALL.
CC Photosynthesis; Carbon dioxide fixation; Photorespiration;
KW Lyase; Oxidoreductase; Monooxygenase; Chloroplast; Transit peptide.
FT TRANSIT 1 51
FT CHAIN 52 171
FT RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL
FT CHAIN.
SQ SEQUENCE 171 AA; 19312 MW; 8064DB3DDE87A448 CRC64;

Query Match 50.0%; Score 45; DB 1; Length 171;
Best Local Similarity 46.2%; Pred. No. 2.8;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 PPGNPHYVAMY 14
:||| : :|
Db 56 PPGNPHYVAMY 68

RESULT 3
GUXB_CELFI STANDARD; PRT; 1090 AA.

AC P50899;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE EXOGLUCANASE B PRECURSOR (EC 3.2.1.91) (EXOCELLOBIOTRIHYDROLASE B)
DE (1,4-BETA-CELLOBIOTRIHYDROLASE B) (CBP120).
DE CBHB OR CENE.
GN Cellulomonas fimi.
OS Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Micrococcales; Cellulomonadaceae; Cellulomonas.
OX NCBI_TaxID=1708;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 456-461.
RX STRAIN=ATCC 484;
RX MEDLINE=96003898; PubMed=7575482;
RA Shen H., Gilkes N.R., Kilburn D.G., Miller R.C. Jr., Warren R.A.J.;
RT "Cellulobiohydrolase B, a second exo-cellobiohydrolase from the
RT cellulolytic bacterium Cellulomonas fimi.";
RL Biochem. J. 311:67-74(1995).
RN [2]
RP SEQUENCE OF 54-75.
RX MEDLINE=93209933; PubMed=8458833;
RA Meinke A., Gilkes N.R., Kilburn D.G., Miller R.C. Jr., Warren R.A.J.;
RT "Cellulose-binding polypeptides from Cellulomonas fimi: endoglucanase
RT D (Cend), a family A beta-1,4-glucanase.";
RL J. Bacteriol. 175:1910-1918(1993).
RN [3]
RP SEQUENCE OF 54-78.
RX MEDLINE=94197708; PubMed=8147863;
RA Shen H., Tomme P., Meinke A., Gilkes N.R., Kilburn D.G.,
RA Warren R.A.J., Miller R.C. Jr.;
RT "Stereochemical course of hydrolysis catalysed by Cellulomonas fimi
RT Cend, a member of a new family of beta-1,4-glucanases.";
RL Biochem. Biophys. Res. Commun. 199:1223-1228(1994).
CC -1- FUNCTION: HYDROLYSE CELLOHEXAUSE TO A MIXTURE OF CELLOTETRAOSE,
CC CELLOTRIOSE AND CELLOBIOSE, WITH ONLY A TRACE OF GLUCOSE. IT
CC HYDROLYSED CELLOPENTAUSE TO CELLOTRIOSE AND CELLOBIOSE, AND
CC CELLOTETRAUSE TO CELLOBIOSE, BUT IT DID NOT HYDROLYSE CELLOTRIOSE.
CC HAS ALSO WEAK ENDOGLUCANASE ACTIVITY. HYDROLYSES GLUCOSIDIC BONDS
CC WITH INVERSION OF ANOMERIC CONFIGURATION.
CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF 1,4-BETA-D-GLUCOSIDIC LINKAGES
CC IN CELLULOSE AND CELLOTETRAOSE, RELEASING CELLOBIOSE FROM THE NON-
CC REDUCING ENDS OF THE CHAINS.
CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 BACTERIAL-TYPE CELLULOSE-BINDING DOMAIN
CC (CBD).
CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY L (FAMILY 48 OF GLYCOSYL
CC HYDROLASES).
CC
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CC
CC EMBL; L38827; AAB00822.1; -.
CC HSSP; P07986; 1EXH.
CC InterPro; IPR000556; -.
CC InterPro; IPR001777; -.
CC InterPro; IPR001919; -.
CC Pfam; PF00553; CBD_2; 1.
CC Pfam; PF02011; Glyco_hydro_48; 1.
CC Pfam; PF00041; fn3; 3.
CC PRINTS; PR00014; FNTYPEIII.
CC PRINTS; PR00844; GLHYDRLASE48.
CC PROSITE; PS00561; CBD_BACTERIAL; 1.
KW Cellulose degradation; Hydrolase; Glycosidase; Repeat; Signal.
FT SIGNAL 1 33
FT POTENTIAL.

FT PROPEP 34 53
 FT CHAIN 54 1090
 FT DOMAIN 54 699
 FT DOMAIN 700 785
 FT DOMAIN 794 884
 FT DOMAIN 891 978
 FT DOMAIN 989 1090
 FT ACT_SITE 513 513
 FT DISULFID 990 1089
 SQ SEQUENCE 1090 AA; 114829 MW; 046B9D956F2F399 CRC64;

Query Match 48.9%; Score 44; DB 1; Length 1090;
 Best Local Similarity 53.8%; Pred. No. 29;
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 PPGNPHYAMDY 14
 |||||
 Db 446 PPGTPTFGMGY 458

RESULT 4

ID YIKL_YEAST STANDARD; PRT; 647 AA.
 AC P40489;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HYPOTHETICAL 72.7 KDA PROTEIN IN MOB1-SGAI INTERGENIC REGION.
 GN YIKL01C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / AB972;
 RA Barrell B.G., Badcock K., Bankier A.T., Bowmen S., Brown D.,
 RA Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser A.,
 RA Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones M.,
 RA Louis E., Lye G., Moule S., Moutle T., Odell C., Pearson D.,
 RA Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,
 RA Walsh S.V., Whitehead S.;
 RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
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 CC -----
 CC EMBL; Z38125; CAA86279.1; -
 DR PIR; S48471; S48471.
 DR SGD; S0001363; XBPI.
 KW Hypothetical protein.
 SQ SEQUENCE 647 AA; 72687 MW; 5087D00C1D1AC4A5 CRC64;

Query Match 47.8%; Score 43; DB 1; Length 647;
 Best Local Similarity 50.0%; Pred. No. 24;
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PYGNPHYAMDY 14
 |||||
 Db 593 PYGDDHVFLLKY 604

RESULT 5

ID YSO4_AC1AM STANDARD; PRT; 77 AA.
 AC P29088;

DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE HYPOTHETICAL PROTEIN IN SOR 3'REGION (ORF4) (FRAGMENT).
 OC Acidianus ambivalens (Desulfurolobus ambivalens).
 OS Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Acidianus.
 OX NCBI_TaxID=2283;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LEI 10 / DSM 3772;
 RC MEDLINE=92394888; PubMed=1522063;
 RA Kletzin A.;
 RT "Molecular characterization of the sor gene, which encodes the sulfur
 RT oxygenase/reductase of the thermoacidophilic Archaeum Desulfurolobus
 RT ambivalens.";
 RL J. Bacteriol. 174:5854-5859(1992).
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 CC EMBL; X56616; CAA39954.1; -
 DR PIR; S24834; S24834.
 DR PIR; D43331; D43331.
 KW Hypothetical protein.
 FT NON_TER 77 77
 SQ SEQUENCE 77 AA; 8665 MW; 1B954D055CDDAAE1 CRC64;

Query Match 46.7%; Score 42; DB 1; Length 77;
 Best Local Similarity 85.7%; Pred. No. 3.5;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PYGNPHY 9
 |||||
 Db 4 PYGNPHY 10

RESULT 6

ID PPSA_AQUAE STANDARD; PRT; 856 AA.
 AC O67899;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE PHOSPHONOLPYRUVATE SYNTHASE (EC 2.7.9.2) (PYRUVATE, WATER KINASE)
 DE (PEP SYNTHASE).
 GN PPSA OR AQ_2142.
 OS Aquifex aeolicus.
 OC Bacteria; Aquificales; Aquificaceae; Aquifex.
 OX NCBI_TaxID=63363;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VF5;
 RC MEDLINE=98196666; PubMed=9537320;
 RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
 RA Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,
 RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
 RT "The complete genome of the hyperthermophilic bacterium Aquifex
 RT aeolicus.";
 RL Nature 392:353-358(1998).
 CC -|- CATALYTIC ACTIVITY: ATP + PYRUVATE + H(2)O = AMP +
 CC PHOSPHONOLPYRUVATE + PHOSPHATE.
 CC -|- PATHWAY: ESSENTIAL STEP IN GLUCONEOGENESIS WHEN PYRUVATE AND
 CC LACTATE ARE USED AS A CARBON SOURCE.
 CC -|- SIMILARITY: BELONGS TO THE PEP-UTILIZING ENZYMES FAMILY.
 CC -----
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DR EMBL; AE000775; AAC07865.1; -
 DR InterPro; IPR000121; -
 DR InterPro; IPR002192; -
 DR Pfam; PF00391; PEP-utilizers; 2.
 DR Pfam; PF01326; PPK_N-term; 1.
 DR PROSITE; PS00370; PEP_ENZYMES_PHOS_SITE; 1.
 DR PROSITE; PS00742; PEP_ENZYMES_2; 1.
 DR Transferase; Kinase; ATP-binding; Phosphorylation.
 FT MOD_RES 433 433 PHOSPHORYLATION (BY SIMILARITY).
 SQ SEQUENCE 856 AA; 96406 MW; 0CB001DABE289912 CRC64;

Query Match 46.1%; Score 41.5; DB 1; Length 856;
 Best Local Similarity 47.1%; Pred. No. 55;
 Matches 8; Conservative 2; Mismatches 2; Indels 5; Gaps 1;

QY 3 PYG-----NPHYVYAMDY 14
 ||| | : || : ||
 Db 46 PYGVVVTANAYYYFLDY 62

RESULT 7
 OC3B_HUMAN STANDARD; PRT; 265 AA.
 ID OC3B_HUMAN STANDARD; PRT; 265 AA.
 AC P31359;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE OCTAMER-BINDING TRANSCRIPTION FACTOR 3B (OCT-3B).
 GN POU5F1 OR OCT3 OR OCT3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=93027160; PubMed=1408763;
 RA Takeda J., Seino S., Bell G.I.;
 RT "Human Oct3 gene family: cDNA sequences, alternative splicing, gene
 RT organization, chromosomal location, and expression at low levels in
 RT adult tissues.";
 RL Nucleic Acids Res. 20:4613-4620(1992).
 CC -1- FUNCTION: TRANSCRIPTION FACTOR THAT BINDS TO THE OCTAMER MOTIF
 CC GENE.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; OCT-3A (AC Q01860) AND OCT-3B
 CC (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: STRONG TO OTHER "POU" TRANSCRIPTION FACTORS. BELONGS
 CC TO CLASS-5 POU.

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DR EMBL; Z11899; CAA77952.1; -
 DR HSPF; P20263; LOC.
 DR TRANSFAC; T01872; -
 DR MIM; 164177; -
 DR InterPro; IPR000327; -
 DR InterPro; IPR001356; -

DR Pfam; PF00046; homeobox; 1.
 DR Pfam; PF00157; pou; 1.
 DR PRINTS; PR00028; POU DOMAIN.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00035; POU_1; 1.
 DR PROSITE; PS00465; POU_2; 1.
 DR PROSITE; PS0071; HOMEBOX_2; 1.
 KW Homeobox; DNA-binding; Transcription regulation; Nuclear protein;
 KW Alternative splicing; polymorphism.
 FT DOMAIN 47 117 POU
 FT DNA_BIND 135 194 HOMEBOX.
 FT VARIANT 227 227 T->A.
 FT VARIANT 262 262 /FTID=VAR_003774.
 FT M->L.
 FT /FTID=VAR_003775.
 SQ SEQUENCE 265 AA; 30084 MW; 41C21E136EFCBB2 CRC64;

Query Match 45.6%; Score 41; DB 1; Length 265;
 Best Local Similarity 54.5%; Pred. No. 19;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 PPYGNPHYVAM 12
 |||:|:|:|
 Db 228 PYGSPHFAL 238

RESULT 8
 OC3A_HUMAN STANDARD; PRT; 360 AA.
 ID OC3A_HUMAN STANDARD; PRT; 360 AA.
 AC Q01860; Q15167; Q15168; Q16422;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE OCTAMER-BINDING TRANSCRIPTION FACTOR 3A (OCT-3A) (OCT-4).
 GN POU5F1 OR OCT3 OR OCT3 OR OCT4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=93027160; PubMed=1408763;
 RA Takeda J., Seino S., Bell G.I.;
 RT "Human Oct3 gene family: cDNA sequences, alternative splicing, gene
 RT organization, chromosomal location, and expression at low levels in
 RT adult tissues.";
 RL Nucleic Acids Res. 20:4613-4620(1992).
 CC -1- FUNCTION: TRANSCRIPTION FACTOR THAT BINDS TO THE OCTAMER MOTIF
 CC GENE.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; OCT-3A (SHOWN HERE) AND OCT-3B
 CC (AC P31359); ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: STRONG TO OTHER "POU" TRANSCRIPTION FACTORS. BELONGS
 CC TO CLASS-5 POU.
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CC      EMBL; Z11898; CAA77951.1; -
CC      EMBL; Z11963; CAA79974.1; -
CC      EMBL; Z11964; CAA79975.1; -
CC      EMBL; S81255; AAB35990.1; -
CC      PIR; S25561; S25561.
CC      HSSP; P20263; 10CP.
CC      TRNSPAC; T00652; -
CC      MIM; 164177; -
CC      InterPro; IPR000327; -
CC      InterPro; IPR001356; -
CC      Pfam; PF00046; homeobox; 1.
CC      Pfam; PF00157; pou; 1.
CC      PRINTS; PR00028; POU DOMAIN.
CC      PROSITE; PS00027; HOMEBOX_1; 1.
CC      PROSITE; PS00035; POU_1; 1.
CC      PROSITE; PS00465; POU_2; 1.
CC      PROSITE; PS50071; HOMEBOX_2; 1.
CC      Homeobox; DNA-binding; Transcription regulation; Nuclear protein;
CC      Alternative splicing.
CC      DOMAIN 142 212 POU.
CC      DNA_BIND 230 289
CC      CONFLICT 189 189 A -> G (IN REF. 2; Z11963).
CC      CONFLICT 220 220 I -> T (IN REF. 2; Z11963).
CC      CONFLICT 227 227 V -> L (IN REF. 2; Z11963).
CC      CONFLICT 230 230 R -> G (IN REF. 2; Z11963).
CC      CONFLICT 240 240 Q -> R (IN REF. 2; Z11963).
CC      CONFLICT 251 251 R -> Q (IN REF. 2; Z11963).
CC      CONFLICT 276 276 V -> VVRV (IN REF. 3).
CC      SEQUENCE 360 AA; 38570 MW; 934C58DAEA0C535B CRC64;

Query Match 45.6%; Score 41; DB 1; Length 360;
Best Local Similarity 54.5%; Pred. No. 26;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 2 PPYGNPHYAM 12
Db 323 PGYGSHPHTAL 333

RESULT 9
MURC_MYCLE STANDARD; PRT; 407 AA.
AC O69552;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE UDP-N-ACETYLGLUCOSAMINE--N-ACETYL-MURAMYL-(PENTAPEPTIDE)
DE PYROPHOSPHORYL-UNDECAPRENOL N-ACETYLGLUCOSAMINE TRANSFERASE
DE (EC 2.4.1.-) (UNDECAPRENYL-PP-MURNAC-PENTAPEPTIDE-UDPGLCNAC
DE TRANSFERASE).
DE MURC OR MLCB268.02C.
GN MURC
OS Mycobacterium leprae.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.
RA Brown D., Churcher C.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RA Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CELL WALL FORMATION. CATALYZES THE TRANSFER OF A GLCNAC
CC SUBUNIT ON UNDECAPRENYL-PYROPHOSPHORYL-MURNAC-PENTAPEPTIDE (LIPID
CC INTERMEDIATE I) TO FORM UNDECAPRENYL-PYROPHOSPHORYL-MURNAC-
CC (PENTAPEPTIDE)GLCNAC (LIPID INTERMEDIATE II) (BY SIMILARITY).
CC -1- PATHWAY: LAST STEP OF PEPTIDOGLYCAN BIOSYNTHESIS.

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CC      -1- SUBCELLULAR LOCATION: MEMBRANE ASSOCIATED (BY SIMILARITY).
CC      -1- SIMILARITY: BELONGS TO THE MURG FAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).


EMBL; AL022602; CAA18668.1; -  

Transferrase; Glycosyltransferase; Cell division; Cell wall;  

Membrane; Peptidoglycan synthesis.  

SQ SEQUENCE 407 AA; 42422 MW; B757B73C092C53F9 CRC64;



Query Match 45.6%; Score 41; DB 1; Length 407;  

Best Local Similarity 53.8%; Pred. No. 30;  

Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;



Oy 2 PPYGNPHYAMDY 14  

| | | | | | |  

Db 267 PEYGEPPYVAVPY 279



RESULT 10  

GTF2_STRDO  

ID GTF2_STRDO STANDARD; PRT; 1592 AA.  

AC P27470;  

DT 01-AUG-1992 (Rel. 23, Created)  

DT 01-AUG-1992 (Rel. 23, Last sequence update)  

DT 15-DEC-1998 (Rel. 37, Last annotation update)  

DE GLUCOSYLTRANSFERASE-I PRECURSOR (EC 2.4.1.5) (GTF-I) (DEXTRANSUCRASE)  

DE (SUCCROSE 6-GLUCOSYLTRANSFERASE)  

OS Streptococcus downei (Streptococcus sobrinus).  

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;  

OC Streptococcus.  

OX NCBI_TaxID=1317;  

RN [1]  

RP SEQUENCE FROM N.A.  

RC STRAIN=6715;  

RX MEDLINE=91123227; PubMed=1704006;  

RA Abo H., Matsumura T., Kodama T., Ohta H., Fukui K., Kato K.,  

RA Kagawa H.;  

RT "Peptide sequences for sucrose splitting and glucan binding within  

RT Streptococcus sobrinus glucosyltransferase (water-insoluble glucan  

RT synthetase).";  

RL J. Bacteriol. 173:989-996(1991).  

CC -1- FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT  

CC TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAUSE  

CC OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE THE  

CC AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.  

CC -1- CATALYTIC ACTIVITY: SUCCROSE + (1,6-ALPHA-D-GLUCOSYL)(N) -  

CC D-FRUCTOSE + (1,6-ALPHA-D-GLUCOSYL)(N+1).  

CC -1- SUBCELLULAR LOCATION: SECRETED.  

CC -1- DISEASE: DENTAL CARIES.  

CC -1- MISCELLANEOUS: GTF-I SYNTHESIZES WATER-INSOLUBLE GLUCANS (ALPHA  

CC 1,3-LINKED GLUCOSE AND SOME 1,6 LINKAGES), GTF-S SYNTHESIZES  

CC WATER-SOLUBLE GLUCANS (ALPHA 1,6-GLUCOSE). GTF-SI SYNTHESIZES BOTH  

CC FORMS OF GLUCANS  

CC -1- SIMILARITY: TO OTHER GLUCOSYLTRANSFERASES AND SOME TO A GLUCAN-  

CC BINDING PROTEIN FROM S.MUTANS.  

CC -----  

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EMBL; D90213; BAA14241.1; -  

DR


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DR PIR: A38175; A38175.
DR HSP: P00695; 2HEE.
DR InterPro: IPR002479; -.
DR Pfam: PF01473; CW_binding_1; 16.
KW Transferase; Glycosyltransferase; Signal; Repeat; Dental caries.
FT SIGNAL 1 38 POTENTIAL.
FT CHAIN 39 1592 GLUCOSYLTRANSFERASE-I.
FT DOMAIN 39 1044 CATALYTIC (APPROXIMATE).
FT DOMAIN 1093 1592 GLUCAN-BINDING (APPROXIMATE).
FT DOMAIN 1093 1592 6.5 X TANDEM REPEATS.
FT REPEAT 1093 1142 1.
FT REPEAT 1158 1207 2.
FT REPEAT 1222 1272 3.
FT REPEAT 1287 1337 4.
FT REPEAT 1402 1451 5.
FT REPEAT 1514 1563 6.
FT REPEAT 1577 1592 7 (INCOMPLETE).
SQ SEQUENCE 1592 AA; 176167 MW; BCOA66D079351ECF CRC64;

Query Match 45.6%; Score 41; DB 1; Length 1592;
Best Local Similarity 77.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GNPHYAMD 13
Db 1133 GNSHYAMD 1141

RESULT 11
ZAN_PIG STANDARD; PRT; 2476 AA.
AC Q28983;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE ZONADHESIN PRECURSOR.
GN ZAN.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MEISHAN; TISSUE=Testis;
RX MEDLINE=96064658; PubMed=7592795;
RA Hardy D.M., Garbers D.L.;
RT "A sperm membrane protein that binds in a species-specific manner to
the egg extracellular matrix is homologous to von Willebrand
factor."
RL J. Biol. Chem. 270:26025-26028(1995).
CC -!- FUNCTION: BINDS IN A SPECIES-SPECIFIC MANNER TO THE ZONA PELLUCIDA
OF THE EGG.
CC -!- SUBUNIT: PROBABLY FORMS COVALENT OLIGOMERS.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: IN TESTIS, PRIMARILY IN HAPLOID SPERMATIDS.
CC NOT IN LUNG, LIVER, HEART, SPLEEN, BRAIN, KIDNEY, EPIDIDYMIS.
CC -!- DOMAIN: THE UNIQUE N-TERMINAL DOMAIN AND THE MUCIN-LIKE DOMAINS
ARE MISSING FROM THE ZONADHESIN THAT BINDS TO THE EGG
EXTRACELLULAR MATRIX. PROCESSING MIGHT OCCUR DURING SPERM
MATURATION AND/OR CAPACITATION.
CC -!- DOMAIN: THE UNIQUE N-TERMINAL DOMAIN PROBABLY MEDIATES SPERM
ADHESION TO THE ZONA PELLUCIDA.
CC -!- DOMAIN: DURING SPERM MIGRATION THROUGH THE REPRODUCTIVE TRACTS,
THE MUCIN-LIKE DOMAIN MIGHT INHIBIT INAPPROPRIATE TRAPPING OF
SPERMATOZOIA OR PROMOTING ADHESION TO THE OVIDUCTAL ISTHMUS.
CC -!- DOMAIN: THE VWFD DOMAINS 1 AND 2 MAY MEDIATE COVALENT
OLIGOMERIZATION (BY SIMILARITY TO HUMAN INTESTINAL MUCIN MUC2).
CC -!- SIMILARITY: CONTAINS 1 MAM DOMAIN.
CC -!- SIMILARITY: CONTAINS 4.5 VWFD DOMAINS.
CC -!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC -----
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CC -----
CC EMBL: U40024; AAC48486.1; -.
CC InterPro: IPR000561; -.
CC InterPro: IPR000998; -.
CC InterPro: IPR001846; -.
CC InterPro: IPR002919; -.
CC Pfam: PF00629; MAM; 2.
CC Pfam: PF01826; TIL; 5.
CC Pfam: PF00094; vwd; 4.
CC PROSITE: PS00022; EGF_1; 1.
CC PROSITE: PS00740; MAM_1; 1.
CC PROSITE: PS01186; EGF_2; 4.
CC PROSITE: PS00060; MAM_2; 2.
CC Signal; Glycoprotein; Transmembrane; EGF-like domain; Cell adhesion;
KW Repeat.
KW SIGNAL 1 29 POTENTIAL.
KW CHAIN 30 2476 ZONADHESIN.
KW DOMAIN 30 2418 EXTRACELLULAR (POTENTIAL).
KW TRANSMEM 2419 2439 POTENTIAL.
KW DOMAIN 2440 2476 CYTOPLASMIC (POTENTIAL).
KW DOMAIN 144 312 MAM.
KW DOMAIN 319 687 53 X HEPTAPEPTIDE REPEATS (APPROXIMATE)
(MUCIN-LIKE DOMAIN).
KW DOMAIN 688 799 VWFD 1 (PARTIAL).
KW DOMAIN 800 1184 VWFD 2.
KW DOMAIN 1185 1573 VWFD 3.
KW DOMAIN 1574 1968 VWFD 4.
KW DOMAIN 1969 2370 VWFD 5.
KW DOMAIN 2366 2402 EGF-LIKE.
KW DISULFID 2370 2381 BY SIMILARITY.
KW DISULFID 2375 2390 BY SIMILARITY.
KW DISULFID 2392 2401 BY SIMILARITY.
KW CARBOHYD 109 109 N-LINKED (GLCNAC. .) (POTENTIAL).
KW CARBOHYD 269 269 N-LINKED (GLCNAC. .) (POTENTIAL).
KW CARBOHYD 735 735 N-LINKED (GLCNAC. .) (POTENTIAL).
KW CARBOHYD 758 758 N-LINKED (GLCNAC. .) (POTENTIAL).
KW CARBOHYD 833 833 N-LINKED (GLCNAC. .) (POTENTIAL).
KW CARBOHYD 1154 1154 N-LINKED (GLCNAC. .) (POTENTIAL).
KW CARBOHYD 1329 1329 N-LINKED (GLCNAC. .) (POTENTIAL).
KW CARBOHYD 1448 1448 N-LINKED (GLCNAC. .) (POTENTIAL).
KW CARBOHYD 1544 1544 N-LINKED (GLCNAC. .) (POTENTIAL).
KW CARBOHYD 1596 1596 N-LINKED (GLCNAC. .) (POTENTIAL).
KW CARBOHYD 1654 1654 N-LINKED (GLCNAC. .) (POTENTIAL).
KW CARBOHYD 1843 1843 N-LINKED (GLCNAC. .) (POTENTIAL).
KW CARBOHYD 1965 1965 N-LINKED (GLCNAC. .) (POTENTIAL).
KW CARBOHYD 2122 2122 N-LINKED (GLCNAC. .) (POTENTIAL).
KW CARBOHYD 2165 2165 N-LINKED (GLCNAC. .) (POTENTIAL).
KW CARBOHYD 2178 2178 N-LINKED (GLCNAC. .) (POTENTIAL).
KW CARBOHYD 2329 2329 N-LINKED (GLCNAC. .) (POTENTIAL).
KW CARBOHYD 2359 2359 N-LINKED (GLCNAC. .) (POTENTIAL).
KW SEQUENCE 2476 AA; 270364 MW; A13B690375A6548C CRC64;

Query Match 45.6%; Score 41; DB 1; Length 2476;
Best Local Similarity 60.0%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 4 YGNPHYAMD 13
Db 804 YGDPHYLTFD 813

RESULT 12
SFR9_HUMAN STANDARD; PRT; 221 AA.
AC Q13242;
DT 15-DEC-1998 (Rel. 37, Created)

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RA Reymond P., Geourjon C., Roux B., Durand R., Fevre M.;
 RT "Sequence of the phosphoenolpyruvate carboxykinase-encoding cDNA from
 RL the rumen anaerobic fungus Neocallimastix frontalis: comparison of
 RL the amino acid sequence with animals and yeast."
 RL Gene 110:57-63(1992).
 CC -!- CATALYTIC ACTIVITY: GTP + OXALOACETATE = GDP + PHOSPHOENOLPYRUVATE
 CC + CO(2).
 CC -!- PATHWAY: RATE-LIMITING GLUCONEOGENIC ENZYME.
 CC -!- SIMILARITY: BELONGS TO THE PHOSPHOENOLPYRUVATE CARBOXYKINASE [GTP]
 CC FAMILY.
 CC -----
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 CC -----
 DR EMBL; M59372; AAA33553.1; -
 DR PIR; JQ1462; JQ1462.
 DR InterPro; IPR000364; -
 DR Pfam; PF00821; PEPC_K; 1.
 DR PROSITE; PS00505; PEPC_K_GTP; 1.
 KW Gluconeogenesis; Lyase; Decarboxylase; GTP-binding.
 FT NP_BIND 217 224 GTP (POTENTIAL).
 FT ACT_SITE 269 269 POTENTIAL.
 SQ SEQUENCE 608 AA; 66904 MW; C4D2B249A92B7D26 CRC64;

 Query Match 44.4%; Score 40; DB 1; Length 608;
 Best Local Similarity 54.5%; Pred. No. 65;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 3 PYGNPHYVAMD 13
 DB 397 PVGPGYALE 407

 RESULT 15
 TFLB_MOUSE
 ID TFLB_MOUSE STANDARD; PRT; 834 AA.
 AC Q62318; P70391;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (KRAB-A INTERACTING PROTEIN)
 DE (KRIP-1).
 GN TIF1B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97133299; PubMed=8978696;
 RA le Douarin B., Nielsen A.L., Garnier J.M., Ichinose H., Jeanmougin F.,
 RA Losson R., Chambon P.;
 RA "A possible involvement of TIF1 alpha and TIF1 beta in the epigenetic
 RT control of transcription by nuclear receptors.";
 RL EMBO J. 15:6701-6715(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Kidney;
 RC MEDLINE=97140325; PubMed=8986806;
 RA Kim S.-S., Chen Y.-M., O'Leary E., Witzgall R., Vidal M.,
 RA Bonventre J.V.;
 RA "A novel member of the RING finger family, KRIP-1, associates with
 RT the KRAB-A transcriptional repressor domain of zinc finger
 RT proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:15299-15304(1996).
 CC -!- FUNCTION: FORMS A COMPLEX WITH A KRAB-DOMAIN TRANSCRIPTION FACTOR
 CC AND INCREASES THE EFFICIENCY OF KRAB-MEDIATED REPRESSION.

CC -!- SUBCELLULAR LOCATION: NUCLEAR.
 CC -!- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
 CC -!- SIMILARITY: CONTAINS 1 PHD ZINC-FINGER DOMAIN.
 CC -----
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 CC -----
 DR EMBL; X99644; CAA67963.1; -
 DR EMBL; U67303; AAB17272.1; -
 DR HSSP; P04002; LWFA.
 DR MGD; MGI:109274; Tif1b.
 DR InterPro; IPR001841; -
 DR InterPro; IPR001965; -
 DR InterPro; IPR002991; -
 DR Pfam; PF00628; PHD; 1.
 DR Pfam; PF00643; zf-B_box; 1.
 DR Pfam; PF00597; zf-C3HC4; 1.
 DR PROSITE; PS00518; ZINC_FINGER_C3HC4; FALSE_NEG.
 KW Transcription regulation; Repressor; Nuclear protein; Zinc-finger.
 FT DOMAIN 42 49 POLY-ALA.
 FT DOMAIN 54 57 POLY-GLY.
 FT ZN_FING 66 121 C3HC4-TYPE.
 FT DOMAIN 526 531 POLY-ALA.
 FT ZN_FING 628 669 PHD-FINGER.
 FT CONFLICT 530 530 A -> S (IN REF. 2).
 SQ SEQUENCE 834 AA; 88847 MW; DB87AAA5DC67BB8B CRC64;

 Query Match 44.4%; Score 40; DB 1; Length 834;
 Best Local Similarity 50.0%; Pred. No. 92;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 2 PPYGNPHYVAMD 13
 DB 753 PPYSPQEFQAD 764

 Search completed: June 28, 2001, 15:54:38
 Job time: 126 sec

